Inhibition and Stimulation of Intestinal and Hepatic CYP3A Activity: Studies in Humanized CYP3A4 Transgenic Mice Using Triazolam

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ABSTRACT:
CYP3A4 is an important determinant of drug-drug interactions. In this study, we evaluated whether cytochrome P450 3A knockout mice [Cyp3a(−/−)] and CYP3A4 transgenic [CYP3A4-Tg] mice can be used to study drug-drug interactions in the liver and intestine. Triazolam was used as a probe drug because it is a highly specific CYP3A substrate and not a P-glycoprotein substrate. Triazolam metabolism was profoundly reduced in Cyp3a(−/−) mice both in vitro and in vivo. In vitro studies revealed clear species differences in humans and mice, but triazolam metabolism in microsomes derived from CYP3A4-Tg “humanized” mice closely resembled that in human microsomes. It is interesting to note that studies with tissue-specific CYP3A4-Tg mice revealed that intestinal CYP3A4 has a major impact on oral triazolam exposure, whereas the effect of hepatic CYP3A4 was limited. To mimic a drug-drug interaction, we coadministered triazolam with the prototypical CYP3A inhibitor ketoconazole, which increased triazolam exposure in all the CYP3A4-proficient mouse strains but not in Cyp3a(−/−) mice. We further found that the antiangioma drug gefitinib is a potent stimulator of 1’-OH triazolam formation in vitro. It is noteworthy that we could also show in vivo stimulation of triazolam metabolism by gefitinib, resulting in a lower oral triazolam exposure. To our knowledge, this is the first in vivo example of direct stimulation of CYP3A4 activity after oral drug administration. Overall, this study illustrates how Cyp3a(−/−) and CYP3A4-Tg mice can be used to study drug-drug interactions. The data clarify that for drugs that are not P-glycoprotein substrates, intestinal metabolism also can be more important than hepatic metabolism after oral administration.

CYP3A enzymes represent one of the most important drug-metabolizing systems, affecting ~50% of currently prescribed drugs (Guengerich, 1999). Because so many drugs are substrates and/or inhibitors for CYP3A, the enzyme is also an important determinant of many drug-drug interactions (Thummel and Wilkinson, 1998; Dresser et al., 2000). The most common type of CYP3A-mediated drug-drug interaction is that one drug inhibits CYP3A activity, which leads to higher levels of other drugs metabolized by CYP3A, potentially leading to toxicity. For example, this was the case for the antihistaminic terfenadine and the antihypertensive mibefradil, which were consequently both withdrawn from the market. Although most drug-drug interactions are undesirable, in certain cases CYP3A can be inhibited on purpose to improve drug therapy. For example, the CYP3A inhibitor ritonavir is given in combination with lopinavir, which improves the lopinavir oral bioavailability considerably (Kumar et al., 1999). Not only drugs but also food constituents can be potent inhibitors of CYP3A. For example, components of grapefruit juice potently inhibit CYP3A, and several clinically relevant drug-grapefruit juice interactions have been described previously (Dresser and Bailey, 2003; Paine and Oberlies, 2007).

Another possible mechanism of a drug-drug interaction is that one drug directly increases the rate of CYP3A-mediated metabolism of another drug. This stimulation of the metabolism is also known as heterotropic positive cooperativity (Tang and Stearns, 2001; Hutzler and Tracy, 2002; Houston and Galetin, 2005). Stimulation of metabolism could be of clinical relevance as it could result in subtherapeutic drug levels. A classic example of a drug that is known to stimulate several CYP3A-mediated reactions is 7,8-benzoflavone, which increases the metabolism of diazepam and aflatoxin B1 in vitro (Andersson et al., 1994; Ueng et al., 1997). It has to be noted that although many in vitro examples of CYP3A stimulation have been published, there is only very limited in vivo evidence for this particular drug-drug interaction (Hutzler and Tracy, 2002; Wienkers and Heath, 2005).

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ABBREVIATIONS: Cyp3a(−/−), cytochrome P450 3A knockout mice; Tg, transgenic; P-gp, P-glycoprotein; P450, cytochrome P450; Cyp3a(−/−)Tg3A4444, Cyp3a knockout mice with liver-specific transgenic expression of human CYP3A4; Cyp3a(−/−)Tg3A4444int, Cyp3a knockout mice with intestine-specific transgenic expression of human CYP3A4; HPLC, high-performance liquid chromatography; PEG, polyethylene glycol; LC/MS/MS, liquid chromatography/tandem mass spectrometry; AUC, area under the curve.
Recently, we have generated Cyp3a knockout mice to study this important drug-handling system in vivo (van Herwaarden et al., 2007). In addition, we created cytochrome P450 3A knockout [Cyp3a(-/-)] transgenic (Tg) mice with expression of human CYP3A4 exclusively in the intestine or in the liver (van Herwaarden et al., 2007). We subsequently used these mice to determine the relative importance of intestinal versus hepatic CYP3A4 activity in first-pass drug metabolism. These studies revealed that intestinal CYP3A4 alone was sufficient to virtually abrogate net docetaxel entry from the gut, whereas hepatic CYP3A4 was more important in systemic docetaxel clearance (van Herwaarden et al., 2007). This study clarified the potential significance of intestinal metabolism, which has been a matter of debate for decades (Lin et al., 1999; Doherty and Charman, 2002; Thummel, 2007).

Besides being a good CYP3A4 substrate, however, docetaxel is also a very good substrate of the apical drug transporter P-glycoprotein (P-gp) (Bardelmeijer et al., 2002). It has been hypothesized that the function of P-gp could prevent saturation of intestinal CYP3A4 and give the enzyme repeated access to its substrates, resulting in highly efficient intestinal metabolism (Benet and Cummins, 2001). We considered that P-gp might have contributed greatly to the efficiency of intestinal CYP3A4-mediated docetaxel metabolism. Hence, it is not clear whether intestinal CYP3A4 can also dominate the metabolism of substrates that are not transported by P-gp, such as midazolam. It is unfortunate that useful analysis of midazolam pharmacokinetics in our mouse models was precluded by the up-regulation of (midazolam-metabolizing) mouse CYP2C in the Cyp3a(-/-) mice (van Waterschoot et al., 2008).

In contrast to midazolam, the closely related drug triazolam is a more specific substrate for CYP3A4 compared with other mouse cytochrome P450 (P450) isoforms (Perloff et al., 2000). Therefore, it might be a better probe drug to characterize our Cyp3a(-/-) and CYP3A4-Tg mouse lines. Similar to midazolam, triazolam is also not a P-gp substrate (van Molkte et al., 2004). Therefore, in this study we used triazolam to study the relative contribution of intestinal and hepatic CYP3A4-mediated metabolism. Furthermore, we also assessed whether our mouse models could be used to study in vivo drug-drug interactions such as inhibition and stimulation of CYP3A activity.

Materials and Methods

Materials. Triazolam and 1′-OH triazolam were obtained from Sigma-Aldrich (St. Louis, MO). D3′,5′-Triazolam and D3′-1′-hydroxy-triazolam were both obtained as 100-μg/ml solutions in methanol from Cerilliant Corporation (Round Rock, TX). NADPH-generation system and pooled human liver and intestinal microsomes were obtained from BD Bioscience (Alphen aan den Rijn, The Netherlands). Gefitinib, imatinib, erlotinib, dasatinib, sorafenib, and sunitinib (12.5 μM final concentration) leading to 0.2% dimethyl sulfoxide in the final incubation. Subsequently, triazolam was added and preincubated for 1 min after which the reaction was started by adding the NADPH-regenerating system. Other conditions were similar as described above.

Chemical and Immunoinhibition. For the inhibition experiments, two antibodies targeting rat CYP2C11 were used. Polyclonal anti-CYP2C11 goat antibodies were obtained from Daiichi Pure Chemical Co. (Tokyo, Japan), and monoclonal anti-CYP2C11 mouse antibodies were obtained from Invitrogen (Carlsbad, CA); they were referred to as anti-CYP2C-A and anti-CYP2C-B, respectively. After 10 min of preincubation with ketoconazole (2.5 μM final concentration) or one of two anti-CYP2C11 antibodies, the microsomal reaction mixture was incubated for 20 min. The final concentration of triazolam in the incubations was 50 μM. All the other conditions were as described above.

HPLC. For determination of triazolam and its metabolites, the HPLC mobile phase consisted of 20% acetonitrile, 24% methanol, and 56% 5 mM phosphate buffer, pH 7.4 (0.15% triethylamine), with a flow rate of 0.4 ml/min. The analytical column was a reverse-phase C18 XBridge, 3.0 × 150 mm, 3.5 μm (Waters, Milford, MA). Column effluent was monitored by UV absorption at 230 nm.

Identity and quantity of 1′-OH and 4-OH triazolam metabolites were verified using the retention time and standard curve of an authentic 1′-OH triazolam standard. For determining triazolam in the presence of gefitinib, the mobile phase consisted of two solutions. Solution A consisted of 20% acetonitrile, 30% methanol, and 50% 5 mM phosphate buffer (pH 7.4). Solution B consisted of 60% acetonitrile and 40% 5 mM H2O. From 0 to 5 and from 8 to 20 min after injection, the mobile phase consisted of 100% A. Between 5 and 8 min after injection, the mobile phase consisted of a mix of A and B (10:90).

Triazolam Pharmacokinetics in Vivo. Thirty minutes before triazolam administration, fasted mice (2 mice) received orally either ketoconazole (35 mg/kg) in polyethylene glycol (PEG) 400, gefitinib (25 mg/kg) in PEG 400, or vehicle (PEG 400). At t = 0, triazolam in ethanol and saline (1:99) was administered by oral gavage at 0.5 mg/kg. Ten, 20, 40, 80, 160, and 320 min after triazolam administration, blood samples were collected by tail sampling. Blood was centrifuged for 6 min at 6800g, after which 25 μl of serum was collected and stored at −20°C until further analysis.

Liquid Chromatography/Tandem Mass Spectrometry. Mouse plasma samples were measured by liquid chromatography/tandem mass spectrometry
The triazolam metabolism in liver and intestinal microsomes of Cyp3a(-/-) and CYP3A4-Tg mice. The biotransformation of triazolam by CYP3A enzymes yields 1'-OH and 4'-OH triazolam as the principal metabolites (Kronbach et al., 1989; von Moltke et al., 1996). To evaluate the differences in metabolic activity between wild-type, Cyp3a(-/-), and CYP3A4-Tg mice, we performed microsomal incubations with triazolam. In wild-type mouse liver microsomes, triazolam was metabolized to its 1'-OH and 4'-OH metabolites, and both metabolite formation reactions obeyed normal Michaelis-Menten kinetics (Fig. 1). Note that at lower triazolam concentrations, 1'-OH triazolam is the major metabolite, whereas 4'-OH triazolam becomes more prominent at higher concentrations. These results are consistent with those observed in other mouse strains (Perloff et al., 1999, 2000).

As expected, triazolam metabolism was profoundly reduced in liver microsomes from Cyp3a(-/-) mice, albeit not completely abolished, when compared with wild-type mice (Fig. 1, Table 1). Accordingly, the intrinsic clearance (V_max/K_m) for the 1'-OH formation was reduced more than 40-fold and for 4'-OH triazolam formation more than 14-fold (Table 1). The residual metabolic activity was NADPH-dependent, indicating that other P450s in Cyp3a(-/-) mice can take over the triazolam metabolism to some extent. It is noteworthy that the kinetic profile for the 1'-OH triazolam formation in the Cyp3a(-/-) mouse liver microsomes was clearly different from that observed in wild-type mouse liver microsomes and could be fitted into a substrate inhibition model (K_i = 507 ± 129 μM) (Fig. 1).

In liver microsomes of Cyp3a(-/-)Tg-3A4Hep mice, expressing human CYP3A4 exclusively in the liver, a different kinetic profile for the 1'-OH and 4'-OH triazolam formation was observed when compared with wild-type mouse liver microsomes (Fig. 1). For 1'-OH triazolam formation, although the affinity of human CYP3A4 is 5-fold lower than the (combined) affinity of the mouse CYP3A enzymes, the higher V_max (3-fold) resulted in only a slightly lower intrinsic clearance (1.7-fold) when compared with wild-type (Table 1). For 4'-OH triazolam formation, the intrinsic clearance was increased 2.1-fold. It is important to note that the metabolic and kinetic profile observed in liver microsomes of CYP3A4-Tg mice [Cyp3a(-/-)Tg-3A4Hep, Cyp3a(-/-)Tg-3A4Hep, and Cyp3a(-/-)Tg-3A4Hep, mice and humans. Note marked differences in y-axis scales between panels. Incubations were performed as described under Materials and Methods. Intestinal metabolic rates of wild-type, Cyp3a(-/-), and Cyp3a(-/-)Tg-3A4Hep mice were below the lower detection limit of our assay (<2.5 pmol/min/mg protein). Note that mouse intestinal microsomes were isolated from the whole tissue, whereas the human intestinal microsomes were isolated after enterocyte isolation and are enriched in P450. Data are the mean ± S.D. of triplicate incubations. Corresponding kinetic parameters are given in Table 1.

We also tested liver microsomes from mice that have intestinal specific transgenic CYP3A4 expression [Cyp3a(-/-)Tg-3A4Jun, Tg-3A4Jun]. Note that liver microsomes from these mice have no CYP3A activity and are in essence similar to those of Cyp3a(-/-) mice (van Herwaarden et al., 2007). Indeed, the 1'-OH triazolam formation of these liver microsomes was roughly similar to that observed in liver microsomes of Cyp3a(-/-) mice, including the substrate inhibition characteristics (K_i = 478 ± 43 μM) (Fig. 1).

We also investigated triazolam metabolism in intestinal microsomes. In wild-type microsomes, metabolite formation could only be detected at the highest triazolam incubation concentrations, and kinetic parameters could not be deduced from these data. In addition, no metabolite formation could be detected in intestinal microsomes from Cyp3a(-/-) and Cyp3a(-/-)Tg-3A4Hep mice. In contrast, 1'-OH and 4'-OH metabolite formation could be readily detected in Cyp3a(-/-)
isolated from the whole tissue, whereas the human intestinal microsomes were isolated after enterocyte isolation and are enriched in P450. 

However, the mouse intestinal microsomes were also very similar to human intestinal microsomes. Both 1'-OH triazolam and 4-OH triazolam formation obeyed normal Michaelis-Menten kinetics and CYP3A enzymes were responsible for the residual triazolam metabolism observed in Cyp3a(-/-) mouse liver microsomes. In contrast, CYP3A4 but Not by Mouse CYP3A.

Kinetic parameters for triazolam metabolism by liver and intestinal microsomes

![Table 1](https://www.aspetjournals.org/doi/abs/10.1124/dmd.107.015007)

<table>
<thead>
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<th>Microsome, Strain</th>
<th>1'-OH Triazolam</th>
<th>4-OH Triazolam</th>
</tr>
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<tbody>
<tr>
<td></td>
<td>$K_m$</td>
<td>$V_{max}$</td>
</tr>
<tr>
<td>Liver</td>
<td></td>
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</tr>
<tr>
<td>Wild-type</td>
<td>11.7 ± 1.96</td>
<td>742 ± 16.4</td>
</tr>
<tr>
<td>Cyp3a(-/-)</td>
<td>73.3 ± 18.8$^a$</td>
<td>115 ± 14.2$^a$</td>
</tr>
<tr>
<td>Cyp3a(-/-) Tg-3A4Hep</td>
<td>58.4 ± 8.46</td>
<td>214.5 ± 124</td>
</tr>
<tr>
<td>Cyp3a(-/-) Tg-3A4Int</td>
<td>40.1 ± 2.73$^a$</td>
<td>56.5 ± 3.14$^a$</td>
</tr>
<tr>
<td>Human</td>
<td>37.2 ± 3.27</td>
<td>115.6 ± 42.2</td>
</tr>
</tbody>
</table>

$^a$ Fitted with substrate inhibition model as described under Materials and Methods.

$^b$ Metabolite observed but kinetics could not be assessed.

$^c$ No metabolite detected (<2.5 pmol/min/mg protein).

Collectively, these data indicate that there are clear species differences between mice and humans in the in vitro metabolism of triazolam. Of importance, the data further show that mouse microsomes with transgenic CYP3A4 expression [in a Cyp3a(-/-) background] closely resemble the triazolam metabolism in human hepatic and intestinal microsomes, both in terms of the metabolic kinetic profile (Fig. 1) and the intrinsic clearance (Table 1). Finally, they also confirm the tissue-specific activity of CYP3A4 in the transgenic strains.

Ketoconazole Inhibits Triazolam Metabolism in Wild-Type but Not in Cyp3a(-/-) Microsomes. Coincubation with the CYP3A inhibitor ketoconazole (2.5 μM) resulted in virtually complete inhibition of triazolam metabolite formation in wild-type but not in Cyp3a(-/-) mouse liver microsomes (Fig. 2). To test whether CYP2C enzymes were responsible for the residual triazolam metabolism in Cyp3a(-/-) mouse liver microsomes, we coincubated with one of two antibodies raised against rat-CYP2C11. Antibody A was able to lower the formation of both hydroxy metabolites to around 50% (Fig. 2), indicating that CYP2C enzymes are, at least partly, responsible for the triazolam metabolism in Cyp3a(-/-) mouse liver microsomes. In addition, antibody A also efficiently inhibited the 1'-OH but not the 4-OH triazolam formation. This result suggests specific and efficient inhibition of CYP2C enzymes that have a preference to produce 1'-OH triazolam over 4-OH triazolam by this antibody, in line with previous observations for midazolam (van Waterschoot et al., 2008). Taken together, these results indicate that the low-level, residual triazolam metabolism observed in Cyp3a(-/-) liver microsomes is, for a large part, mediated by CYP2C enzymes, even though in the wild-type situation the contribution of CYP2C is negligible.

Gefitinib Stimulates 1'-OH Triazolam Formation by Human CYP3A4 but Not by Mouse CYP3A4. It was recently shown that the anticancer drug gefitinib stimulates the formation of 1'-OH midazolam in human liver microsomes (Li et al., 2007). Based on the structural similarity between midazolam and triazolam, we hypothesized that gefitinib could also stimulate triazolam metabolism. However, when we coincubated gefitinib with triazolam we did not observe stimulation but rather inhibition of the 1'-OH triazolam formation in wild-type mouse liver microsomes. As expected, no stimulation was observed in Cyp3a(-/-) microsomes. In contrast, 1'-OH triazolam formation was markedly stimulated in human liver microsomes (Fig. 3). Consistent with these observations, we also found potent stimulation in Cyp3a(-/-) Tg-3A4Hep mouse liver microsomes (Fig. 3). We note that the 4-OH triazolam formation was inhibited by gefitinib in both human and Cyp3a(-/-) Tg-3A4Hep liver microsomes (data not shown). Coincubation with imatinib, another
tyrosine kinase inhibitor and known CYP3A4 substrate used as control, showed modest inhibition of 1'-OH triazolam formation in all the preparations.

More detailed examination of the stimulation in Cyp3a(−/−)Tg-3A4Hep mouse microsomes revealed that gefitinib changes both $K_m$ and $V_{max}$ of 1'-OH triazolam formation (Fig. 4; Table 2). The $K_m$ values for 1'-OH triazolam formation decreased 3.5- and 2.8-fold for liver and intestine, respectively (Table 2). In addition, the $V_{max}$ for the same metabolite showed a 2- and 2.2-fold increase, leading to an increase in intrinsic clearance of 6.7- and 6.3-fold for liver and intestine, respectively. In contrast, the formation of 4-OH triazolam was inhibited by gefitinib (Fig. 4), and the intrinsic clearances decreased 2.9- and 4.1-fold for liver and intestine, respectively (Table 2).

We subsequently tested whether more tyrosine kinase inhibitors could stimulate the 1'-OH triazolam formation. In addition to gefitinib, only erlotinib showed some stimulation of the 1'-OH formation in Cyp3a(−/−)Tg-3A4Hep microsomes, although this was clearly less pronounced compared with gefitinib (Fig. 5). All of the other drugs inhibited the 1'-OH triazolam formation, and dasatinib seemed to be the most potent CYP3A4 inhibitor of all the tyrosine kinase inhibitors tested.

Intestinal but Not Hepatic CYP3A4 Determines Oral Triazolam Exposure. Next, we investigated the relative in vivo importance of intestinal and hepatic CYP3A in triazolam pharmacokinetics.
In this study, we show that the metabolism of triazolam is profoundly reduced in Cyp3a(-/-) mice both in vitro and in vivo. Counter to our expectations, our studies with tissue-specific CYP3A4-Tg mice revealed that intestinal CYP3A4 has a major impact on oral triazolam systemic exposure, whereas the effect of hepatic CYP3A4 was relatively modest. We further evaluated whether the CYP3A4-Tg mouse strains could be used to study drug-drug interactions. This evaluation was exemplified by the coadministration of the prototypical CYP3A inhibitor ketoconazole, which increases the triazolam exposure in all the CYP3A proficient mouse strains but not in Cyp3a(-/-) mice. We found that the anticancer drug gefitinib is a potent stimulator of the 1'-OH triazolam formation by CYP3A4 in vitro. It is interesting to note that in vivo, we could show stimulation of triazolam metabolism by gefitinib, resulting in a lower triazolam plasma exposure. Whereas direct in vivo stimulation of CYP3A4 activity has been shown previously after intraportal infusion of a drug (Tang et al., 1999), the observations of the present study represent, to our knowledge, the first example of such a drug-drug interaction after oral drug administration.

Previous efforts to use midazolam as a probe drug for the characterization of the Cyp3a(-/-) and CYP3A4-Tg mouse strains were confounded by the up-regulation of (midazolam-metabolizing) mouse CYP2C enzymes in Cyp3a(-/-) mice. When we gave midazolam at a dose of either 0.5 or 10 mg/kg i.v. there was no significant difference between wild-type and Cyp3a(-/-) mice (van Waterschoot et al., 2008). After oral administration of 2 mg/kg there also were no significant differences between wild-type and Cyp3a(-/-) mice (Supplemental Data 1). In contrast to midazolam, triazolam is considered to be specific for the mouse CYP3A isoforms (Perloff et al., 2008). After oral administration of 2 mg/kg there also were no significant differences between wild-type and Cyp3a(-/-) mice. Nonetheless, here we showed that also in triazolam there is still some residual triazolam metabolism mediated by CYP2C, even though the contribution of CYP2C enzymes in the wild-type situation is negligible. However, compared with the effect on midazolam, this compensatory triazolam metabolism is much lower.

Although the liver has long been considered the most important organ where CYP3A-mediated metabolism takes place, evidence is accumulating that also intestinal CYP3A metabolism can have a pronounced impact on the oral bioavailability of drugs (van Herwaarden et al., 2009). Using Cyp3a(-/-)TgInt and Cyp3a(-/-)TgHep mice, we previously showed that for docetaxel intestinal CYP3A4 metabolism was much more significant than hepatic metabolism after oral administration, whereas after intravenous administration hepatic CYP3A4 metabolism was dominant and the impact of intestinal CYP3A4 was very minor (van Herwaarden et al., 2007). These experiments also illustrated that these transgenic mice have both very

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**Discussion**

In this study, we show that the metabolism of triazolam is profoundly reduced in Cyp3a(-/-) mice both in vitro and in vivo. Counter to our expectations, our studies with tissue-specific CYP3A4-Tg mice revealed that intestinal CYP3A4 has a major impact on oral triazolam systemic exposure, whereas the effect of hepatic CYP3A4 was relatively modest. We further evaluated whether the CYP3A4-Tg mouse strains could be used to study drug-drug interactions. This evaluation was exemplified by the coadministration of the prototypical CYP3A inhibitor ketoconazole, which increases the triazolam exposure in all the CYP3A proficient mouse strains but not in Cyp3a(-/-) mice. We found that the anticancer drug gefitinib is a potent stimulator of the 1'-OH triazolam formation by CYP3A4 in vitro. It is interesting to note that in vivo, we could show stimulation of triazolam metabolism by gefitinib, resulting in a lower triazolam plasma exposure. Whereas direct in vivo stimulation of CYP3A4 activity has been shown previously after intraportal infusion of a drug (Tang et al., 1999), the observations of the present study represent, to our knowledge, the first example of such a drug-drug interaction after oral drug administration.

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substantial hepatic and intestinal CYP3A4 activity. However, although intestinal CYP3A4 is the major determinant of docetaxel oral bioavailability in mice, the question remained whether intestinal metabolism is also important for drugs that are, unlike docetaxel, not a substrate for intestinal drug efflux transporters like P-gp. Therefore, we tested triazolam. It is interesting to note that our mouse data revealed that also for oral triazolam exposure intestinal metabolism by CYP3A4 is more important than hepatic metabolism, qualitatively similar to what we found previously for docetaxel (van Herwaarden et al., 2007). Qualitatively similar results were also obtained with midazolam (Supplemental Data 1). Overall, this also shows that, at least in mice, for drugs that are not substrates for P-gp, intestinal CYP3A4 activity can be a more important determinant of oral bioavailability than hepatic CYP3A4 activity.

The fact that we did not observe a difference in triazolam AUCs between Cyp3a(−/−) and Cyp3a(−/−)Tg-3A4Hep mice would suggest that hepatic metabolism does not play any role after oral administration. However, this might be misleading as we know that CYP2C enzymes are up-regulated in the livers of Cyp3a(−/−) mice but not in Cyp3a(−/−)Tg-3A4Hep mice (van Waterschoot et al., 2009). It is obvious that without the up-regulated CYP2C enzymes there would have been less compensatory metabolism, and triazolam plasma levels would consequently have been higher in Cyp3a(−/−) mice. Thus, although their AUCs appeared to be not different, in Cyp3a(−/−) mice.

FIG. 6. Plasma concentration versus time curves of triazolam (A–C) and 1′-OH triazolam (D–F) after oral triazolam administration (0.5 mg/kg) and coadministration of gefitinib (25 mg/kg, B and E) or ketoconazole (35 mg/kg, C and F) are shown for Cyp3a(−/−), Cyp3a(−/−)Tg-3A4Hep, Cyp3a(−/−)Tg-3A4Int, and Cyp3a(−/−)Tg-3A4Hep/Int mice. Note differences in scale for triazolam and 1′-OH triazolam panels. Data are shown as the mean concentrations, and error bars represent the S.D. (n = 4–5 per time point).

### TABLE 3

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<td>Triazolam</td>
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<tr>
<td>Cyp3a(−/−)Tg-3A4Int</td>
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<td>132 ± 23**</td>
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<td>Wild-type</td>
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<td>1′-OH Triazolam</td>
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AUC<sub>0–320 min</sub> (h · µg/l), area under plasma concentration-time curve up to 320 min. Data are presented as means ± S.D., n = 4–5. *P < 0.05, **P < 0.01, and ***P < 0.001 compared with Cyp3a(−/−) mice; †P < 0.05, ††P < 0.01, and †††P < 0.001 compared with untreated strain. N.D., not determined.
mice the triazolam metabolism could be mainly attributed to the up-regulated CYP2C enzymes, whereas in Cyp3a(−/−)Tg-3A4Hep mice this can be primarily attributed to hepatic CYP3A4. This latter interpretation is also supported by the fact that the CYP3A inhibitor ketoconazole markedly increased the triazolam systemic exposure in Cyp3a(−/−)Tg-3A4Hep mice but not in Cyp3a(−/−) mice (Table 3).

We found that the anticancer drug gefitinib is a potent stimulator of the 1′-OH triazolam formation but inhibits the 4-OH triazolam formation in vitro. Stimulation of CYP3A-mediated metabolism is thought to be attributable to presence of multiple binding sites within the enzyme’s active site (e.g., Tang and Stearns, 2001). Recent crystal structures have verified the possible simultaneous binding of substrates to CYP3A4 and accompanying conformational changes (Ekroos and Sjögren, 2006). Most likely, binding of gefitinib to the active site of CYP3A4 results in a conformational change of the enzymes that favors the 1′-OH but inhibits the 4-OH triazolam formation. Such regioselectivity where one metabolic route is stimulated and the other is inhibited has been observed previously. For example, testosterone could stimulate the 4-OH midazolam formation by CYP3A, but it inhibited the 1′-OH metabolite formation (Wang et al., 2000). In contrast, 7,8-benzoflavone stimulated 1′-OH but inhibited 4-OH midazolam formation (Wang et al., 2000).

It is interesting to note that in vivo coadministration of gefitinib with triazolam also resulted in significantly lower triazolam exposure in Cyp3a(−/−)Tg-3A4Hep and Cyp3a(−/−)Tg-3A4Hep/Int mice but not in Cyp3a(−/−) and Cyp3a(−/−)Tg-3A4Hep mice, indicating that stimulation of CYP3A4 primarily takes place in the liver. Although coadministration of gefitinib with triazolam resulted in lower triazolam plasma levels after oral administration, the effect was less pronounced than what expected from the in vitro results. Clearly, because the in vivo situation is far more complex than an in vitro homogenate, it is not surprising that there is not a simple one-to-one quantitative relationship between in vitro and in vivo quantitative shifts. In the microsomal extract, the only route for removal of triazolam is by metabolic conversion. In contrast, in vivo there are many alternative routes for clearance of triazolam, including clearance by transporters, diffusion, ultrafiltration, and so on. Thus, it is more or less expected that the in vivo impact of CYP3A4 stimulation will be more limited than in vitro. The access of gefitinib to the metabolizing enzyme may be much more limited in vivo than in a simple in vitro extract because we are dealing with intact cells and organs. In addition, as gefitinib itself is a substrate for CYP3A4 (McKillop et al., 2005), a substantial part of the gefitinib dose could already have been metabolized. Finally, administration of gefitinib, 30 min before triazolam administration, was used to obtain significant loading of the body with gefitinib, but the concentration of gefitinib in intestinal epithelial cells may already have started to decrease after 30 min, resulting in levels too low to exert a marked stimulatory effect in the intestine.

Thus far, there are no recognized examples known of clinically relevant drug-drug interactions that can be attributed to the direct stimulation of CYP3A4-mediated metabolism (as opposed to induction of CYP3A expression, which is common). Clearly, because it typically concerns only a specific combination of drugs, stimulation of drug metabolism by CYP3A4 is much more difficult to predict than inhibition. We note that gefitinib does not only stimulate the CYP3A4-mediated metabolism of triazolam but also that of midazolam and the anticancer drug irinotecan in vivo (Fujita et al., 2005; Li et al., 2007). A recent clinical study also reported a drug-drug interaction between gefitinib and sorafenib (Adjei et al., 2007). When both drugs were given simultaneously, the AUC of gefitinib was reduced (38%) compared with when the drug was given alone, suggesting that sorafenib might stimulate gefitinib metabolism. In contrast, gefitinib had no effect on sorafenib pharmacokinetics. It is clear that because anticancer drugs in general have narrow therapeutic windows and are often combined, direct stimulation of CYP3A4-mediated metabolism could be of clinical relevance.

CYP3A4 is undoubtedly one of the most important players in many drug-drug interactions. It is unfortunate that the prediction of in vivo drug-drug interactions based on in vitro data is not always straightforward (Lin, 2000; Wienkers and Heath, 2005; Obach, 2009). In addition, as the interpretation of differences in CYP3A, animal studies are not always representative of the human situation. The fact that for some drugs the intestine and not the liver is the most important organ for CYP3A4-mediated drug-drug interactions can further complicate predictions. Therefore, humanized mouse models for CYP3A4, as we characterized and used here, could be of great value to better understand and predict drug-drug interactions, especially at a relatively early stage in drug development. Nonetheless, one should always realize that humanized mice are still not humans and that there will always be limitations in using these models for quantitative predictions of drug exposure in humans.

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References


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Supplementary data 1: Plasma concentration versus time curves of midazolam (top panel) and 1’-OH midazolam (lower panel) after oral midazolam administration (2 mg/kg) are shown for wild-type, Cyp3a<sup>−/−</sup>, Cyp3a<sup>−/−</sup>Tg-3A4<sub>Hep</sub>, Cyp3a<sup>−/−</sup>Tg-3A4<sub>Int</sub> and Cyp3a<sup>−/−</sup>Tg-3A4<sub>Hep/Int</sub> mice. Data are shown as the mean concentration, and error bars represent the S.D. (n = 4 per time point). Midazolam levels were not significantly different between Cyp3a<sup>−/−</sup> and wild-type mice. Note that midazolam metabolism in Cyp3a<sup>−/−</sup> mice can be attributed to upregulated CYP2C enzymes (van Waterschoot et al., 2008) and that these upregulated CYP2C levels are (partly) normalized in Cyp3a<sup>−/−</sup>Tg-3A4<sub>Hep</sub> and Cyp3a<sup>−/−</sup>Tg-3A4<sub>Int</sub> mice (van Waterschoot et al., 2009). Exclusive expression of transgenic CYP3A4 in the intestine (Cyp3a<sup>−/−</sup>Tg-3A4<sub>Int</sub>) resulted in a markedly reduced midazolam exposure whereas expression in the liver (Cyp3a<sup>−/−</sup>Tg-3A4<sub>Hep</sub>) resulted in a higher exposure, when compared to Cyp3a<sup>−/−</sup> mice. No difference in midazolam exposure was observed between Cyp3a<sup>−/−</sup>Tg-3A4<sub>Int</sub> and Cyp3a<sup>−/−</sup>Tg-3A4<sub>Hep/Int</sub>. These data demonstrate that intestinal CYP3A4 has a major impact on oral midazolam exposure, whereas the effect of hepatic CYP3A4 is very modest.
Plasma concentration versus time curves of triazolam (A-C) and 1'-OH triazolam (D-F) after oral triazolam administration (0.5 mg/kg) and co-administration of gefitinib (25 mg/kg, B, E) or ketoconazole (35 mg/kg, C, F) are shown for Cyp3a−/−, Cyp3a−/−Tg-3A4Hep, Cyp3a−/−Tg-3A4Int and Cyp3a−/−Tg-3A4HepInt mice. Note differences in scale for triazolam and 1'-OH triazolam panels. Data are shown as the mean concentrations, and error bars represent the S.D. (n = 4-5 per time point).