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SNP Communication

A Novel Single Nucleotide Polymorphism (SNP) of the CYP2C19 Gene in a Japanese Subject with Lowered Capacity of Mephobarbital 4′-Hydroxylation

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Summary: We sequenced all nine exons and exon-intron junctions of the cytochrome P450 2C19 (*CYP2C19*) gene from a Japanese subject with a lowered capacity of CYP2C19-mediated 4′-hydroxylation after an oral administration of mephobarbital. We found a novel single nucleotide polymorphism (SNP) of *CYP2C19* gene as follows: SNP, 040110MoritaJ001; GENENAME: *CYP2C19*; ACCESSION NUMBER: NT_030059.8; LENGTH; 25 bases; 5′-GAGGGCCTGGCCC/TGCATGGAGCTGT-3′. The SNP (168946C>T) induced an amino acid alteration (Arg442Cys) located in exon 9 close to the heme-binding region of CYP2C19, which may result in the decrease in the catalytic properties of CYP2C19. A new allele having this SNP was designated as *CYP2C19*16*.

Key words: ***CYP2C19*; novel SNP; amino acid substitution; Japanese**

Introduction

Mephobarbital is metabolized to 4′-hydroxymephobarbital by CYP2C19 in human liver microsomes.[1)] Recently, we investigated the pharmacokinetic disposition and metabolism of mephobarbital in extensive metabolizers and poor metabolizers of CYP2C19 recruited from a Japanese population. Through the study, we found that a heterozygote of defective allele, *CYP2C19*2*, had a lower capacity for the 4′-hydroxylation of mephobarbital compared with the other heterozygotes. Urinary excretion rate of 4′-hydroxymephobarbital collected in 0 to 24 hours after an oral administration of mephobarbital in the subject was only one third of those in the other heterozygotes of defective alleles, *CYP2C19*2* or *CYP2C19*3* (Kobayashi *et al*[1]). Although all of known SNPs of *CYP2C19* gene (see http://www.imm.ki.se/CYPalleles/) have been analyzed, none of these mutated alleles were existed in the genomic DNA of this outlier, except for *CYP2C19*2*. Therefore, we sequenced all nine exons and exon-intron junctions of *CYP2C19* gene from the outlier and identified a novel SNP located in exon 9 of *CYP2C19* gene and the SNP was also analyzed in 80 Japanese reported herein.

Materials and Methods

Human DNA samples: Genomic DNA was isolated from whole blood of healthy volunteers using GFX genomic Blood DNA Purification kit (Amersham Biosciences, Piscataway, NJ, USA) in accordance with the manufacture's instructions. Informed consent was obtained, and the study including phenotyping and

Until January 27, 2004, the SNP reported herein has not been reported in the "Human cytochrome P450 (CYP) Allele Nomenclature Committee database (http://www.imm.ki.se/CYPalleles/) or the "JSNPs data base (http://snp.ims.u.tokyo.ac.jp/)".

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Table 1. Primers used for the specific amplification and direct sequencing analysis of *CYP2C19* gene

amplified region	forward primer (5′ to 3′)	reverse primer (5′ to 3′)
Exon1	AGTGGGCCTAGGTGATTGGCCACTT	TCAAAGTATTTTACTTTACAATGATCTC
Exons 2 and 3	TAAATATGAATCTAAGTCAGGCTTAGT	GGAGAGCAGTCCAGAAAGGTCAGTGATA
Exon 4	TGCTTTTAAGGGGAGTCATAGG	CAAATGTACTTCAGGGCTTGG
Exon 5	CAACCAGAGCTTGGCATATTG	TGATGCTTACTGGATATTCATGC
Intron 5	AAACCTTGCTTTTATGGAAAGTG	ATAACTAAGCTTTTGTTAACATGTT
Exon 6	AAAACTGGCACAAGACAGGGATG	AAATTGGGACAGATTACAGCTGCG
Exon 7	AATTGCTAGAACAAATGTTCCATTTC	AGAGGGTAAGAATCATACTGTGA
Exon 8	CCACTGTTTCATAAACCATCGTGA	GAAGGCACATGTAAGTTCCAACTGA
Exon 9	ATCTACTCATCCCTCCTATGATTCACCG	ATGTGGCACTCAATGTAACTATTATAGA

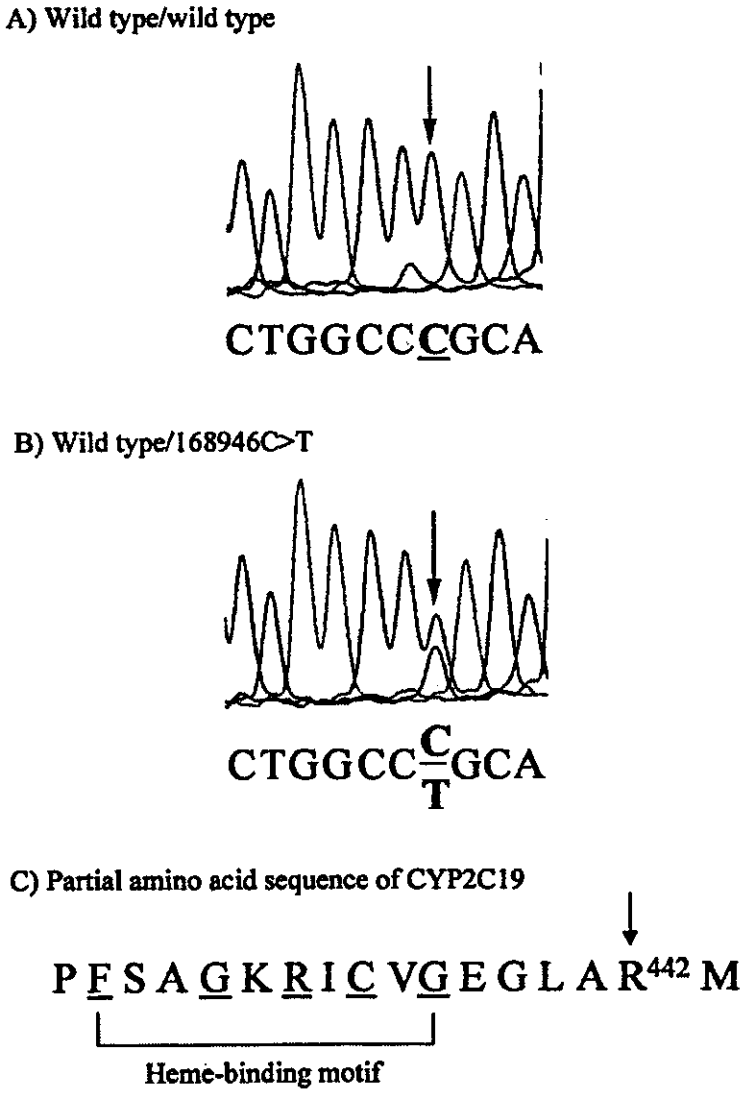

Fig. 1. The nucleotide sequences of the *CYP2C19* gene in exon 9 containing 168946C>T polymorphism (Arg442Cys). Although the sequences are shown only for sense strands, both the strands were sequenced. The first A of the translational initiation codon ATG of exon 1 is defined as position +1. A) Wild type/wild type. B) Wild type/168946C>T. C) Partial amino acid sequence of CYP2C19 showing the conserved heme-binding motif (FXXGXRXCXG). Arrows indicate variant nucleotide and amino acid positions. Underlines indicate the conserved heme-binding motif of cytochrome P450.

genotyping tests was approved by the ethics review board of Kyushu Pharmacology Research Clinic and by the ethics committee of Graduate School of Pharmaceutical Sciences, Chiba University, Chiba Japan.

PCR conditions and DNA sequencing: The PCR was conducted in a reaction mixture (25 μL) containing 100 ng of genomic DNA, 0.63 U Ampli Taq Gold (Applied Biosystems, Foster City, CA, USA), 10×PCR Gold Buffer, 2.5 mM $MgCl_2$ and 0.2 mM dNTPs with 0.2 μM of each primer. PCR conditions consisted of an initial denaturation at 94°C for 10 min, followed by 35 cycles of denaturation at 94°C for 1 min, annealing at for 57°C 1 min and extension at 72°C for 1 min, except that annealing was performed at 65°C for amplification of exon 1. Sequences were determined using Cycle Sequencing with Quick Start Kit (Beckman coulter Fulleton, California, USA) and CEQ2000XL DNA analysis system (Beckman coulter). The primers used for the PCR amplification and sequencing are shown in **Table 1.** The SNP was confirmed by the repeated sequence analyses on PCR products generated by new genomic DNA amplification.

Mephobarbital phenotyping protocol: Thirty male healthy volunteers received an oral 200-mg dose of racemic mephobarbital (1 tablet of Prominal®, Winthrop Laboratories, Sydney, Australia). Urine samples were collected at 0 to 24 hours. The concentration of 4′-hydroxymephobarbital in urine was measured by the HPLC method. (Kobayashi *et al*[1]). The genotypic backgrounds of CYP2C19 of thirty male healthy subjects were the nine homo extensive metabolizers (*2C19*1/2C19*1*), ten hetero extensive metabolizers (*2C19*1/2C19*2, 2C19*1/2C19*3*) and eleven poor metabolizers (*2C19*2/2C19*2, 2C19*2/2C19*3, 2C19*3/2C19*3*).

Results and Discussion

We found the following novel SNP (168946 C>T) from the outlier subject with a lowered capacity for CYP2C19-mediated 4′-hydroxylation of mephobarbital.

SNP: 040110MoritaJ001; GENENAME: *CYP2C19*; ACCESSION NUMBER: NT_030059.8; LENGTH; 25 bases; 5′-GAGGGCCTGGCCC/TGCATGGAGCTGT-3′.

The SNP was 168946C>T in exon 9 resulting in an amino acid change of Arg442Cys (**Fig. 1**). The outlier was heterozygous for the Arg442Cys allele. As shown in **Fig. 1C**, the amino acid substitution (Arg442Cys) is closely located in the heme-binding region.[2] Thus, the novel SNP is expected to decrease the catalytic properties of CYP2C19. In fact, urinary excretion rate of 4′-hydroxymephobarbital collected in 0 to 24 hours after an oral administration of mephobarbital in the subject was lower than those in the other heterozygotes with defective alleles, *CYP2C19*2* or *CYP2C19*3*, or the homozygotes of *CYP2C19*1* (3.5% vs. 10.1±1.1 or 10.9±1.5% of dose). However, the rate in the subject was not as low as those in poor metabolizers of CYP2C19 (0.53±0.31% of dose).

Until now, it has been known that the only two defective alleles (i.e., *CYP2C19*2* and *CYP2C19*3*) account for >99% of poor metabolizer alleles in the Japanese population.[3,4] On the other hand, more than 10 variants (designed as *CYP2C19*4* to *CYP2C19*15*) of *CYP2C19* gene have been reported from the other ethnic groups (see http://www.imm.ki.se/CYPalleles/). The novel SNP would be able to explain the poor metabolizer status of CYP2C19 which cannot be explained by *CYP2C19*2* and *CYP2C19*3* in a Japanese population. However, since this novel SNP was not found in another 80 DNA samples of Japanese subjects, further studies are definitely required for the more exact frequency of the SNP and its functional characteristics in Japanese and the other races.

In conclusion, the novel SNP (Arg442Cys) located in exon 9 of the *CYP2C19* gene was found in a Japanese subject with an impaired activity of CYP2C19. This outlier appears to be a heterozygote for *CYP2C19*2* and this new SNP, although haplotypes of the subject have not been evaluated. Further studies are undergone to establish whether the newly identified SNP (Arg422Cys) affects the CYP2C19 function in our laboratory.

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SNP Communication

A Novel Variant Allele of OATP-C (SLCO1B1) Found in a Japanese Patient with Pravastatin-induced Myopathy

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Summary: We have recently found that the frequency of *OATP-C*15* is significantly higher in patients who experienced myopathy after receiving pravastatin or atorvastatin than in patients without myopathy. However, there were two patients who experienced pravastatin-induced myopathy despite the fact that they did not possess *OATP-C*15* or other known mutations of *OATP-C* that have been reported to decrease the function of OATP-C. In this study, we sequenced all of the exons and exon-intron junctions of *OATP-C* of the two patients and found a novel mutation in exon 12 of *OATP-C* in one of the patients. In this mutation (1628T>G), there is a substitution of Leu to Trp at position 543 in transmembrane-spanning domain 10 of OATP-C. However, the frequency of this mutation in the Japanese population appears to be very low (<1%).

Key words: ***OATP-C (SLCO1B1)*; novel variant allele; nonsynonymous; statins**

Introduction

3-Hydroxy-3-methylglutaryl coenzyme A reductase inhibitors, also known as statins, are the most effective drugs for treatment of elevated concentration of low-density lipoprotein cholesterol, and they have been shown to reduce cardiovascular events of coronary heart disease and cardiovascular-related morbidity and mortality rates.[1] These drugs are tolerated well by most patients, but they can produce a variety of muscle-related complaints like myopathy and rhabdomyolysis, which have been the major clinical complication for statin treatment.[2] We have recently studied genetic factors contributing to the risk of statin-induced myopathy and found that the frequency of *OATP-C*15*, a mutant allele of *OATP-C* (OATP1B1, gene *SLC21A6/SLCO1B1*), was significantly higher in patients with myopathy who were receiving pravastatin or atorvastatin than in patients without myopathy.[3] We also found in another study that transporting activities for pravastatin and atorvastatin decreased significantly in HEK293 cells expressing *OATP-C*15* compared to those in cells expressing *OATP-C*1a*, the reference allele of *OATP-C*.[4] Based on these findings, we speculated that patients treated with pravastatin or atorvastatin who are carrying *OATP-C*15* have increased plasma concentrations of these drugs and are thus more susceptible to the myotoxic effects of these statins than are non-carrier patients treated with pravastatin or atorvastatin.

However, in our study two of seven patients who experienced myopathy after receiving pravastatin or atorvastatin did not possess *OATP-C*15* or mutated alleles of *OATP-C* that have been reported to decrease the function of OATP-C. Therefore, we sequenced all of the exons and exon-intron junctions of *OATP-C* for the DNA samples of these patients, and we found a novel nonsynonymous mutation of *OATP-C* located in exon 12 of this gene.

Materials and Methods

Human genomic DNA samples: DNA samples obtained from the two patients who experienced myopathy after receiving pravastatin or atorvastatin but did not possess *OATP-C*15* were used in the present study. None of the known mutant alleles of *OATP-C* that have

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Until October 11, 2004, the mutation described herein has not been registered in the NCBI dbSNP or JSNP database

Table 1. Primer sequences used for the analysis of *OATP-C*

Exon	Forward Primer (5′→3′)	Reverse Primer (5′→3′)	Note
2	CATTGACCTAGCAGAGTGGTAACG	GTGATCAATCCAAAACCAAAGAG	PCR and sequence
3	GAAATGATGCTTTATCAGTGTAGTGA	CCTGTGCAGTTATGACAACCAC	PCR and sequence
4	CATCTCCATTTTTCTTCATTCCA	GTACACACTTAGTGGGTATCTTC	PCR and sequence
	CATTGTCTTTGAGGGAAGGCACT		sequence
5	GTACTCTGGTAATTTGGGGAAGA	CTGTGTTGTTAATGGGCGAACT	PCR and sequence
	GTACTCTGGTAATTTGGGGAAGA		sequence
6–7	GGACTAATACACCATATTGTCAAAG	GCTGGATTTTATATTTATTCTGATT	PCR and sequence
6	TTGTAATAGAAATGCTAAAAT		sequence
7	TCCCTTTGTCTACTTTTGAA		sequence
8	CCTAGACAGTATCTGTTGCATTATGTCA	CTTCCACTTGTTATGTGCTCAAGA	PCR and sequence
9	TGTAAAGTACCCAGGATAACC	AGAGCAATAGTGACATCACAAGT	PCR and sequence
10	TTGATAGGTGCAGCAAACCAC	CAACCTATGTTGCTTCTCTTTAG	PCR and sequence
11	CTCTGCTTTCACTTTACTTC	CCTGATTGTGCCCTAAGCAGAC	PCR and sequence
12	GTCCAAAAGAGTATGTGCTCTGC	CAGCCTTGAGAGTTCATAGTA	PCR and sequence
	TGTATTTGCAGCACTGTTAGG		sequence

been reported to decrease its activity[5] were found in the DNA samples obtained from these patients. Written informed consent was obtained from the patients, and the study was approved by the Ethics Committee of the Graduate School of Pharmaceutical Sciences, Chiba University. We also studied fifty DNA samples obtained from healthy Japanese volunteers for the determination of allele frequency. Written informed consent was obtained from all of the volunteers, and the study was also approved by the Ethics Committee of the Graduate School of Pharmaceutical Sciences, Chiba University.

Polymerase chain reaction (PCR) conditions for sequencing: All exons and exon/intron boundaries of the *OATP-C* in the DNA samples obtained from the two patients were analyzed by PCR and direct sequencing. The primers used for amplification of the genomic DNA and direct sequencing are summarized in **Table 1.** DNA amplification was conducted in a reaction mixture (50 μL) containing 1–2 μg/mL genomic DNA, 1.2 mM $MgSO_4$, 5 mM dNTPs, 5 mM KOD buffer, 0.02 U/mL KOD-plus-polymerase and 0.2 μM of each primer. Thermocycling conditions consisted of initial denaturation for 3 minutes at 94°C followed by 35 cycles of denaturation at 96°C for 20 seconds, annealing at 57°C (reducing by 2°C every 3 cycles 2 times followed by 26 cycles at 51°C) for 30 seconds, and extension at 68°C for 25 seconds. Terminal elongation was performed at 68°C for 2 minutes. The PCR product was purified using Wizard® SV Gel and PCR Clean-Up System (Promega Corp., Madison, WI, USA) and directly sequenced on a CEQ™ 2000 DNA Analysis System (Beckman Coulter, Inc., Fullarton, CA, USA) with a CEQ™ DTCS Quick start kit (Beckman Coulter, Inc.). The reference sequence of *OATP-C* was obtained from GenBank (NT_000012.9).

DNA samples from healthy volunteers were analyzed by PCR and direct sequencing using the primers used for sequencing exon 12 (**Table 1**). PCR and thermocycling conditions were the same as the described above.

Results and Discussion

A novel nonsynonymous single nucleotide polymorphism (SNP) was found in one of the DNA samples from the two patients.

SNP: 041015OishiT001; GENENAME: *SLCO1B1*; ACCESSION NUMBER: NT_000012.9; LENGTH: 25 bases; 5′-CAATACAAGTCT T/G GAATTTATTTT-TC-3′. The SNP was 1628T>G in exon 12 of *OATP-C* (**Fig. 1**). In this SNP, Leu is substituted by Trp at position 543 in transmembrane-spanning domain 10 of OATP-C. Although the functional significance of this SNP is not known, it may cause functional impairment of OATP-C because it has been reported that nonsynonymous SNPs within the putative transmembrane domains in OATP-C result in severely reduced function of OATP-C due to its decreased plasma membrane expression.[5] This novel SNP was not found in any of the 50 DNA samples from healthy Japanese volunteers. The results suggest that the allele frequency of this novel variant allele of *OATP-C* is very low (<1%) in the Japanese population. However, OATP-C is responsible for the hepatocellular uptake of a broad range of endogenous and xenobiotic compounds, including bile acid, glucuronide and sulfate conjugates, methotrexate, pravastatin, rosuvastatin and cerivastatin.[6-9] Therefore, further studies are required to clarify the exact frequency in the Japanese population and the functional characteristics of this novel variant allele of *OATP-C*.

In conclusion, we found a novel nonsynonymous mutation (1628T>G) located in exon 12 of *OATP-C* in a DNA sample from a patient who experienced myopathy after receiving pravastatin. In this mutation, there is a substitution of Leu to Trp at position 543 in transmembrane-spanning domain 10 of OATP-C. The

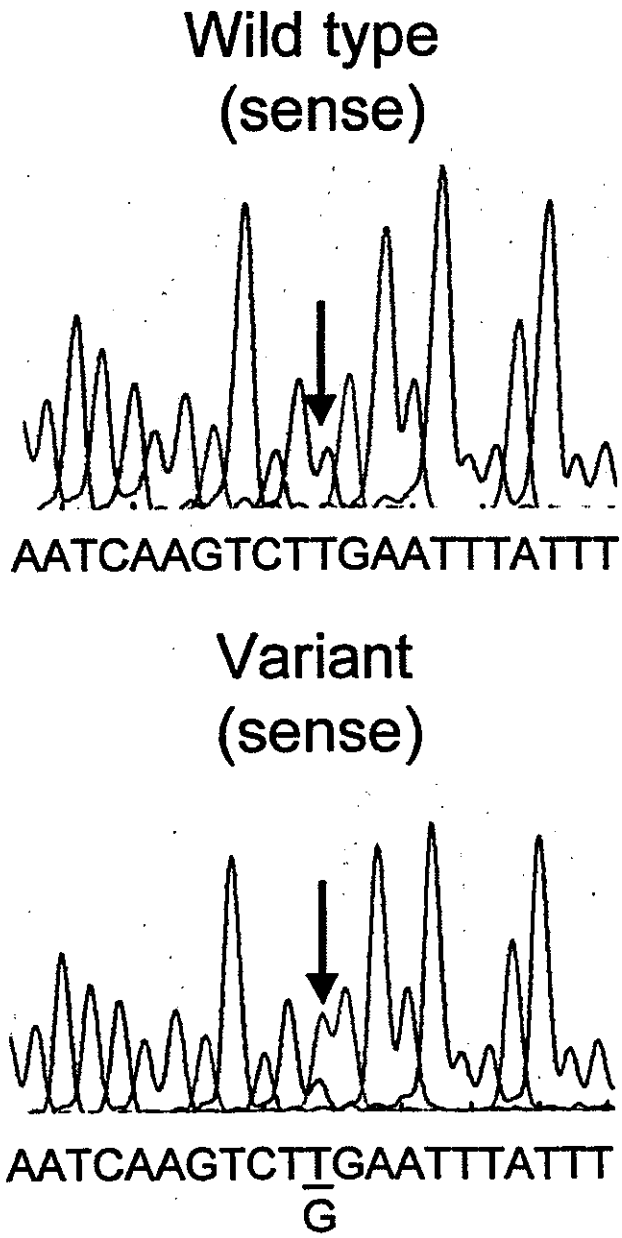

Fig. 1. Nucleotide sequences of *OATP-C* containing novel variant 041015OishiT001 (1628T>G) in exon 12. Arrows indicate the positions of the nucleotide change.

frequency of this mutation in the Japanese population appears to be very low (<1%).

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Pharmacogenetic roles of CYP2C19 and CYP2B6 in the metabolism of *R*- and *S*-mephobarbital in humans

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Objectives and methods **We assessed the relationship between the metabolism of *R*- and *S*-mephobarbital (MPB) and genetic polymorphisms of cytochrome P450 (CYP) 2C19 and CYP2B6. Nine homozygous extensive metabolizers (homo-EMs, *2C19*1/2C19*1*) of CYP2C19, ten heterozygous EMs (hetero-EMs, *2C19*1/2C19*2*, *2C19*1/2C19*3*) and eleven poor metabolizers (PMs, *2C19*2/2C19*2*, *2C19*3/2C19*3*, *2C19*2/2C19*3*) recruited from a Japanese population, received an oral 200 mg-dose of racemic MPB. Blood and urine samples were collected, and *R*-MPB, *S*-MPB and the metabolites, phenobarbital (PB) and 4′-hydroxy-MPB, were measured. Each subject was also genotyped for *CYP2B6* gene.**

Results **The mean area under the plasma concentration–time curve (AUC) of *R*-MPB was 92-fold greater in PMs than in homo-EMs. *R/S* ratios for AUC of MPB were much higher in PMs than in EMs (homo- and hetero-). The cumulative urinary excretion of 4′-hydroxy-MPB up to 24 h postdose was 21-fold less in PMs than in homo-EMs. The metabolic ratio of $AUC_{PB}/(AUC_{S\text{-}MPB} + AUC_{R\text{-}MPB})$ was higher in PMs than in EMs (homo- and hetero-). In addition, this metabolic ratio was lower in the carriers of *CYP2B6*6* compared with that in its non-carriers.**

Conclusions **Our results indicate that the 4′-hydroxylation of *R*-MPB is mediated via CYP2C19 and that the rapid 4′-hydroxylation of *R*-MPB results in a marked difference in the pharmacokinetic profiles between *R*-MPB and *S*-MPB in the different CYP2C19 genotypic individuals. In addition, a minor fraction of the interindividual variability in PB formation from MPB may be explainable by the *CYP2B6*6* allele. *Pharmacogenetics* 14:549–556 © 2004 Lippincott Williams & Wilkins**

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Keywords: CYP2C19, CYP2B6, genetic polymorphism, mephobarbital, stereoselective metabolism

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Introduction

Mephobarbital (MPB, 5-ethyl-1-methyl-5-phenylbarbituric acid) is a chiral barbiturate which has been used as a racemate in the treatment of epilepsy since 1932. This drug undergoes an extensive hepatic metabolism in humans. Two routes of the metabolism have been described in humans [1–3]: aromatic hydroxylation to 4′-hydroxymephobarbital (OH-MPB) and *N*-demethylation to phenobarbital (PB). In addition, the *R*-enantiomer of MPB (*R*-MPB) is rapidly 4′-hydroxylated to yield OH-MPB, whereas *S*-enantiomer is principally *N*-demethylated to yield PB, the major metabolite in plasma [4,5]. As a result of this metabolic stereoselectivity, the oral clearance of *R*-MPB was much greater than that of *S*-MPB [5]. OH-MPB undergoes glucronidation and is mainly excreted in urine [3].

Küpfer and Branch [4] reported that the urinary recovery of OH-MPB after an oral administration of racemic MPB was not detected in the poor metabolizers (PMs) of *S*-mephenytoin and that OH-MPB in urine was not recovered in an extensive metabolizer (EM) administrated only *S*-MPB (90 mg), although it was recovered 33% in the EM administered the equal dose of *R*-MPB. In addition, our *in vitro* study demonstrated that the 4′-hydroxylation of MPB is preferential for *R*-enantiomer and its reaction is catalyzed by CYP2C19 [6]. These findings suggest that OH-MPB is exclusively formed from *R*-MPB by CYP2C19. However, the stereoselective disposition of MPB has only been studied in EMs, and no study in PMs of CYP2C19 has been conducted so far.

On the other hand, the *N*-demethylase activity of *S*-MPB appears to depend mainly on the catalytic capacity of CYP2B6 in human liver microsomes [7].

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CYP2B6 is involved in the biotransformation of many drugs including cyclophosphamide, which showed a substantial interindividual difference in the metabolism *in vitro* and *in vivo* [8,9]. A part of such interindividual variabilities can be caused by the genetic polymorphism of CYP2B6. Indeed, Lang *et al.* [10] have identified nine mutations of *CYP2B6* gene in a white population and termed the six different alleles as *CYP2B6*1* (wild-type), *CYP2B6*2*, *CYP2B6*3*, *CYP2B6*4*, *CYP2B6*5*, *CYP2B6*6* and *CYP2B6*7* by the haplotype analysis. Moreover, Lamba *et al.* [11] have reported the new additional alleles, *CYP2B6*8* and *CYP2B6*9*. However, very little has been reported on the effects of genetic polymorphism of CYP2B6 on the catalytic function *in vivo* or clinical implication [12].

The present study, therefore, was undertaken to investigate the stereoselective pharmacokinetic disposition and metabolism of MPB in the homo-EM, hetero-EM and PM groups of CYP2C19 recruited from a Japanese population. We also investigated the pharmacokinetic disposition of MPB in relation to the genetic polymorphism of CYP2B6.

Materials and methods

Drugs and chemicals

Racemic MPB was supplied by Mitsubishi Pharma Corp. (Osaka, Japan). OH-MPB was prepared from 4'-hydroxy-PB *via* *N*-methylation as described by Hiers and Hager [13].

Subjects

Thirty unrelated healthy Japanese male volunteers were enrolled in the current panel study. The subjects were interviewed and were judged as an identical Japanese ethnicity by lineage and birth. None had taken any drugs and beverages containing grapefruit for at least 1 week before the study. Each subject was physically normal and had no antecedent history of significant medical illness or hypersensitivity to any drugs. The study protocol was approved in advance by the ethics review board of Kyushu Pharmacology Research Clinic and by the ethics committee of Graduate School of Pharmaceutical Sciences, Chiba University. Each subject gave his written informed consent before the study.

Study protocol

Each volunteer received an oral 200-mg dose of racemic MPB (one tablet of Prominal, Winthrop Laboratories, Sydney, Australia) with 200 ml of water (around 8:00 am) after an overnight fast. Lunch and evening meals were provided at approximately 4 and 9 h after dosing, respectively. Serial venous blood samples (5 ml each) were collected at 0 (predose), 0.5, 1, 1.5, 2, 3, 4, 6, 8 and 12 h and 1, 2, 4, 8, 12 and 20 days after the dosing. Urine samples were collected at 0 to 24 h.

Analytical method

Concentrations of MPB enantiomers and PB in plasma were determined by a high pressure liquid chromatography (HPLC) method. Plasma (0.5 ml), 100 µl of 0.2 M K_2HPO_4 and 50 µl of secobarbital (as an internal standard) solution (10 µg/ml in methanol) were extracted with 5 ml of dichloromethane. The organic layer was evaporated and the residue was reconstituted with 200 µl of the mobile phase. Twenty µl of reconstituted filtrate by a 0.45 µm filter was injected onto the Jasco HPLC system (Tokyo, Japan) and a TSK-GEL ENANTIO OVM column (4.6 × 150 mm, Tosoh, Tokyo, Japan). The mobile phase consisted of potassium phosphate buffer (25 mM, pH 5.0)/ethanol in the proportion 100/7.5 v/v at a flow rate of 1.0 ml/min. The eluate was monitored at 215 nm.

The concentration of OH-MPB in urine was measured by HPLC after deconjugation. Urine (0.1 ml) was incubated at 37 °C for 2 h with 500 units of β-glucuronidase in 0.1 ml of potassium phosphate buffer (pH 5.0, 0.1 M). The deconjugated urine sample was extracted with 5 ml of dichloromethane after adding 50 µl of cyclobarbital (as an internal standard) solution (20 µg/ml in methanol) and 30 mg of NaCl. The organic layer was shaken with 2 ml of 0.5 N NaOH. The aqueous layer (1.5 ml) and 0.1 ml of 35% hydrochloride were extracted with 5 ml of dichloromethane. The residue of evaporated organic layer was reconstituted with 100 µl of the mobile phase, and 20 µl was directly injected onto the Hitachi HPLC system (Tokyo, Japan) and a CAPCELL PAK C_{18} UG120 column (4.6 × 250 mm, 5 µm; Shiseido, Tokyo, Japan). The mobile phase consisted of 50 mM potassium phosphate buffer (pH 5.0) and acetonitrile at a ratio of 75:25 (v/v) and a flow rate of 1 ml/min. The eluate was monitored at 215 nm.

Genotyping

The two *CYP2C19* mutants, *CYP2C19*2* and *CYP2C19*3* alleles, were genotyped by a polymerase chain reaction–restriction fragment length polymorphism (PCR–RFLP) method as described by Kubota *et al.* [14]. For *CYP2B6* mutants, *CYP2B6*2*, *CYP2B6*3*, *CYP2B6*4*, *CYP2B6*5*, *CYP2B6*6* and *CYP2B6*7* alleles were genotyped by using the PCR-RFLP method as described by Lang *et al.* [10], and the genotyping analysis was verified with a direct sequencing.

Pharmacokinetic and statistical analyses

Peak concentrations (C_{max}) and times to C_{max} (T_{max}) of *R*-MPB, *S*-MPB and PB were obtained directly from the plasma concentration–time data. The area under the plasma concentration–time curve (AUC) was calculated by the trapezoidal rule with extrapolation to the infinity. The elimination half-life ($t_{1/2}$) was calculated by linear regression analysis from the slope (k) of log-linear terminal concentration–time phases ($t_{1/2} = 0.693/$

k). The apparent oral clearance (CL/F) of *R*-MPB or *S*-MPB was estimated as follows: CL/F = dose/2/AUC/body weight, where dose represents that of racemic MPB (i.e. 200 mg). Urinary excretion of OH-MPB during the 0 to 24-h postdose period was calculated as the percentage molar amount of OH-MPB relative to the administered dose of racemic MPB.

All pharmacokinetic data are given as the mean ± standard deviation (SD). The statistical differences between the various group parameters were determined with either a paired Student's t-test or non-parametric Mann-Whitney U-test. A P value of <0.05 was considered as statistically significant.

Results

No clinically undesirable signs and symptoms possibly attributed to the administration of MPB were recognizable throughout the study period. All subjects completed the study according to the protocol.

Demographic and genotypic characteristics

The demographic and genotypic characteristics of the thirty normal healthy male volunteers enrolled in our study are summarized in Table 1.

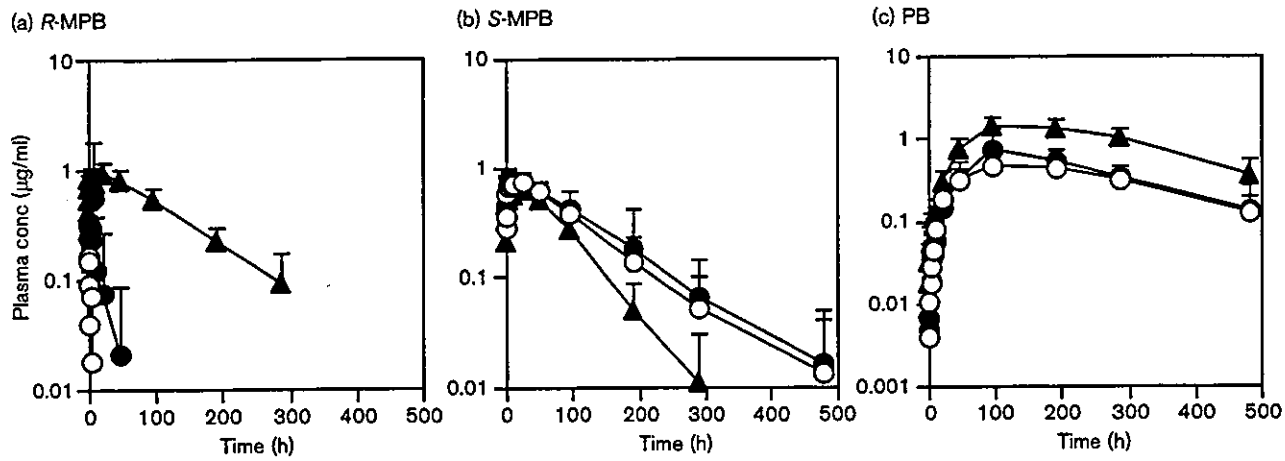
Plasma concentration–time profiles of *R*-MPB, *S*-MPB and PB versus CYP2C19 genotypes

The mean (± SD) plasma concentration–time curves of *R*-MPB, *S*-MPB and its primary metabolite, PB, in the homo-EM (*2C19*1/2C19*1*), hetero-EM (*2C19*1/2C19*2*, *2C19*1/2C19*3*) and PM (*2C19*2/2C19*2*, *2C19*2/2C19*3*, *2C19*3/2C19*3*) groups of CYP2C19 who took an oral 200-mg dose of racemic MPB are shown in Fig. 1(a, b and c, respectively). The mean plasma concentrations of *R*-MPB markedly differed among the three groups (Fig. 1a). In case of the EM status, *R*-MPB in plasma was undetectable throughout the total sampling time period in two homo-EMs and detectable at only one sampling time in two homo-EMs and a hetero-EM. Thus, the mean kinetic data on *R*-MPB (Table 2) could be estimated from the data

Table 1 Individual demographic characteristics and genotypic backgrounds of *CYP2C19* and *CYP2B6* of thirty male healthy subjects enrolled in the study

				Genotype	
Subject number	Age (yr)	Weight (kg)	Height (cm)	*CYP2C19*	*CYP2B6*
Group 1 (homo-EM for CYP2C19)					
2	21	54.1	166.9	*1/*1	*4/*6
3	21	51.7	171.3	*1/*1	*1/*1
7	28	62.3	175.8	*1/*1	*2/*6
9	22	62.6	172.2	*1/*1	*1/*6
19	22	59.6	174.0	*1/*1	*1/*6
20	21	70.5	172.1	*1/*1	*1/*1
23	20	64.6	169.1	*1/*1	*1/*1
27	21	54.9	167.3	*1/*1	*1/*1
29	23	66.1	168.6	*1/*1	*1/*1
Mean	22.1	60.7	170.8		
± SD	2.4	6.2	3.1		
Group 2 (hetero-EM for CYP2C19)					
1	20	69.3	172.7	*1/*2	*6/*6
5	20	54.3	161.7	*1/*2	*2/*6
6	23	53.6	168.2	*1/*2	*1/*1
10	33	69.5	176.8	*1/*2	*1/*6
11	20	74.7	175.1	*1/*2	*6/*6
12	21	58.7	173.7	*1/*2	*1/*6
18	22	71.1	178.4	*1/*3	*1/*1
22	23	60.5	165.4	*1/*2	*1/*1
26	25	54.7	168.3	*1/*2	*2/*6
28	23	72.3	181.7	*1/*2	*1/*1
Mean	23.0	63.9	172.2		
± SD	3.9	8.3	6.2		
Group 3 (PM for CYP2C19)					
4	31	79.9	182.8	*2/*2	*4/*6
8	30	59.9	172.3	*3/*3	*1/*6
13	23	54.4	170.6	*2/*3	*1/*1
14	28	59.2	180.1	*2/*2	*1/*1
15	21	71.4	175.5	*2/*3	*1/*1
16	21	50.0	158.8	*2/*3	*1/*2
17	40	61.2	169.7	*2/*2	*1/*1
21	21	66.6	181.7	*3/*3	*1/*4
24	20	57.4	168.0	*3/*3	*1/*1
25	23	67.1	173.3	*2/*2	*1/*2
30	24	75.0	175.3	*2/*2	*2/*4
Mean	25.6	63.8	173.5		
± SD	6.1	9.1	6.9		

Fig. 1



Plasma concentration–time profiles of *R*-mephobarbital (a), *S*-mephobarbital (b) and phenobarbital (c) after an oral 200-mg dose of racemic mephobarbital to the homo-EM ($n = 9$, open circles), hetero-EM ($n = 10$, closed circles) and PM groups of CYP2C19 ($n = 11$, closed triangles). Data are expressed as mean ± SD. MPB, mephobarbital; PB, phenobarbital.

Table 2 Pharmacokinetic parameters of *R*- and *S*-mephobarbital and phenobarbital obtained from the homo-EM, hetero-EM and PM groups of CYP2C19

Parameters	Homo EM ($n = 9$)	Hetero EM ($n = 10$)	PM ($n = 11$)
R-mephobarbital			
C_{max} (μg/ml)	0.3 ± 0.1	0.4 ± 0.3	1.0 ± 0.2***,†††
T_{max} (h)	1.3 ± 0.6	2.0 ±1.6	20.6 ± 13.0***,†††
AUC (μg/h/ml)	1.5 ± 0.3	6.6 ± 10.7	138.0 ± 37.5***,†††
$t_{1/2}$ (hr)	3.6 ± 1.5	6.8 ± 5.4	87.8 ± 19.9***,†††
CL/F (ml/h/kg)	1131.7 ± 286.7	730.2 ± 479.5*	12.2 ± 3.2***,††
S-mephobarbital			
C_{max} (μg/ml)	0.9 ± 0.2	0.8 ± 0.2	0.7 ± 0.2
T_{max} (h)	8.4 ± 9.1	10.6 ± 9.7	6.6 ± 8.7
AUC (μg/h/ml)	100.9 ± 20.0	113.7 ± 59.7	73.9 ± 36.2
$t_{1/2}$ (h)	76.4 ± 31.5	84.6 ± 37.1	68.7 ± 37.3
CL/F (ml/h/kg)	17.0 ± 3.7	16.0 ± 5.5	25.2 ± 9.8*,†
Phenobarbital			
C_{max} (μg/ml)	0.5 ± 0.2	0.7 ± 0.6	1.5 ± 0.4***,††
T_{max} (h)	128.0 ± 48.0	134.4 ± 49.6	139.6 ± 66.0
AUC (μg/h/ml)	184.4 ± 59.0	233.4 ± 164.2	519.2 ± 208.8***,††
$t_{1/2}$ (h)	184.0 ± 63.6	185.8 ± 93.2	143.3 ± 34.2

Data are expressed as means ± SD.
The mean kinetic data on *R*-mephobarbital are estimated from the data obtained from five homo-EMs and nine hetero-EMs.
*$P < 0.05$; and ***$P < 0.001$ versus homo-EM group.
†††$P < 0.001$; ††$P < 0.01$; and †$P < 0.05$ versus hetero-EM group.

obtained from the remaining five homo-EMs and nine hetero-EMs.

The mean plasma concentration–time curves of *S*-MPB (Fig. 1b) also indicated an intergenotypic difference in the CYP2C19 status. The mean plasma *S*-MPB concentrations at 96 to 288 h postdose were lower in the PM group than in the EM (homo- and hetero-) groups, implying that the elimination of *S*-MPB is considerably accelerated in the PM group. However, the mean plasma concentrations up to 48 h postdose revealed no differences among the three groups.

The plasma concentration–time profile of PB (Fig. 1c) showed a trend similar to that of *R*-MPB (Fig. 1a). There were the intergenotypic differences in the mean plasma PB concentrations between the PM and EM (homo- and hetero-) groups from 24 to 480 h postdose.

Pharmacokinetic analyses of *R*-MPB, *S*-MPB and PB versus CYP2C19 genotypes

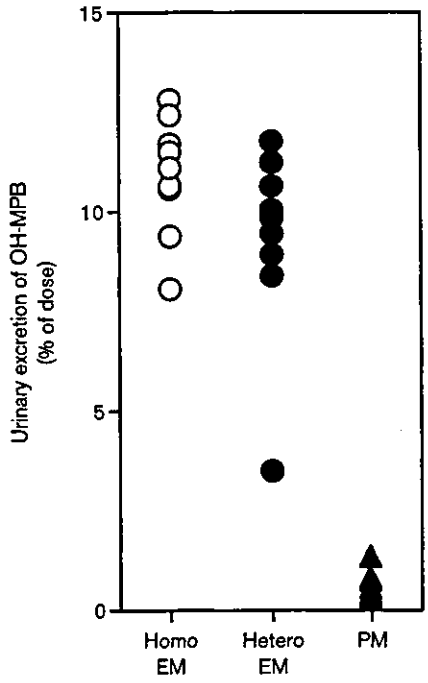
The mean (± SD) pharmacokinetic data obtained from the three different genotypic groups are summarized in Table 2. There was a highly significant ($P < 0.001$) intergenotypic difference between the homo-EM and

PM groups in the mean kinetic parameters of *R*-MPB (Table 2). The mean C_{max}, T_{max}, AUC, $t_{1/2}$ and CL/F values were three-fold higher, 16-fold longer, 92-fold greater, 24-fold longer and 93-fold smaller, respectively, in the PM than in the homo-EM group. The mean kinetic values for PB showed similar differences between the PM and homo-EM groups as observed with *R*-MPB. The mean C_{max} and AUC values were significantly ($P < 0.001$) greater in the PM than in the homo-EM group. On the other hand, the mean kinetic data on *S*-MPB showed a behaviour opposite to those on *R*-MPB and PB. The mean AUC and $t_{1/2}$ were smaller and shorter, respectively, in the PM than in the homo-EM group, although the differences did not reach statistical significance. However, the mean CL/F value was significantly ($P < 0.05$) greater in the PM than in the homo-EM group.

Urinary excretion of OH-MPB versus CYP2C19 genotypes

The individual urinary excretion data of OH-MPB derived from the 0 to 24-h postdose period in the homo-EM, hetero-EM and PM groups are shown in Fig. 2. The mean (± SD) cumulative excretion at 24 h postdose was 10.9 ± 1.5% in homo-EMs, 9.5 ± 2.3% in hetero-EMs and 0.53 ± 0.31% in PMs. A subject (#12) with hetero-EM genotype (Table 1) showed a lower urinary excretion of OH-MPB (3.5% of dose) than the other subjects with the same hetero-EM genotype of CYP2C19 (8.4 to 11.7% of dose). PB was unmeasurable in urine samples of any of the subjects collected up to 24 h postdose.

Fig. 2



Individual data on urinary excretion of 4'-hydroxymephobarbital (% of dose) measured in 0 to 24 h after an oral 200-mg dose of racemic mephobarbital to the homo-EMs ($n = 9$, open circles), hetero-EMs ($n = 10$, closed circles) and PMs of CYP2C19 ($n = 11$, closed triangles). OH-MPB, 4'-hydroxymephobarbital.

R/S metabolic ratio for MPB

The mean (± SD) ratio of AUC for *R*-MPB to that for *S*-MPB (*R/S* metabolic ratio for AUC), was markedly greater in the PM than in the homo-EM group of CYP2C19 (2.069 ± 0.610 versus 0.014 ± 0.003). Subject 12, with the CYP2C19 hetero-EM genotype (Table 1) showed a greater *R/S* metabolic ratio for AUC than the ranging values observed in the other subjects with hetero-EM (0.543 versus 0.013–0.042). The mean *R/S* ratio for AUC in the hetero-EM group (0.023 ± 0.012), except for subject 12, was higher than that in the homo-EM and lower than that in the PM group.

CYP2B6 genotyping

Genotyping for six *CYP2B6* alleles was carried out in all 30 subjects recruited in this study (Table 1). The frequencies of *CYP2B6*2*, *CYP2B6*3*, *CYP2B6*4*, *CYP2B6*5*, *CYP2B6*6* and *CYP2B6*7* alleles were 10.0, 0, 6.7, 0, 23.3 and 0%, respectively. The present study showed a frequency pattern similar to the previous study performed in a Japanese population by Hiratsuka *et al.* [15].

PB formation index versus CYP2B6

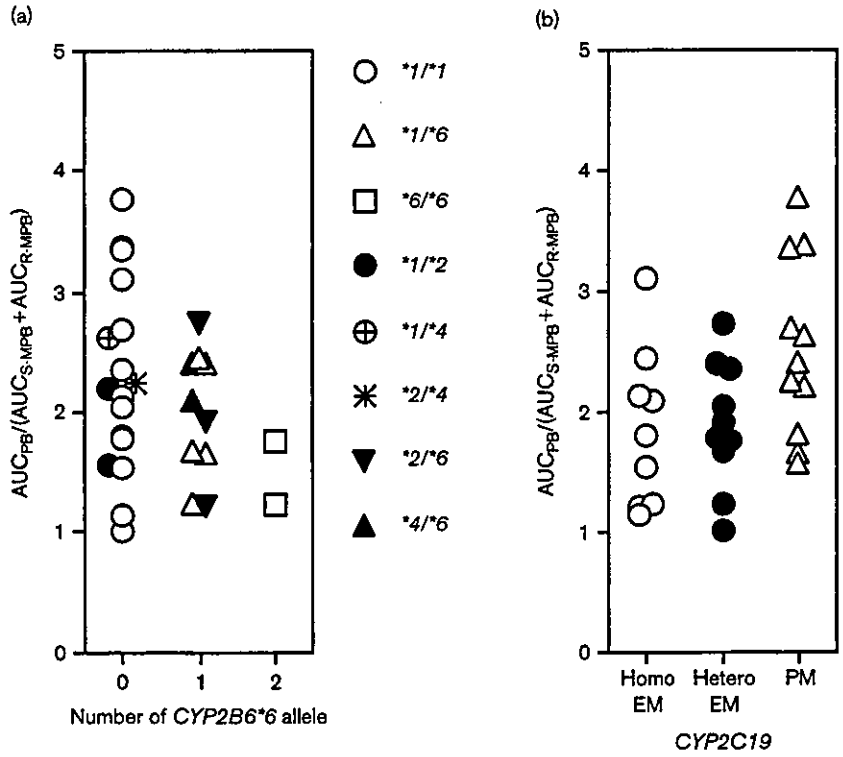
To investigate the possible effect of *CYP2B6* alleles (*CYP2B6*2*, *CYP2B6*4* and *CYP2B6*6*) on the PB formation from MPB, the metabolic ratio (MR) of $AUC_{PB}/(AUC_{S\text{-MPB}} + AUC_{R\text{-MPB}})$ was calculated and used as a CYP2B6 metabolic activity index. As shown in Fig. 3a, the individuals carrying one or two *CYP2B6*6* alleles tended to have a lower MR in light of the MR in the individuals who are the *CYP2B6*6* non-carriers, although the differences among the 0, 1 and 2 *CYP2B6*6* carrier groups were not statistically significant. The mean MR of the individuals carrying one *CYP2B6*2* or one *CYP2B6*4* allele did not differ from that in all other subjects without carrying *CYP2B6*2* or *CYP2B6*4* allele.

The MR of $AUC_{PB}/(AUC_{S\text{-MPB}} + AUC_{R\text{-MPB}})$ was also compared among the three different *CYP2C19* genotype (homo-EM, hetero-EM and PM) groups. As shown in Fig. 3b, the mean MR in the PM group of CYP2C19 (2.5 ± 0.7) was significantly ($P < 0.05$) higher than that in the homo-EM (1.9 ± 0.7, by Mann–Whitney *U*-test) or hetero-EM group (1.9 ± 0.5, by Student's *t*-test).

Discussion

The present study indicated that the $t_{1/2}$ and AUC of *R*-MPB after an oral intake of racemic MPB was

Fig. 3



(a) Individual data on AUC ratio in carriers of two *CYP2B6*6* alleles ($n = 2$) and one *CYP2B6*6* allele ($n = 10$) and non-carriers of *CYP2B6*6* allele ($n = 18$). (b) Individual data on AUC ratio in homo-EMs ($n = 9$), hetero-EMs ($n = 10$) and PMs of CYP2C19 ($n = 11$). Area under the plasma concentration–time curve, AUC; AUC_{PB}, AUC for phenobarbital; $AUC_{S\text{-}MPB}$, AUC for *S*-mephobarbital; and $AUC_{R\text{-}MPB}$, AUC for *R*-mephobarbital.

markedly longer and greater (Fig. 1 and Table 2) in the PM group than in the (homo- and hetero-) EM groups of CYP2C19, respectively, and the urinary excretion of OH-MPB in the PM group of CYP2C19 was 21-fold lower than that in the EM groups (Fig. 2). Küpfer and Branch [4] reported that the urinary recovery of OH-MPB after the oral administration of racemic MPB was not detected in the PMs of CYP2C19, but that OH-MPB in urine was recovered in an EM administered *R*-MPB. In addition, our *in vitro* study demonstrated that the 4′-hydroxylation of MPB is preferential for *R*-enantiomer and its reaction is catalyzed by CYP2C19 [6]. Therefore, the findings obtained from the present *in vivo* study strongly indicate that the 4′-hydroxylation of *R*-MPB in humans *in vivo* is mainly catalyzed by CYP2C19 and this pathway of *R*-MPB is impaired in the PM individuals of CYP2C19.

On the other hand, the AUC of *S*-MPB in the PM group of CYP2C19 did not significantly differ from that in the EM groups of CYP2C19 (Table 2). The results obtained from the present *in vivo* study are consistent with the *in vitro* observation that *R*-MPB is 4′-hydroxylated by CYP2C19, but the metabolism of *S*-MPB is not catalyzed by CYP2C19 [6], in agreement with the *in vivo* observation that OH-MPB in urine was not recovered in an EM of CYP2C19 administrated only *S*-MPB [4]. Therefore, it is suggested that CYP2C19 is not responsible for the elimination of *S*-MPB from the human body.

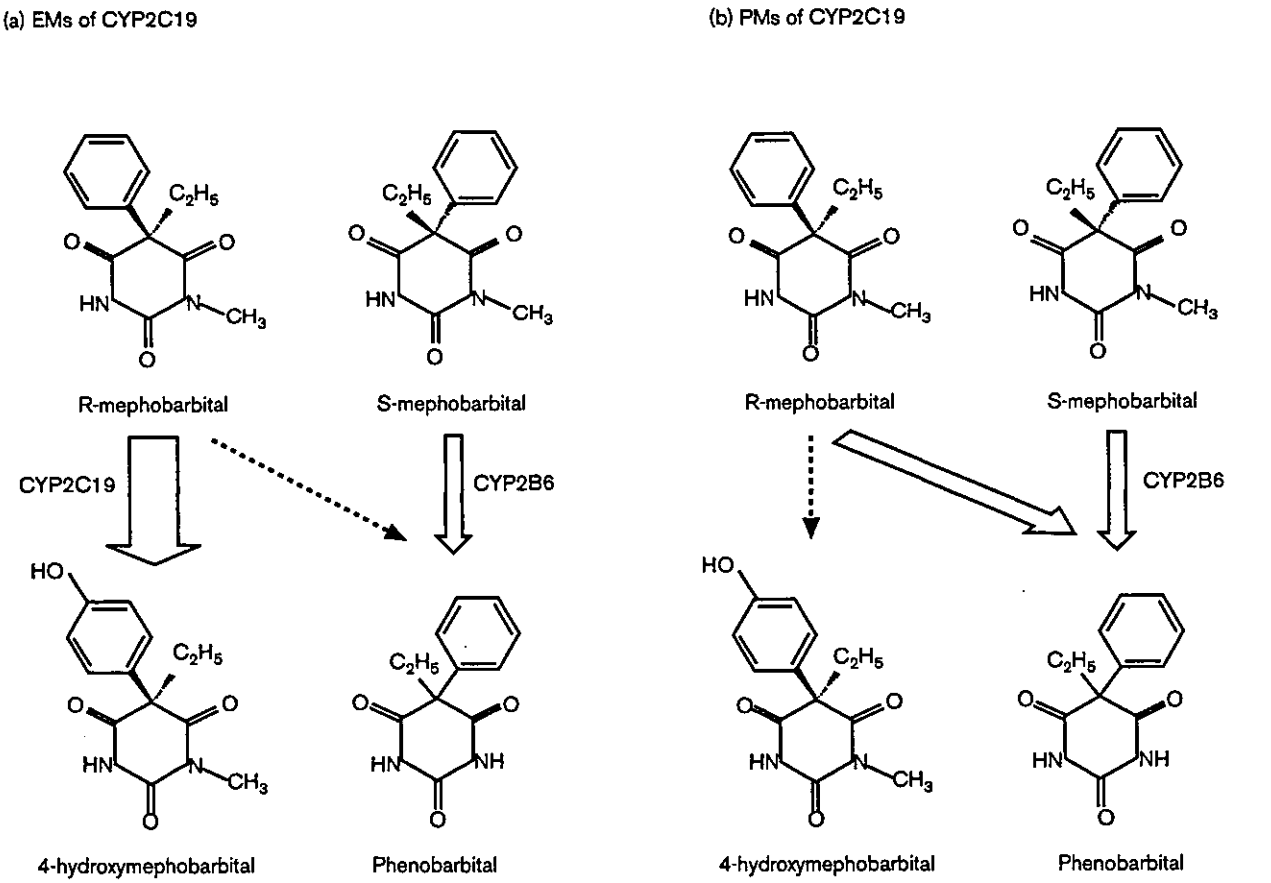
As shown in Fig. 2, one data point derived from subject 12 (Table 1) deviated from the other data plots of the hetero-EMs, and, therefore, this hetero-EM individual was assumed to be an outlier in the group. The results suggested that subject 12, who was genotyped as *2C19*1/2C19*2* (Table 1), might have been a poor or low metabolizer of *R*-MPB, such as a PM of CYP2C19. To our knowledge, previous studies indicated that the two mutant alleles of *CYP2C19*, *CYP2C19*2* and *CYP2C19*3*, explain 100% of the PMs in the Japanese population [14]. To confirm the possibility that subject 12 may carry a novel mutant allele of *CYP2C19* in addition to *CYP2C19*2* allele, we sequenced all nine exons and exon–intron junctions of *CYP2C19* gene from the outlier and finally identified a novel SNP as *CYP2C19*16* [16].

One of the primary metabolites of MPB, PB, showed higher plasma levels in the PMs than in EMs of

CYP2C19 (Fig. 1 and Table 2). Our preliminary results from the *in vitro* experiments with human liver microsomes indicated that the formation of PB (i.e. via *N*-demethylation of MPB) occurred in a less stereoselective fashion and to a similar extent between the CYP2C19 EM- and PM-related liver microsomes (unpublished data), providing the following possibilities: (1) since *R*-MPB was extensively 4'-hydroxylated and rapidly eliminated in the EM individuals, PB should exclusively be formed from *S*-MPB; (2) in the PMs with the defective 4'-hydroxylation of *R*-MPB, *R*-MPB would be more available for the alternative route of metabolism by *N*-demethylation; and (3) if both *R*-MPB and *S*-MPB are presumed to contribute to the PB formation, plasma concentrations of PB should be higher in the PM than in the EM group. Nevertheless, no clinical signs and symptoms (e.g. sedation) possibly attributed to the administration of MPB were recognizable throughout the present study period in either of the EM or PM subjects of CYP2C19. This might occur because plasma concentrations of MPB and PB (i.e. <3 μg/ml) were much lower than therapeutic levels (i.e. for PB, 15 to 40 μg/ml is the therapeutic window). On the basis of the overall results obtained from the present study, we wish to propose a scheme of the assumptive metabolic pathways (i.e. via 4'-hydroxylation and *N*-demethylation) of MPB enantiomers and CYP isoforms involved in their pathways in EMs and PMs of CYP2C19 (Fig. 4).

Previously, Eadie *et al.* [17] reported that patients who were pretreated with PB showed a greater clearance of MPB (due probably to an induction by PB) and a rapid appearance of PB after administration of MPB than did the untreated patients. Since *S*-MPB is primarily metabolized to PB by CYP2B6 [7], pretreatment with PB

Fig. 4



Proposed scheme of metabolic pathways of mephobarbital enantiomers and CYP isoforms involved in their pathways in EMs and PMs of CYP2C19. The thicknesses of open arrows indicate an assumptive degree of each of the two enzymes involved in the metabolic pathways of the two enantiomers of mephobarbital. The solid arrows with the dotted lines indicate a minor metabolic pathway of *R*-mephobarbital in the CYP2C19 EM and PM individuals. Whether *R*-mephobarbital would be metabolized to phenobarbital in humans and what CYP enzyme(s) would be involved in this pathway have remained unknown, although the authors have had their preliminary *in vitro* data with human liver microsomes, suggesting that *R*-mephobarbital is converted to phenobarbital (see Discussion).

would induce CYP2B6, thereby resulting in an accelerated elimination of *S*-MPB and production of PB. In this study, the PM group of CYP2C19 showed a slightly rapid elimination of *S*-MPB compared with the EM groups of CYP2C19 (Fig. 1b). In addition, the MR of $AUC_{PB}/(AUC_{S\text{-}MPB} + AUC_{R\text{-}MPB})$ was also higher in the PMs than in the EMs of CYP2C19 (Fig. 3b). These observations might have been due to an induction of CYP2B6 by PB, because the PM group of CYP2C19 had about three-fold higher plasma levels of PB than the EM groups (Fig. 1c).

Although the MR of $AUC_{PB}/(AUC_{S\text{-}MPB} + AUC_{R\text{-}MPB})$ was used for the metabolic index of MPB mediated via CYP2B6, no apparent outliers were observed (Fig. 3a). Among the six different *CYP2B6* alleles examined, only *CYP2B6*6* appeared to be associated with a moderately decreased MR, but due to the small sample size this difference did not reach statistical significance among the zero, one and two *CYP2B6*6* carriers. In the analysis of the *CYP2B6*6* allele in microsomes of human liver samples, a lower protein expression of CYP2B6.6, which was encoded by *CYP2B6*6*, has been reported [9,10]. On the other hand, V_{max} of recombinant CYP2B6.6 was higher than that of recombinant CYP2B6.1 [18,19]. Thus, the findings for the functional role of CYP2B6.6 obtained from the *in vitro* studies remain conflicting or inconclusive, but the lower protein expression would be compatible with our *in vivo* data. Since the subjects carrying *CYP2B6*2* or *CYP2B6*4* allele were rare and homozygotes of these alleles did not exist in our study subjects, further study is needed to assess whether *CYP2B6*2* and/or *CYP2B6*4* alleles would affect the MR. Moreover, Lamba *et al.* [11] have recently reported two new additional alleles of *CYP2B6* gene, *CYP2B6*8* and *CYP2B6*9*. Since *CYP2B6*6* (516G>T and 785A>G) overlapped with *CYP2B6*4* (785A>G) and *CYP2B6*9* (516G>T), it is not negated that some of our subjects genotyped as *2B6*1/2B6*6* in the present study might be carrying a genotype of *2B6*4/2B6*9*. However, *CYP2B6*9* has not yet been detected in Japanese population [15].

In conclusion, the present *in vivo* study strongly suggests that the 4′-hydroxylation of *R*-MPB is mediated via CYP2C19 in humans and that the stereoselective 4′-hydroxylation by this enzyme results in a marked difference in the pharmacokinetic profiles of *R*-MPB and *S*-MPB between the EM and PM individuals of CYP2C19. In addition, *CYP2B6*6* carriers tended to have a lower MR compared with that in other *CYP2B6*6* allele non-carriers, suggesting that a minor fraction of the interindividual variability in PB formation from MPB may be explainable by the absence or presence of *CYP2B6*6* allele.

Acknowledgement

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Short Communication

CATALYTIC ROLES OF CYP2C9 AND ITS VARIANTS (CYP2C9*2 AND CYP2C9*3) IN LORNOXICAM 5′-HYDROXYLATION

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ABSTRACT:

The effects of allelic variants of CYP2C9 (*CYP2C9*2* and *CYP2C9*3*) on lornoxicam 5′-hydroxylation were studied using the corresponding variant protein expressed in baculovirus-infected insect cells and human liver microsomes of known genotypes of CYP2C9. The results of the baculovirus expression system showed that CYP2C9.3 gives higher K_m and lower V_{max} values for lornoxicam 5′-hydroxylation than does CYP2C9.1. In contrast, K_m and V_{max} values of CYP2C9.1 and CYP2C9.2 for the reaction were comparable. Lornoxicam 5′-hydroxylation was also determined in liver microsomes of 12 humans genotyped for the *CYP2C9* gene (1/*1*, n = 7; **1/*2*, n = 2; **1/*3*, n = 2; **3/*3*, n = 1). A sample genotyped as **3/*3* exhibited 8- to 50-fold lower intrinsic clearance for lornoxicam 5′-hydroxylation than did samples genotyped as **1/*1*. However, the values for intrinsic clearance for **1/*3* were within the range of values exhibited by samples of **1/*1*. In addition, no appreciable differences were observed in kinetic parameters for lornoxicam 5′-hydroxylation between **1/*1* and **1/*2*. In conclusion, this study showed that lornoxicam 5′-hydroxylation via CYP2C9 was markedly decreased by the substitution of Ile359Leu (CYP2C9.3), whereas the effect of the substitution of Arg144Cys (CYP2C9.2) was nonexistent or negligible. Additional in vivo studies are required to confirm that individuals with homologous *CYP2C9*3* allele exhibit impaired lornoxicam clearance.**

Lornoxicam (also known as chlortenoxicam) [6-chloro-4-hydroxy-2-methyl-*n*-2-pyridyl-5*H*-thieno(2,3-*e*)-[1,2]-thiazine-2-carboxamide-1,1-dioxide] is a nonsteroidal anti-inflammatory drug that decreases prostaglandin synthesis by inhibiting cyclooxygenase (Radhofer-Welte and Rabasseda, 2000). Exhibiting analgesic, antipyretic, and anti-inflammatory effects, lornoxicam has been clinically available in certain European countries since 1995. Since no unchanged form is detectable in excreted material, lornoxicam appears to be eliminated predominantly by hepatic biotransformation. The enzyme responsible for the main metabolic pathway, 5′-hydroxylation of lornoxicam, is cytochrome P450 2C9 (CYP2C9) (Bonnabry et al., 1996).

CYP2C9 is the principal enzyme responsible for the metabolism of numerous clinically important drugs, such as amitriptyline, fluoxetine, losartan, phenytoin, *S*-warfarin, tolbutamide, and many nonsteroidal antirheumatics, including oxicams (Miners and Birkett, 1998). To date, more than 10 allelic variants have been described for the *CYP2C9* gene (Goldstein, 2002). Among them, *CYP2C9*2* (Arg144Cys), *CYP2C9*3* (Ile359Leu), *CYP2C9*5* (Asp360Glu), and *CYP2C9*6* (frame shift by the deletion of an adenine at the 818 cDNA base pair) have been reported to affect the metabolism and clinical toxicity of drugs in vitro and in vivo (Dickmann et al., 2001; Kidd et al., 2001). However, the degree of reduction of activity and changes in kinetic parameters appear to be highly substrate-dependent (Takanashi et al., 2000). In addition, a few studies have been performed regarding whether heterozygotes of the *CYP2C9* alleles exhibit lower metabolic activity than homozygotes of the *CYP2C9*1* allele (Bhasker et al., 1997; Yamazaki et al., 1998; Hermida et al., 2002; Lee et al., 2002).

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In the present study, we examined the effects of allelic variants of CYP2C9 on lornoxicam 5′-hydroxylation by comparing the kinetic parameters of lornoxicam 5′-hydroxylation with CYP2C9.1, CYP2C9.2, or CYP2C9.3, which are the CYP2C9 proteins corresponding to *CYP2C9*1*, *CYP2C9*2*, or *CYP2C9*3* alleles, expressed in baculovirus-infected insect cells and liver microsomes of 12 white people genotyped for the *CYP2C9* gene.

Materials and Methods

Chemicals. Lornoxicam was synthesized at Taisho Pharmaceutical Co., Ltd. (Saitama, Japan). 5′-Hydroxylornoxicam was supplied by Nycomed (Roskilde, Denmark). Piroxicam was purchased from ICN Biomedicals Inc. (Costa Mesa, CA). Other chemicals and reagents used in this study were of the highest quality commercially available.

Enzyme Preparations. Microsomes from baculovirus-infected insect cells expressing CYP2C9.1, CYP2C9.2, and CYP2C9.3 (catalog numbers, P218, P209, and P242) were obtained from BD Gentest (Woburn, MA). These were coexpressed with NADPH-P450[1] oxidoreductase. The P450 contents in recombinant CYP2C9.1, CYP2C9.2, and CYP2C9.3 were 667, 426, and 741 pmol P450/mg protein, whereas the values for the cytochrome *c* reductase activity were 980, 590, and 800 nmol/min/mg protein, respectively. Individual human liver microsomes (HG3, HG23, HG30, HG42, HG43, HG56, HG66, HG70, HG89, HG93, HG112, and HK27) were also purchased from BD Gentest. The genotyping of the liver samples used in this study was carried out for the detection of *CYP2C9*2* and *CYP2C9*3* by BD Gentest. Table 1 lists the donor genotypes for the *CYP2C9* gene.

Lornoxicam 5′-Hydroxylase Activity. Lornoxicam 5′-hydroxylase activities in human liver microsomes or microsomes from the expression system were determined by HPLC. The standard incubation conditions were chosen based on the results of preliminary experiments varying both incubation times and concentrations of microsomal proteins. A typical incubation mixture (0.2 ml of the total volume) contained 100 mM Tris buffer (pH 7.4), an NADPH-

[1] Abbreviations used are: used are: P450, cytochrome P450; HPLC, high performance liquid chromatography.

TABLE 1

Kinetic parameters for 5'-hydroxylornoxicam formation from lornoxicam in cDNA-expressed CYP2C9 recombinant systems and human liver microsomes

	K_m	V_{max}	V_{max}/K_m
	μM	*pmol/min/pmol total P450*	*μl/min/pmol total P450*
cDNA-expressed CYP2C9 recombinant systems			
CYP2C9.1	0.83 ± 0.15[a]	0.406 ± 0.016	0.489 ± 0.065
CYP2C9.2	0.91 ± 0.08	0.495 ± 0.010[b]	0.544 ± 0.041
CYP2C9.3	1.95 ± 0.09[b]	0.097 ± 0.001[b]	0.050 ± 0.002[b]
Human liver microsomes			
HG23 **1/*1*	0.79	0.256	0.324
HG30 **1/*1*	0.81	0.278	0.343
HG42 **1/*1*	1.28	0.069	0.054
HG66 **1/*1*	0.76	0.142	0.187
HG70 **1/*1*	0.77	0.189	0.245
HG89 **1/*1*	0.66	0.168	0.255
HG112 **1/*1*	1.08	0.182	0.169
HG43 **1/*2*	0.83	0.106	0.128
HG56 **1/*2*	0.81	0.115	0.142
HG3 **1/*3*	0.72	0.143	0.199
HG93 **1/*3*	1.72	0.145	0.084
HK27 **3/*3*	2.82	0.019	0.007

[a] Kinetic parameters expressed as mean ± SD (n = 3).
[b] $p < 0.05$ vs. CYP2C9.1.

generating system (1 mM $NADP^+$, 8 mM glucose 6-phosphate, 5 mM $MgCl_2$, 2 IU/ml glucose-6-phosphate dehydrogenase), lornoxicam, and 0.25 mg/ml microsomal protein of human livers. The reaction was initiated by the addition of the microsomes after 5-min preincubation at 37°C. The reaction mixtures were incubated for 20 min, and reactions were terminated by the addition of 0.1 ml of acetonitrile, including 3 μM piroxicam as an internal standard. After removal of the protein by centrifugation at 10,000 rpm for 5 min, a 10-μl portion of the supernatant was subjected to HPLC. For recombinant P450s, the incubation mixture was of the same composition as mentioned above, except that 25, 25, or 200 pmol P450/ml, respectively, were used for microsomes from baculovirus-infected insect cells expressing CYP2C9.1, CYP2C9.2, or CYP2C9.3. For kinetic determinations, lornoxicam concentrations ranging from 0.5 to 125 μM were used.

HPLC analyses were performed according to the method of Suwa et al. (1993), with slight modifications. The HPLC system consisted of a 2690 separation module Alliance system equipped with a Millennium32 chromatointegrator and a 2487 dual λUV-visible spectrophotomonitor (Waters, Tokyo, Japan). Chromatography was performed on an XTerra RP18 column (50 × 2.1 mm; particle size = 3.5 μm; Waters) eluted at 0.2 ml/min with the following mobile phase: 14.5% acetonitrile, 50 mM KH_2PO_4. The eluent was monitored at 380 nm. The column temperature was 60°C.

Statistical Analysis. All experiments were performed in triplicate, and the mean values for each data point were used for analysis. Enzyme kinetic parameters (K_m, V_{max}) were estimated by curve-fitting metabolite formation rate data by the single-enzyme Michaelis-Menten equation and Eadie-Hofstee plot. All graphical analyses were performed by nonlinear regression using SAS Version 6.1 (SAS Institute, Cary, NC). Differences in kinetic parameters among different *CYP2C9* genotypes were evaluated for statistical significance by Dunnett's multiple comparison.

Results and Discussion

Figure 1A shows the formation of 5'-hydroxylornoxicam by recombinant systems prepared from the cell line expressing the variants of CYP2C9. Simple Michaelis-Menten kinetics were noted for lornoxicam metabolism in all samples studied. The kinetic parameters of lornoxicam 5'-hydroxylation for CYP2C9.1, CYP2C9.2, and CYP2C9.3 are shown in Table 1. CYP2C9.3 (Leu359) had higher K_m values and lower V_{max} than did CYP2C9.1 (wild-type, Ile359) for lornoxicam 5'-hydroxylation. The differences in K_m and V_{max} values between CYP2C9.1 and CYP2C9.3 were about 2- and 4-fold, respectively.

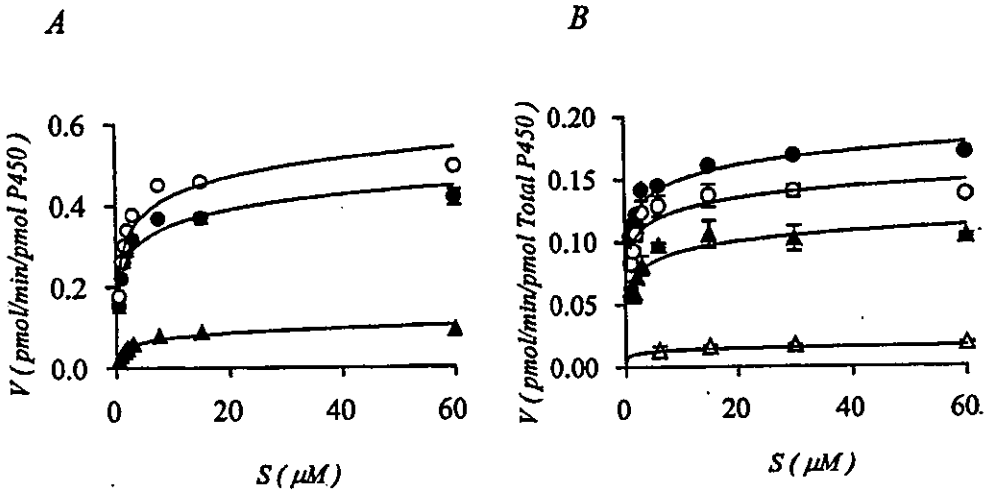

FIG. 1. *Michaelis-Menten plots for 5'-hydroxylation of lornoxicam by cDNA-expressed CYP2C9.1 (●), CYP2C9.2 (○), and CYP2C9.3 (▲) (A), and representative Michaelis-Menten plots for 5'-hydroxylation of lornoxicam by human liver microsomes from four genotyped livers (B).*

In A, results are expressed as mean ± S.D. of triplicate experiments. In B, liver microsomes of HG89 (●, genotyped as **1/*1*), HG3 (▲, genotyped as **1/*2*), HG43 (○, genotyped as **1/*3*), and HK27 (△, genotyped as **3/*3*) were used for the plots.

In terms of intrinsic clearance (V_{max}/K_m, the intrinsic capacity of an enzyme to metabolize a substrate), the values for CYP2C9.3 showed 10-fold smaller V_{max}/K_m values for the reaction than did CYP2C9.1. This finding is in good agreement with a previous report of Takanashi et al. (2000) in which CYP2C9.3 expressed in yeast cells exhibited lower intrinsic clearance than did CYP2C9.1 for oxidation of other oxicams, such as tenoxicam 5′-hydroxylation and piroxicam 5′-hydroxylation. These results suggest that the amino acid substitution of Ile359 for Leu359 also affects the metabolic capacity of CYP2C9 in addition to the affinity of CYP2C9 for lornoxicam. The effect of this change on both the K_m and V_{max} values may be explained by the proposal that CYP2C9 amino acid 359 lies within putative substrate recognition sequence 5 in the CYP2 family (Lewis, 2002).

In contrast, K_m, V_{max}, and intrinsic clearance (V_{max}/K_m) of lornoxicam 5′-hydroxylation for CYP2C9.1 (wild-type, Arg144) and CYP2C9.2 (Cys144) expressed in baculovirus-infected insect cells were comparable (Table 1). There was no significant difference between CYP2C9.1 and CYP2C9.2 in V_{max}/K_m values for the reaction. This finding is consistent with previous reports that CYP2C9.2 has catalytic functions similar to those of CYP2C9.1 for the oxidation of tolbutamide, *S*-warfarin, and torsemide (Sullivan-Klose et al., 1996; Miners et al., 2000). However, Rettie et al. (1994) reported that the V_{max} values of the CYP2C9.2 for *S*-warfarin 7-hydroxylation were lower than that of CYP2C9.1. Crespi and Miller (1997) showed that the magnitude of the difference in V_{max} for *S*-warfarin between CYP2C9.1 and CYP2C9.2 depends on the expression system used, and is influenced by the ratio of NADPH-P450 oxidoreductase to P450. Thus, it is necessary to use human liver samples genotyped as **2/*2* to clarify the effect of the substitution of Arg144Cys for CYP2C9 on the activity in human liver microsomes.

We determined the kinetic parameters of lornoxicam 5′-hydroxylation from liver microsomes derived from 12 human samples genotyped for the *CYP2C9* gene. The formation of 5′-hydroxylornoxicam by human liver microsomes showed simple Michaelis-Menten kinetic behavior (Fig. 1B). Using Eadie-Hofstee plots, we confirmed that a single kinetic parameter could be determined in the reaction. As shown in Table 1, apparent K_m values for lornoxicam 5′-hydroxylation ranged from 0.76 to 1.28 μM in microsomes of livers genotyped as **1/*1*. The K_m values for liver microsomes of samples genotyped as **1/*2* or **1/*3* ranged from 0.72 to 1.72 μM. Only a microsome sample genotyped as **3/*3* exhibited a high K_m value (2.82 μM). The sample genotyped as **3/*3* exhibited a lower V_{max} value (0.019 pmol/min/pmol total P450) than the other samples genotyped as **1/*1*, **1/*2*, or **1/*3* (0.069–0.278 pmol/min/pmol total P450). Thus, samples genotyped as **3/*3* showed 8- to 50-fold lower intrinsic clearance (V_{max}/K_m, 0.007 μl/min/pmol total P450) than samples genotyped as **1/*1* and other heterozygous alleles of *CYP2C9* (0.054–0.343 μl/min/pmol total P450), although only one sample was genotyped as **3/*3*. The substitution of Ile359Leu for CYP2C9 also appears to decrease the intrinsic clearance of lornoxicam 5′-hydroxylation in human liver microsomes. In addition, the present study using human liver microsomes containing samples genotyped as **1/*2* or **1/*3* showed that the heterozygous alleles of *CYP2C9*2* or *CYP2C9*3* did not always have lower intrinsic clearance for lornoxicam 5′-hydroxylation than **1/*1*.

Rare cases of subjects with higher than expected plasma concentrations after the administration of lornoxicam have been reported (Turner and Johnston, 1990; Ravic et al., 1991). Since 5′-hydroxylation is the main metabolic pathway of lornoxicam in humans, it has been speculated that the increase in plasma concentrations is attributable to defective metabolism of lornoxicam. Our results indicate that it may be possible that certain subjects, exhibiting high area under the curve and C_{max} values associated with delayed elimination, are the poor-metabolizer phenotypes of CYP2C9, although their actual genotypes were unknown.

In conclusion, the present study showed that the lornoxicam 5′-hydroxylation via CYP2C9 was markedly reduced by the substitution of Ile359 for Leu359 (CYP2C9.3), whereas the effect of the substitution of Arg144 for Cys144 (CYP2C9.2) was nonexistent or negligible. Additional in vivo studies are required to confirm that individuals with the homologous *CYP2C9*3* allele exhibit impaired lornoxicam clearance.

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総説

薬物トランスポーターの遺伝的多型と臨床的意義

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〔SUMMARY〕 薬物の吸収，分布，排泄を規定する薬物トランスポーターが数多くクローニングされ，その発現部位，輸送方向性，基質薬物が明らかとされつつある．同時に遺伝子多型によるヒト生体中での機能評価ならびに個人差の解明が急ピッチで進んでいる．その結果，薬物トランスポーターは相互作用などを含む薬物療法全般に重要な役割を果たすことが指摘されるに至っている．薬物代謝酵素に加え薬物トランスポーターの遺伝子多型情報は個別適正化使用―オーダーメイド医療―を一歩前進させる情報と期待される．〔臨床検査　48：139-147，2004〕

〔KEYWORDS〕 薬物輸送蛋白，薬物トランスポーター，遺伝的多型，機能変化

はじめに

薬物の体内動態や効果に見る大きな個人差の原因が関与する蛋白をコードする遺伝子の多型から説明されつつある．その代表は，薬物代謝酵素であるが，代謝を受けるためには肝臓に薬物が運ばれる，すなわち分布する必要がある．近年，この分布のみならず，吸収や排泄過程に関与する薬物輸送蛋白(薬物トランスポーター)が数多く同定され，その機能が明らかにされるとともに，代謝酵素と同様にその機能の差が遺伝子多型から予測されようとしている．薬物トランスポーターの生体機能を考える場合には，その基質薬物，発現部位，輸送方向性が重要となる．本稿では，現在までに日本人を中心に詳細な遺伝子多型解析が行われ，その機能への関与が明らかとなった薬物トランスポーターを取り上げ，遺伝子多型診断に基づいた医薬品適正使用の一端を紹介する．

主な薬物トランスポーターの種類

薬物トランスポーターは，肝，腎，小腸などの消化管，脳，肺といった様々な組織の上皮細胞(あるいは血管内皮細胞)に発現し，薬物の生体膜輸送(取り込みや汲み出し)に重要な役割を果たしている．表1には，現在までにヒトで確認されている主な薬物トランスポーターをまとめた．薬物トランスポーターは，ABCトランスポーター(ATP binding cassette)と溶質トランスポーター(solute carrier superfamily；SLC)の2つに大別される．前者は，ATPの加水分解エネルギーを駆動力とし，細胞内から細胞外へ薬物を排出する．P-糖蛋白(P-gp，遺伝子名が*MDR1*)やMRP1，MRP2(別名cMOAT)などが代表的であり，癌細胞に見られる抗癌剤の多剤耐性の原因蛋白としてよく知られている．有機イオントランスポータースーパーファミリー(SLC22A)は有機アニオントランスポーター(OAT)，有機カチオントランスポーター(OCT)，カルニチントランスポーター(OCTN)の3種類のファミリーで構成されており，主に低脂肪性イオン薬物の細胞内への取り込み過程に関与する．一方，脂溶性の比較的高いアニオン性薬物の取り込みには，OATファミリーとは構造的にも異なるOATPファミリ

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