CYP3A5 Genotype-Phenotype Analysis in the Human Kidney Reveals a Strong Site-Specific Expression of CYP3A5 in the Proximal Tubule in Carriers of the CYP3A5*1 Allele

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ABSTRACT:

Interindividual variability in the drug-metabolizing activity of the CYP3A5 enzyme is mainly due to a single nucleotide polymorphism in CYP3A5, leading to low expression in homozygous CYP3A5*3/*3 individuals compared with CYP3A5*1/*3 allele carriers. In the human kidney, expression of CYP3A5 has been implicated in blood pressure regulation and calcineurin inhibitor-associated nephrotoxicity. The effect of the CYP3A5*1/*3 polymorphism on the expression level and protein distribution within the human kidney is not well characterized. Therefore, we performed a genotype-phenotype analysis of CYP3A5 mRNA and protein expression in the human kidney. To this end, we analyzed sections of normal kidney tissue obtained from 93 white individuals undergoing nephrectomy by quantitative mRNA expression analysis. Qualitative protein expression analysis of CYP3A5 was performed by immunohistochemistry. Mean renal mRNA expression of carriers of the CYP3A5*1 (n = 12) allele was more than 18-fold higher than that of CYP3A5*3/*3 carriers (n = 81, p < 0.001). Immunohistochemical analysis demonstrated CYP3A5 protein in all epithelia of the nephron in kidney sections with the CYP3A5*3/*3 genotype. In carriers of the CYP3A5*1 allele, a strong increase in protein expression of CYP3A5 was detected, and this was confined to the proximal tubule. This study confirms a significant effect of the CYP3A5*1/*3 polymorphism on CYP3A5 expression in the normal human kidney and reveals a strong nephron segment-specific difference in the CYP3A5 protein expression limited to the proximal tubule.

Introduction

A striking interindividual difference in the CYP3A5 enzyme expression is linked to a single nucleotide polymorphism in CYP3A5 leading to only low expression in homozygous CYP3A5*3/*3 individuals compared with CYP3A5*1/*3 allele carriers (Kuehl et al., 2001; Wojnowski, 2004). Data suggested a role for CYP3A5 in salt-sensitive blood pressure regulation and indicated an association with hypertension (Givens et al., 2003; Kreutz et al., 2004, 2005; Fromm et al., 2005; Ho et al., 2005; Kivistö et al., 2005; Bochud et al., 2006; Lieb et al., 2006; Eap et al., 2007; Langae et al., 2007; Zhang et al., 2010). Although controversial results regarding this association have been obtained, it has been hypothesized that CYP3A5 modifies renal tubular sodium reabsorption via protection of the mineralocorticoid receptor from glucocorticoid binding in the distal tubular cells (Fromm et al., 2005; Kreutz et al., 2005). Another hypothesis states a gene-gene-interaction between CYP3A5 and ATP-binding cassette, subfamily B, member 1 (ABCB1), which codes for the multidrug transporter P-glycoprotein, affecting blood pressure regulation in humans (Eap et al., 2007; Bochud et al., 2009).

So far, a detailed analysis of the genotype-dependent CYP3A5 mRNA expression has been described mainly for liver (Kuehl et al., 2001; Lin et al., 2002), whereas data on genotype-dependent CYP3A5 levels in the human kidney are scarce. Nevertheless, renal CYP3A5 expression has been implicated in calcineurin inhibitor-associated nephrotoxicity (Joy et al., 2007; Kuypers et al., 2010). We therefore performed a genotype-phenotype analysis of CYP3A5 mRNA and protein expression in kidneys from white individuals.

Materials and Methods

Tissue Samples. Kidney samples from 93 patients were obtained during surgical interventions conducted at the Department of Urology, Campus Benjamin Franklin, Charité–Universitätsmedizin Berlin. The kidney samples originated from normal tissue surrounding different kidney tumors (see Table 1 for detailed characteristics of the study cohort). All patients gave written informed consent, and the local ethics committee approved the use of patient samples. DNA and RNA of all tissue samples were isolated simultaneously using the QIAGEN AllPrep DNA/RNA Mini Kit including a DNase digestion step (Qiagen GmbH, Hilden, Germany).

Genotyping and mRNA Quantification. Genotyping of CYP3A5 (rs776746) was performed as described previously (Kreutz et al., 2005). Correctness of genotyping results was confirmed by direct sequencing using the ABI Prism 3130 Genetic Analyzer (Applied Biosystems, Foster City, CA). After reverse transcription of total RNA (n = 93 samples) using the First Strand cDNA Synthesis Kit (Fermentas GmbH, St. Leon-Rot, Germany), mRNA expression levels of genes of interest, i.e., CYP3A4 and CYP3A5, were quantified as reported previously (Gálvez-Prieto et al., 2008). Details of the primers and probes used for quantitative real-time polymerase chain reaction are summarized in Supplemental Table 1. To normalize our expression data, we used hydroxymethylbilane synthase (HMBS; also known as porphobilino-

ABBREVIATIONS: ABCB1, ATP-binding cassette, subfamily B, member 1; HMBS, hydroxymethylbilane synthase.
gen (deaminase) as a housekeeping gene. All primers and fluorogenic probes were designed using the Primer Express software (Applied Biosystems) and were synthesized by TIB Molbiol (Berlin, Germany). Quantification was performed using the standard curve method with calculation of the transcript number in each sample and dividing it through the respective HMBS transcript number. Specificity of the products was confirmed by direct sequencing.

**Immunohistochemistry.** Immunostaining for CYP3A5 protein was performed on paraffin sections using a polyclonal primary antibody directed toward human CYP3A5 (ab22692; Abcam, Cambridge, UK) and second step amplification by Envision and DAB-plus from Dako Denmark A/S (Glostrup, Denmark) as described previously (Mooyaart et al., 2009). For this purpose, 20 different renal biopsies were screened, as well as a panel of seven normal human kidneys from Eurotransplant. Sections were counterstained with hematoxylin and were mounted. Only the second step conjugates were used as negative controls.

**Statistical Analysis.** Data are presented as mean ± S.E.M. Regarding CYP3A5*1 allele carriers (CYP3A5*1/*1 and CYP3A5*1/*3) and CYP3A5*3/*3 individuals, differences in categorical measures were compared using Fisher’s exact test, and differences in continuous measures were analyzed using the Mann-Whitney U test or Student’s t test. All reported p values are two-sided; a p value of less than 0.05 was considered to indicate statistical significance.

**Results**

No significant differences in gender proportion, mean age, and frequency of hypertension were found between CYP3A5*1 allele carriers and CYP3A5*1/*3 individuals (Table 1). In the hypertensive and normotensive groups of patients, we observed allele frequencies of 10.9 and 15.8%, respectively, for the CYP3A5*1 allele (p = 0.54). The genotype distribution of all polymorphisms investigated was in Hardy-Weinberg equilibrium. The allele frequencies of the CYP3A5*1 and CYP3A5*3 allele were 7.5 and 92.5%, respectively, and thus were similar to those reported previously in a large cohort of white persons (Kreutz et al., 2005).

The highest levels of CYP3A5 mRNA were found in CYP3A5*1/*1 individuals (n = 2), intermediate levels were found in heterozygotes (n = 10), and lowest levels were found in CYP3A5*3/*3 individuals (n = 81). The comparison between genotype groups indicated a significant effect of the CYP3A5*1 allele on CYP3A5 mRNA levels expressed as CYP3A5 transcript number/HMBS transcript number (CYP3A5*1/*1 individuals, 5.18 ± not applicable; CYP3A5*1/*3 individuals, 1.74 ± 0.31; and CYP3A5*3/*3 individuals, 0.28 ± 0.03, p < 0.05 and p < 0.001, respectively) (Fig. 1a). Mean CYP3A4 mRNA content was almost 5-fold lower than the mean CYP3A5 mRNA level of CYP3A5*3/*3 individuals (0.06 ± 0.02 versus 0.28 ± 0.03 CYP3A4 or CYP3A5 transcript/HMBS transcript number, p < 0.001).

Immunohistochemistry revealed staining for CYP3A5 protein in all renal epithelia. Compared with kidney samples with a CYP3A5*3/*3 genotype (n = 5), higher expression of CYP3A5 was detected in kidneys of CYP3A5*1 allele carriers (n = 2). This genotype-dependent differential expression was exclusively observed in epithelial cells of the proximal tubule, whereas no influence of the genotype was observed in distal epithelium, collecting ducts, or glomeruli (Fig. 1b).

**Discussion**

Thus far, a detailed analysis of the genotype-dependent CYP3A5 mRNA expression has been described mainly for liver (Kuehl et al., 2001; Lin et al., 2002) or only a small number of kidney samples (Koch et al., 2002). In this respect, this is the first study showing the strong genotype-phenotype correlation between CYP3A5 genotype and its renal mRNA expression levels on a large set of normal human kidney samples from white individuals. Regarding the genotype-dependent effects on the CYP3A5 protein content in the human kidney, a significant difference between heterozygous CYP3A5*1/*3 allele carriers and CYP3A5*3/*3 individuals was reported previously in microsomal preparations from 21 human kidneys (Givens et al., 2003). In the current study, immunohistochemical analysis in normal kidneys confirmed the genetically determined variability in renal CYP3A5 expression with an increased staining intensity in CYP3A5*1/*3 allele carriers. Of note, the increased expression observed in CYP3A5*1 allele carriers is restricted to the proximal tubule. Although immunohistochemical localization of renal CYP3A5 protein has been reported previously in biopsies of transplanted kidneys (Joy et al., 2007; Metalidis et al., 2011), no genotype-dependent differences in the CYP3A5 staining pattern have been detected thus far (Metalidis et al., 2011). This discrepancy might result from technical differences including antigen retrieval and subsequent amplification of the first antibody, as well as the use of a different primary antibody. Moreover, it should be noted that the aforementioned studies were performed on transplanted kidneys with and without signs of calcineurin inhibitor-associated nephrotoxicity (Joy et al., 2007; Metalidis et al., 2011). In contrast, we...
analyzed well preserved normal kidneys before transplantation. We cannot exclude the possibility that ischemia reperfusion injury after transplantation may affect the expression level of CYP3A5 in proximal epithelium.

In accordance with other reports (Koch et al., 2002; Givens et al., 2003), we found either very low or no CYP3A4 mRNA expression levels compared with CYP3A5, which consolidates the presumption of CYP3A5 being the predominant CYP3A isoenzyme in the human kidney.

Hepatic CYP3A4 mRNA expression has been shown to be influenced by the ABCB1 2677 polymorphism (Lamba et al., 2006), and an interaction between CYP3A5 and ABCB1 with effects on blood pressure has been reported in individuals of East African descent (Eap et al., 2007; Bochud et al., 2009). For CYP3A5 mRNA levels in carriers sure has been reported in individuals of East African descent (Eap et al., 2007; Bochud et al., 2009). For CYP3A5 mRNA levels in carriers of the CYP3A5*1 allele, we did not observe a significant influence of the ABCB1 TTT-haplotype, which is derived from the three ABCB1 genotypes 1236C>T, 2677G>T (rs2032582), and 3435C>T (rs1045642) (Eap et al., 2007; Bochud et al., 2009) (data not shown). However, we realize that the analyzed subcohort of 12 individuals is too small to draw negative conclusions; this association necessitates further investigation. The same applies to the observation that no significant association between presence of CYP3A5*1 allele and the diagnosis of hypertension was observed, although numerically the CYP3A5*1 allele frequency was higher in the normotensive group.

In summary, we confirmed a genotype-dependent variation in renal CYP3A5 mRNA content as has been described mainly for liver so far. Furthermore, we showed that the morphologic correlative of this relationship is a strong nephron segment-specific difference in the CYP3A5 protein expression limited to the proximal tubule.

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References


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CYP3A5 genotype - phenotype analysis in the human kidney reveals a strong site-specific expression of CYP3A5 in the proximal tubule in carriers of the CYP3A5*1 allele

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Drug Metabolism and Disposition

Supplemental Table 1: Primers and probes used for quantitative RT-PCR analysis

<table>
<thead>
<tr>
<th>Transcript</th>
<th>Primer forward (F), reverse (R)</th>
<th>Probe</th>
</tr>
</thead>
<tbody>
<tr>
<td>CYP3A5*1</td>
<td>F: TCGTCAGGGTCTCTGGAAATTT</td>
<td>AAGTATGGAAAAATGTGGGGAACGTATGAAGGT</td>
</tr>
<tr>
<td></td>
<td>R: TCTGATCACGTCGGGATCTG</td>
<td></td>
</tr>
<tr>
<td>CYP3A4 exon primers</td>
<td>F: GAACTGAATGAGAACCAACAAAGTAAA</td>
<td>TTTGGTCATTGTAATCAGTGTGCGTG</td>
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<tr>
<td></td>
<td>R: CAATGGCGCAAAGTCACAGTGGAT</td>
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<tr>
<td>CYP3A4 intron primers</td>
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<tr>
<td></td>
<td>R: AACTCAATGATTTAATGGCAAA</td>
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</tr>
<tr>
<td>HMBD (PBGD)</td>
<td>F: CCACACACAGCCTACTTTTCCAA</td>
<td>CCATGTCTGGTAACGGCAATGCGG</td>
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<tr>
<td></td>
<td>R: ACGCGAATCACTCTCATCTTTT</td>
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*a No specific probe was designed for this assay; instead, we used SYBR Green for unspecific DNA intercalation.