Table VI. Pharmacokinetic parameters of pravastatin after a single dose (10 mg) in various OATP-C genotypic patterns

	Polymorphism							
130	151	174	336	Genotype	No.			
Asn/Asn	Asn/Asn	Val/Val	Pro/Pro	OATP-C*la/*la	2			
Asn/Asp	Asn/Asn	Val/Val	Pro/Pro	OATP-C*1a/*1b	4			
Asp/Asp	Asn/Asn	Val/Val	Pro/Pro	OATP-C*1b/*1b	4			
Asp/Asp	Asn/Asn	Val/Ala	Pro/Pro	OATP-C*1b/*15	9			
Asp/Asp	Asn/Asn	Ala/Ala	Pro/Pro	OATP-C*15/*15	1			
Asn/Asp	Asn/Ser	Val/Val	Pro/Pro	OATP-C*1b/*16	2			
Asp/Asp	Asn/Asn	Val/Ala	Pro/Arg	Unidentilled	- 1			

AUC, Area under concentration-time curve; CL_u , total clearance; CL_{uv} , nonrenal clearance; k_u , terminal rate constant for elimination. †SignilCantly different from values in $OATP-C^*1b/^*1b$ subjects as determined by Mann-Whitney U test (P < .05).

race and that most Japanese subjects who have a Val174Ala polymorphism also have an Asn130Asp polymorphism simultaneously.

Genetic variations have been examined in some transporter genes such as MDR1 (multidrug resistance 1), MRP1 (multidrug resistance protein 1), MRP2 (multidrug resistance protein 2), and OATP-8. The numbers of nonsynonymous SNPs in MDR1, MRP1, MRP2, and OATP-8 genes were reported to be 4, 4, 4, and 2, respectively, with allelic frequencies ranging from 21.8% to 49.0%, 1% to 7.3%, 1% to 12.5%, and 55% to respectively, among healthy Japanese subjects.32-34 Although the data for these transporter genes are not sufficient for conclusions to be made, it appears that nonsynonymous SNPs in the OAT3 gene (only one nonsynonymous with an allelic frequency of <1% in this study) occur at a lower frequency than these genes, including OATP-C. These observations are consistent with a recent Unding of a lower frequency of nonsynonymous SNPs in the OCT2 (organic cation transporter 2) gene.35 Similar to OAT3, the OCT2 protein is located on the basolateral membrane of the proximal tubule epithelium and is suggested to govern the entry of organic cations from the blood into the renal tubule, thereby controlling the Urst step in renal secretion of organic cations. Thus, as has been suggested for OCT2, OAT3 may also be relatively intolerant of nonsynonymous changes.35

In vivo phenotypic data on the most common non-synonymous variant revealed functional differences between subjects with the OATP-C reference and the variant. Subjects with the OATP-C*15 allele had signill cantly lower Cl_t and Cl_{nr} values than did those with a reference form of OATP-C (ie, *1a and *1b alleles), suggesting a functional consequence of the *15 allele in the pharmacokinetics of pravastatin. Hepatic clearance of pravastatin is rate-limited by uptake. ^{11,31} The hepatic

uptake clearance of pravastatin determined in vivo by integration plot analysis was comparable to the blood low rate, suggesting high extraction in the liver during a single pass. 5 Thus low transport activity of OATP-C may lead to a reduction in hepatocellular uptake of pravastatin, resulting in lower total clearance. In addition, the possibility of an increasing F cannot be negated. Although the net in vivo effect of reduced transport activity on the overall pharmacokinetics of pravastatin remains unclear, these pharmacokinetic data from the subjects with the *15 allele are consistent with previous in vitro Undings showing that the Ala174 variant (OATP-C*5) signilicantly reduced estrone sulfate and estradiol-17β-D-glucuronide transport activity by using OATP-C variants generated in HeLa cells. 15 In vitro intrinsic clearance was markedly lower for the OATP-C*5 variant than for the reference allele (OATP-C*1b), with a mean reduction rate of 75%. 15 These values were found to be very close to those in our healthy volunteers (35%-60%). It should be noted that Val174Ala is present in OATP-C*5 and *15, and the only difference between these 2 alleles is the presence of Asn130Asp in OATP-C*15. In contrast, the effect of the *1b allele (Asp130) did not appear as evident as that of the *15 allele. The absence of functional changes in the *1b allele is consistent with previous in vitro Undings reported from 3 independent laboratories. 15-17 Nevertheless, caution must be taken with regard to the in vivo effects of Asn130Asp, because amino acid substitutions in extracellular loop 2 of the OATP-C are presumed to affect substrate specificity. The Asn130Asp variant is located in extracellular loop 2.

One subject with the Arg336 variant had a high AUC value and low values for CL_t and CL_{nr} of pravastatin. Tirona et al¹⁵ reported that all polymorphisms that localized to the putative transmembrane-spanning domain (MSD) were associated with a signil cant reduc-

AUC (ng·h/mL)	$(L \cdot kg^{-1} \cdot h^{-1})$	$CL_r \\ (L \cdot kg^{-I} \cdot h^{-I})$	$CL_{nr} (L \cdot kg^{-1} \cdot h^{-1})$	$CL_{sec} (L \cdot kg^{-I} \cdot h^{-I})$	k_e (h^{-1})
60.5	2.66	0.44	2.22	0.29	0.171
47.2 ± 27.4	1.95 ± 0.72	0.51 ± 0.12	1.45 ± 0.72	0.40 ± 0.12	0.279 ± 0.093
44.2 ± 6.38	2.39 ± 0.44	0.38 ± 0.03	2.01 ± 0.42	0.25 ± 0.03	0.312 ± 0.090
62.1 ± 21.8	$1.57 \pm 0.32 \dagger$	0.46 ± 0.13	$1.11 \pm 0.34 \dagger$	0.34 ± 0.12	0.255 ± 0.091
111.8	0.79	0.51	0.28	0.37	0.212
60.0	2.55	0.43	2.12	0.31	0.260
110.3	1.22	0.41	0.81	0.30	0.213

tion in transporting activity. The Pro336Arg variant is localized within MSD7.

As shown in Fig 1, mean serum concentration-time curves of pravastatin were different among the 3 genotypic groups. There was, however, a relatively large intergenotypic variability, particularly for the heterozygous carriers. These results indicate that unidentilled factors may also contribute to the overall pharmacokinetics of pravastatin. Tamai et al³⁶ reported that pravastatin was weakly but signilicantly taken up by HEK293 cells transfected with OATP-B, another member of the OATP family expressed in human hepatocytes. In addition, some transporters may be involved in oral absorption of pravastatin.³⁷ These Indings suggest that the multitransporter-mediated transport is involved in the distribution and disposition kinetics of pravastatin. A phenotyping probe that is highly specilic for OATP-C would be extremely useful to further explore the genetics behind this variability in the pharmacokinetics of pravastatin.

Two polymorphisms in the OAT3 gene, T723A and Ala389Val, were unlikely to be associated with differences in either Cl_r or CL_{sec} . CL_r of pravastatin ranged from 0.38 to 0.51 $L \ge kg^{-1} \cdot h^{-1}$ and was much higher than the glomerular [Itration rate, indicating that tubular secretion is a predominant mechanism in renal excretion.20 In addition, given that OAT3 is predominantly expressed in the kidney, 21,22 both clearance values were used as phenotypic indexes in this study. The lack of change in CL_r and CL_{sec} of pravastatin was somewhat unexpected, because the less frequent nonsynonymous variants in OCT2 were reported to result in signill cantly reduced and deleterious transport activities.35 Both OAT3 and OCT2 are members of the SLC22 superfamily and have a similar localization in the proximal tubule epithelium but differ in their charge specilicity; OCT2 transports positively charged compounds, whereas OAT3 transports anionic compounds.

As described earlier, the allelic frequency of Ala389Val was extremely low among Japanese subjects. Thus, with these results taken into consideration, the 2 polymorphisms in the OAT3 gene may not be a major determinant of the large interindividual variability in the pharmacokinetics of pravastatin.

In this study 23 healthy volunteers were not selected for a specilic genotype. For a better understanding of the potential effects of genetic variation, a statistically signilcant number of subjects should be included in each genotype group for each gene. However, because of the low frequency of individuals who are homozygous for the variant allele in the Japanese population and because of various genotypic patterns across the 2 genes of interest, this aim could not be achieved. Obviously, the small number of subjects is a drawback in our study. Considerable variation in pharmacokinetic parameters among various genotype groups makes it difucult to attribute pharmacokinetic changes to one single allele. For instance, although differences in AUC values between *1a/*1a and *1b/*1b subjects were in the same range as those observed between *1b/*1b and *1b/*15 subjects, signil cant changes in clearance values were only observed for the *1b/*1b-*1b/*15 comparison and not for the *1a/*1a-*1b/*1b comparison. It is clear that these results should be confirmed in a population study involving larger numbers of subjects. Nevertheless, this report provides for the possibility that OATP-C gene polymorphism contributes to in vivo activity.

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CORRECTION

In "A comparison of three methods for predicting lithium doses in Chinese psychiatric patients" (Chang Y, Huang H, Chou M, Lin M. Clin Pharmacol Ther 2003;73:P88), the aflliation was printed incorrectly. It should have been Taipei Veterans General Hospital, Yu-Li Psychiatric Hospital, Taipei, Taiwan.

トランスポーターの臨床的意義遺伝子多型から見る薬物療法への寄与

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1 はじめに

薬理遺伝学や薬理ゲノミクスの台頭は薬物の個別 適正化使用に大きなインパクトを与えている。その 中では、薬物代謝酵素が代表として挙げられるが、 吸収や分布、排泄過程に見る個人差の原因を薬物輸 送タンパク(トランスポーター)遺伝子多型から解明 する研究が精力的に進められている。本稿では、遺 伝子多型を利用したトランスポーターの生体中での 機能評価と相互作用をはじめとする薬物療法へのさ まざまな関与について、現在までの知見を整理する とともに、この領域の研究が抱える問題点について 考えてみたい。

2 トランスポーター遺伝子多型と機能評価

トランスポーター遺伝子多型の研究は(遺伝)疾患との関連が先行したため、薬効や体内動態との関連

が注目されたのは、ここ 2、3年と言える。表1には、多型の機能評価が加えられている主なトランスポーターを挙げた。発現細胞による輸送実験、諸臓器での発現量への影響といった in vitro 評価、健常成人による臨床試験、薬効や副作用、さらには疾患との関連(in vivo)について評価が加えられている。検討が加えられるトランスポーターは増えつつあるが、P-糖タンパク質(P-gp)をコードする MDR 1 が先行し、情報量が最も多い。ここでは、MDR 1 とOATP-Cを取り上げる。

1. MDR1 遺伝子

Mickley 6^{11} が最初に 2 種類の変異を同定して以来,MDRI 遺伝子の広範囲にわたるスクリーニングが行われ,現在までに 20 種類以上の変異が確認されている。 2^{-41} 変異の特徴を挙げると,①変異の様式はすべてが 1 塩基置換 (SNPs) で,代謝酵素などに見られる全領域の欠損や挿入などは報告されていない.②日本人 100 名の解析では,すべての検体において,必ずどこかに最低 1 か所の変異がみられる.

表 1 遺伝子多型に基づいた機能評価が加えられている主なトランスポーター

トランスポーター	In vitro 評価	In vivo 評価
MDR 1 (multidrug resistance 1)	0	©
MRP 1 (multidrug resistance-associated protein 1)	0	なし
MRP 2/cMOAT (multidrug resistance protein 2)	0	0
BCRP (breast cancer resistance protein)	0	なし
OATP-C (organic anion transporting polypeptide-C)	0	0
OAT 3 (organic anion transporter-3)	なし	0
OCT-1 (organic cation transporter-1)	0	なし
OCT-2 (organic cation transporter-2)	0	なし

本表には疾患との関連や動物実験、遺伝子改変による構造活性評価は含んでいない。

表2 MDR1 遺伝子多型のヒトでの機能評価

変異部位	基質薬物	対象	薬効,体内動態,副作用への影響	文献 No.
C 3435 T	ジゴキシン	健常成人	T/T>C/C(最高血中濃度)	2
C 3435 T	フェニトイン	健常成人	T/T>C/C(血中濃度)	5
C 3435 T G 2677 T	ジゴキシン	健常成人	M/M>W/M>W/W(吸収率) W/W>W/M>M/M(腎,尿細管分泌クリアランス)	6
C 3435 T	シクロスポリン	腎移植患者	T/T=T/C=C/C(トラフ濃度,拒絶反応の頻度)	7
C 3435 T	フェキソフェナジン	健常成人	T/T=C/C(血中濃度時間曲線下面積)	8
C 3435 T G 2677 T/A	タリノロール	健常成人	W/W=W/M=M/M(血中濃度時間曲線下面積)	9
C 3435 T	ドセタキセル	がん患者	T/T=T/C=C/C(全身クリアランス)	10
*2 haplotype	フェキソフェナジン	健常成人	*1/*1>*1/*2>*2/*2(血中濃度時間曲線下面積)	11
C 3435 T	ジゴキシン	健常成人	C/C>C/T=T/T(血中濃度時間曲線下面積)	12
C 3435 T	ノルトリプチリン	鬱患者	T/T>T/C>C/C(薬剤性低血圧)	13
C 3435 T	ネルフィナビル エファビレンツ	HIV-1 感染患者	T/T>C/T>C/C(CD 4 細胞数と免疫機能改善) C/C>C/T>T/T(トラフ濃度)	14
C 3435 T G 2677 T	ステロイド	小児心臟移植患者	W/W>W/M>M/M(免疫療法におけるステロイドの使用期間)	15

表中の遺伝子型の記載について、例えば、T/T、T/C、W/W、M/M はそれぞれ、チミンのホモ接合型、チミンとシトシンのヘテロ接合型、野生型(C 3435 T であれば、数値の前の塩基でシトシンを意味する、また、C 3435 T と C 2677 T のハブロタイプの場合は、シトシンとグアニンの組み合わせが野生型となる)のホモ接合型、変異(3435 位では、チミン、ハブロタイプの場合は両部位がチミンとなる)のホモ接合型を意味する。

それほど、変異の存在は珍しくない。③現在、多くの研究者が3435位のシトシンからチミンへの変異(C3435 T)に注目した検討を加えているが、この変異はアミノ酸の置換を伴わない。④幾つかの変異がハプロタイプを構成している。すなわち、C1236 T、G2677 T/A、C3435 T の3種類の変異を同時に保有する確立が高い。G2677 T/A は893 番目のアラニンがそれぞれスレオニン、セリンに変わる数少ないアミノ酸の置換を伴う変異である。

表2には、現在までに報告されている変異のヒトでの機能評価の一部をまとめた。10種類程度の基質薬物による検討が報告され、いずれにおいても、変異のターゲットはC1236 T, G2677 T/A, C3435 Tである。体内動態に関するものが中心となっているが、免疫抑制剤と臓器移植後の拒絶反応、三環系抗うつ薬による副作用、HIV治療薬による免疫機能改善など、薬効に対する影響も検討が加えられている。しかし、特に、体内動態への関与をみると、報告間で異なる知見が得られている。例えば、ジゴキシンを用いた検討では、変異によるP-gp機能(排出(efflux))の低下を指摘する知見^{2.61}がある一方で、機能亢進を指摘する知見¹²²が報告されている。同様な現象はフェキソフェナジンでも生じている。ターゲットとしている変異箇所、すなわち、対象ボラン

ティアの遺伝子背景(すべての報告に共通の変異は C 3435 T のみ), 評価に用いる速度論パラメータが報告間で厳密には異なっているものの, コンセンサスが得られていないのが現状と言える. この問題については, 今後のトランスポーターのヒトでの機能を評価する上で重要な問題になるので, 別項で考えてみたい.

2. OATP-C 遺伝子

OATP-C は主に肝臓に発現し、肝への薬物の取 り込み(uptake)に働くトランスポーターとして知 られている。現在までに15種類の変異が確認され ている. その中で頻度, アミノ酸の置換から Asn 130 Asp, Val 174 Ala の 2 種類の変異が注目される. HMG-CoA 還元酵素阻害剤であるプラバスタチンは 肝に選択的に取り込まれることで薬効を示すが、そ の取り込みに OATP-C が重要な働きをすると考え られる、130 D/D 174 V/V(I群), 130 D/D 174 V/ A(Ⅱ群)、130 D/D 174 A/A(Ⅲ群)の遺伝子型で層 別した被検者にプラバスタチンを単回投与した際の 血中濃度推移を図1に示した. Ⅱ群, Ⅲ群, すなわ ち130位と174位両部位に変異を有する被検者で は、全身クリアランスの低下と血中濃度の上昇が認 められている。特に、ホモ型変異保有者(Ⅲ群)の頻 度は低いがクリアランスは I 群の 50% 程度となっ



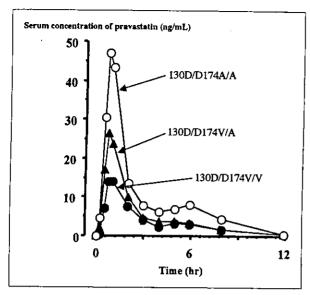


図 1 OATP-C 遺伝子型とブラバスタチン血中濃度推移

ている. 174 位の変異の寄与を強く示唆する結果であるが、被検者で見られた体内動態の変化は発現系を用いた in vitro 実験結果と良好な一致を見る. 161 OATP-C 遺伝子多型の機能評価は少なく、追試が必要であるが、130 位の変異の基質特異性なども指摘されている. 177 スタチン系には、横紋筋融解症などの重篤な副作用が知られている. プラバスタチン以外のスタチンは肝代謝されるため、代謝物や筋肉側の要因を考慮する必要があるが、横紋筋融解症などの副作用は高い血中濃度の維持が原因の1つと指摘されていることから、これらの変異との関連が臨床的にも課題となる.

3 トランスポーターと薬物相互作用

トランスポーターを介した薬物相互作用については、詳細な総説®があるので参照されたいが、ここでは臨床的に重要と考えられる点のみを取り上げる.
1. 投与経路

PGP は広範囲な薬物を基質とすることから、誘導や阻害に基づく薬物相互作用を生じやすいとされる。キニジンやクラリスロマイシン併用によるジゴキシン血中濃度の上昇やリファンピシン併用によるジゴキシンやタリノロールの濃度低下は、それぞれ腎や腸管での P-gp の阻害と誘導によるものと考えられる。また、シクロスポリンは強力な P-gp のモ

ジュレーターであることから, エトポシドやドキソ ・ルビシンなどの基質薬物の輸送を阻害し、 重篤な白 血球減少や中枢性毒性を招く. ところが, 最近の研 究により、一部の相互作用が投与経路により左右さ れることが明らかとなりつつある。先に述べたジゴ キシンとリファンビシン併用によるジゴキシン血中 濃度の低下はジゴキシンを経口投与した時のみに生 じ,静脈内投与時には生じない. また,併用による 経口時 AUC の低下は誘導された腸管の P-gp 発現 量と有意な相関が得られている.19) 同様な現象はタ リノロールとリファンピシン,201 ジゴキシンとクラ リスロマイシン0との相互作用で見られる. これら の知見は腸管に発現する P-gp が、どの程度作用を 受ける薬物の吸収率に影響するかに左右されるもの と考えられるが、その定量的予測の確立の必要性と ともに臨床における相互作用を考える際には、頭の 片隅に置く必要がある.

2. 多型の関与

トランスポーターが関与する薬物相互作用を遺伝子多型から検討した研究は少なく MDR1を取り扱った数報に限られる. いずれも, ジゴキシンとレボチロキシン, 21) リファンピシン, 22 クラリスロマイシン60との相互作用である. MDRI 遺伝子型の違いで相互作用の程度に差が認められる結果が得られており, 相互作用の個人差を考える新規のメカニズムとして注目される. しかし, 多型の関与は先に述べた体内動態と同様に報告数が少ない上に, 報告間で一致した知見が得られていないことから, 更なる検討が必要と言える.

3. グレープフルーツジュース(GFJ)と薬物相互作用 GFJ はテルフェナジン, サキナビル, トリアゾラム, シクロスポリンなどの多くの薬物の腸管でのチトクローム P4503A による代謝を阻害し,吸収率,血中濃度の上昇を招くことから要チェック食品である. 最近, 代謝に加え, トランスポーターとの興味ある相互作用が報告されている. フェキソフェナジンを GFJ とともに服用すると, それまでの概念とは異なり, フェキソフェナジンの吸収率や血中濃度が低下する. 22,23)

P-gp と OATP はともに小腸の管腔側に発現するが、異なった輸送方向を示す。P-gp は細胞内に到

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達した薬物を再度腸管へ排出する(吸収の低下に働く)のに対し、OATPs は逆に血液側に輸送する(吸収の増加に働く)、GFJ は両輸送タンパクの機能を阻害するが、より低濃度で強力に OATPs の輸送を阻害することが in vitro 実験で明らかとなった. 吸収率や血中濃度の低下は GFJ による OATPs が担う吸収の阻害がその背景と考えられる. 本現象に関与する OATP の同定など、多くの課題が残るものの、GFJ を介した薬物相互作用には様々なメカニズムがその背景にあることに留意する必要がある.

4 ヒトにおけるトランスポーター研究が 抱える問題点

ヒトにおけるトランスポーターの機能評価法の1つとして、遺伝子多型からのアプローチは有効と思われる.しかし、表2に示すように、P-gp については一定の知見が得られていない.この原因を考察することは、今後の研究を展開する上で重要であろう.

a. 基質特異性 先に GFJ とフェキソフェナジンの相互作用を述べたが、この報告はフェキソフェナジンの吸収には、少なくとも 2 種類のトランスポーターの関与を考える必要があることを明確に示している。また、ジゴキシンも P-gp の他に OATP-8 が輸送に関与していることが明らかとなっている。それぞれの輸送タンパクの体全体での寄与率などは不明である。同様なことは薬物代謝酵素でも言え、多型を有する代謝酵素のみで代謝される薬物ほど、その影響は著明に現れる。特異的な基質薬物を用いた評価が望まれる。

b. ハプロタイプ 冒頭でも述べたが MDRI 遺伝子には多数の変異が見られ、そのうち数種類は同時に生じている。1種類の変異のみに注目するのではなく、同時に生じる変異のパターンによる評価が行われている。アロブテロールによる気管支拡張作用の個人差は、このパターンの評価により明らかとされた。20 一部の報告では、機能に重要な MDR 1 多型パターンが指摘されつつある。

c. その他の要因 ヒト DNA 上に見られる CpG 領域のシトシンは高度にメチル化されており、タン

パクの発現に関与する. 細胞やがん組織間にみられる P-gp 発現量の違いがメチル化の違いによることを指摘する研究が多く報告されている.

5 おわりに

ノックアウトマウスや in vitro 研究により、トランスポーターが薬物の体内動態や効果に大きく関与することが明らかとなりつつある.しかし、生体中での機能、さらには薬物療法への関与については、P-gp を除き、ほとんど検討が加えられていない.一方、MDRI 遺伝子多型を通した機能評価からは、基質特異性などの問題点が指摘されるに至っている.加えて、薬物輸送では細胞や臓器の入口と出口で異なったトランスポーターの関与を考える必要がある.これらのことから、数種類のトランスポーターとその遺伝子の寄与を視野に入れた臨床試験等の展開が必要になることが予想されてくる.基礎研究で得られた数多くの知見を整理した効率的なヒトでの研究が望まれる.

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Genetic Polymorphism of Organic Anion and Cation Transporters: Pharmacokinetic and Pharmacodynamic Consequences in Pharmacotherapy

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Abstract: It has been suggested that genetic polymorphisms in drug transporters as well as drug-metabolizing enzymes are associated with interindividual differences in drug disposition, efficacy, and toxicity and in disease. Organic anion and cation transporters are expressed in the selective or multiple tissues such as small intestine, liver and kidney, and mediate the transport of many clinically useful drugs. Polymorphisms of drug transporter genes have recently been identified and demonstrated to have functional significance for transporter activity and expression. For example, genetic variants in the OATP-C (SLC21A6) gene are associated with alterations in pravastatin and rifampin uptake into liver. In addition, homozygotes for OCTN2 (SLC22A5) mutant alleles cause systemic carnitine deficiency because of a disruption of



carnitine reabsorption in the kidney. Since a growing number of preclinical and clinical studies have demonstrated that the polymorphisms of various drug transporter genes may be responsible for overall outcomes of pharmacokinetics and pharmacotherapy of certain drugs, further understanding of the physiology and biochemistry of drug transporters with respect to genetic variations will be important to establish individualized pharmacotherapy with clinically used drugs.

Key Words: Anion and cation transporters, Genetic polymorphisms, Clinically useful drugs, Pharmacokinetics, Pharmacodynamics

INTRODUCTION

Genetic polymorphisms in the genes encoding drugmetabolizing enzymes contribute to variations in the kinetic disposition and pharmacological effects of clinically useful drugs [Evans and Relling, 1999]. For example, cytochrome P450 (CYP) 2C9 is the key enzyme for the metabolism of phenytoin and warfarin, and at least three single-nucleotide polymorphisms (SNPs) in this enzyme are known to alter the pharmacokinetics of these drugs [Mamiya et al., 1998; Ninomiya et al., 2000; Scordo et al., 2002; Takahashi et al., 2003]. The variants of CYP2C9 (e.g., CYP2C9*3) are associated with large interindividual differences in the dose of warfarin required for appropriate anticoagulant efficiency, and an increased risk of major bleeding complications [Aithal et al., 1998]. Also, the cure rate for H.pylori infection by proton pump inhibitors (omeprazol or rabeprazole) is significantly higher in poor metabolizers (PMs) than extensive metabolizers (EMs) of CYP2C19, another polymorphic CYP2C isoenzyme, because of high serum concentrations in PM patients [Furuta et al., 1998; 2001]. In addition, many drugs interact with specific target proteins to exert pharmacological effects, such as receptors and channels. In schizophrenic treatment, genetic polymorphisms in neurotransmitter receptor-related genes determine the clinical response to clozapine [Arranz et al., 2000].

Genetic variations in several drug transporters, which play an important role in drug absorption, distribution and

elimination processes, have recently been reported. Among various drug transporters, P-glycoprotein, the MDR1 gene product, is one of the best studied and characterized; Pglycoprotein is an ATP-binding cassette transporter and functions as an energy-dependent efflux pump involved in drug disposition as well as multidrug-resistance. An SNP in exon 26 (C3435T) of MDR1 was found to be associated with reduced absorption and renal clearance of digoxin [Hoffmeyer et al., 2000; Kurata et al., 2002]. In addition to C3435T, G2677T determines success or failure in the antiviral treatment of HIV-1-infected patients [Fellay et al., 2002] and chemotherapy for acute myeloid leukemia [Illmer et al., 2002]. Mutations of multidrug resistance associated protein-2 (MRP2 / cMOAT) are known to cause a hyperbilirubinemia (Dubin-Johnson syndrome) by reducing bilirubin excretion [Wada et al., 1998; Toh et al., 1999]. These observations clearly indicate that genetic variations in drug transporters as well as drug-metabolizing enzymes, receptors and targeting proteins lead to the interindividual difference in the efficacy and toxicity of drugs.

Organic anion and cation transporters are expressed in human tissues such as liver and kidney along the major routes of drug elimination, and thus play key roles in various pharmacokinetic stages. To date, physiological and functional properties of several organic anion transporters (OATs), organic anion transporting polypeptides (OATPs) and organic cation transporters (OCTs and OCTNs), isolated from human tissues, have been evaluated. More recently, genetic polymorphisms have been identified in genes encoding these transporters. In the present review, we summarize the current available data on the impact of genetic polymorphisms in organic anion and cation transporters on their pharmacokinetics and pharmacodynamics.

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HUMAN OATP / OAT FAMILY

1-1. Tissue Distribution and Functional Characterization (a). OATP Family

OATP-A (SLC21A3/OATP/OATP1), initially isolated from human liver, is expressed in brain and liver [Kullak-Ublick et al., 1995; Abe et al., 1999; Tamai et al., 2000]. A recent report has described that OATP-A protein is expressed in brain microvessels and capillary endothelial cells, and can regulate the influx of opioid peptides across the blood-brain barrier [Gao et al., 2000]. The transport of thyroid hormones is also mediated by OATP-A [Fujiwara et al., 2001; Kullak-Ublick et al., 2001].

OATP-C (SLC21A6/LST-1/OATP2) and OATP8 (SLC21A8) are selectively expressed in human liver and located on the basolateral membrane of hepatocytes [Abe et al., 1999; Hsiang et al., 1999; König et al., 2000a, 2000b]. While OATP-C and OATP8 control the uptake of a broad range of substrates such as thyroid hormone [Abe et al., 1999; Hsiang et al., 1999; Kullak-Ublick et al., 2001], methotrexate [Abe et al., 2001; Tirona et al., 2001]and rifampin [Tirona et al., 2003], the uptake of unconjugated bilirubin is mediated by OATP-C but not OATP8 [Cui et al., 2001]. Pravastatin [Hsiang et al., 1999; Nakai et al., 2001] and digoxin [Kullak-Ublick et al., 2001] are reportedly transported by OATP-C and OATP8, respectively.

OATP-B (SLC21A9) has a broad tissue distribution when compared with other OATPs [Tamai et al., 2000; Kullak-Ublick et al., 2001]. OATP-B is localized to the basolateral side of human hepatocytes and facilitates substrate uptake from the portal circulation [Kullak-Ublick et al., 2001]. However, the importance of OATP-B in the hepatic disposition of therapeutic drugs is currently unclear, since the substrate specificity of OATP-B is restricted compared with that of OATP-A, OATP-B and OATP-C [Kullak-Ublick et al., 2001].

OATP-D (SLC21A11) and OATP-E (SLC21A12) are abundantly expressed in various peripheral tissues [Tamai et al., 2000; Fujiwara et al., 2001]. However, little is known about the physiological and pharmacological functions of OATP-D with the exception of the tissue distribution of its mRNA. OATP-E contributes to the transport of thyroid hormone in peripheral tissues [Fujiwara et al, 2001]. OATP-E is also predominantly localized to the apical side of human placenta [Sato et al., 2003]. In a recent study, OATP-F has been identified as high affinity thyroid hormone transporter, which is predominantly expressed in brain and testis [Pizzagalli et al., 2002].

(b). OAT Family

Currently, four human organic anion transporters have been identified. OAT1 (SLC22A6) [Race et al., 1999; Hosoyamada et al., 1999; Sun et al., 2001] and OAT3 (SLC22A7) [Race et al., 1999; Cha et al., 2001; Sun et al., 2001] are mainly expressed in the kidney. OAT1 protein is localized on the basolateral membrane of the S2 segment of proximal tubules in the kidney [Hosoyamada et al., 1999], whereas OAT3 protein is localized on the S1, S2 and S3 segments [Cha et al., 2001]. OAT1, but not OAT3, exhibits

the properties of an exchange-type transporter [Hosoyamada et al., 1999; Cha et al., 2001]. Although, in general, the OAT family is mainly expressed in the kidney, OAT2 is abundantly expressed in the liver (basolateral membrane) and, to a lesser extent, in the kidney [Simonson et al., 1994]. Sekine et al., 1998]. OAT4 (SLC22A9), on the other hand, is expressed predominantly in the kidney and placenta [Cha et al., 2000]. In the kidney, OAT4 protein is localized to the apical side of proximal tubules [Babu et al., 2002a].

Previous studies report that the OAT family transports various clinically important drugs or endogenous anions OAT1, OAT2, OAT3 and OAT4 transport organic anions such as probenecid [Hosoyamada et al., 1999; Race at al., 1999; Cha et al., 2000; Enomoto et al., 2002], prostagrandir (PG) E₂ [Enomoto et al., 2002] and PGF_{2 α} [Enomoto et al., 2002, Kimura et al., 2002]. On the other hand, paminohippurate (PAH) is taken up via OAT1, OAT2, and OAT3 but not OAT4 [Hosoyamada et al., 1999; Race at al., 1999; Cha et al., 2000, 2001; Sun et al., 2001].

In the human kidney, the OAT family seems to play important roles in the process of secreting or transporting various therapeutic drugs through the proximal tubules; OAT1, OAT2 and OAT3 mediate the uptake of organic anions into proximal tubular cells from the blood across the basolateral membrane, and then OAT4 regulates excretion into the proximal tubule fluid across the brush-border membrane. Methotrexate, an antitumor drug, is taken up via OAT1 and OAT3 at the basolateral membrane of proximal tubules and effluxed in the apical membrane of proximal tubules via OAT4 [Takeda et al., 2002b]. Furosemide, a loop diuretic, is transported by OAT1 [Hosoyamada et al., 1999; Race at al., 1999], OAT3 [Cha et al., 2001] and OAT4 [Cha et al., 2000]. Thus, furosemide that is taken up by OAT1 and OAT3 localized at the basolateral membrane in the proximal tubules exhibits a diuretic effect following action on the luminal side of the loop segment, and then excreted via OAT4 in the apical membrane. Other clinically important drugs including nonsteroidal anti-inflammatory drugs (NSAIDs) [Khamdang et al., 2002], angiotensin II receptor antagonist [Race et al., 1999], antiviral nucleotide analogs [Cihlar et al., 1999; Ho et al., 2000; Takeda et al., 2002c], tetracycline [Babu et al., 2002b] and cephalosporin antibiotics [Takeda et al., 2002a] are also substrates for the OAT family (Table.1). Since NSAIDs such as ibuprofen and ketoprofen efficiently inhibit the transport of adefovir by OAT1 in the kidney at clinically relevant concentrations, but are not transported by OAT1 [Mulato et al., 2000], it has been suggested that NSAIDs may reduce adefovirinduced nephrotoxicity [Apiwattanakul et al., 1999; Mulato et al., 2000].

1.2. Impact of OAPT-C Variants on Pharmacokinetics and Pharmacodynamics

1.2.1. Frequency and In Vitro Transport Activity of OATP-C Variants

Recently, a number of SNPs in the human OATP-C gene have been identified in different ethnic populations [Tirona et al., 2001; Nozawa et al., 2002; Nishizato et al., 2003]. At least 17 non-synonymous variants and 16 allelic patterns

Table 1. Summary of organic anion and cation transporters.

Transporter	Gene	Chr.	Tissue distribu	ıtion	Therapeutic /physiological substrates b)	
Transporter	symbol	Cui.	Expression	Polarity *)		Reference
OATP-A	SLC21A3	12	Brain, Liver	BL	fexofenadine, thyroid hormones	Kullak-Ublick et al., 1995; 2001, Abo et al., 1999; Cvetkovic et al., 1999; Tamai et al., 2000; Fujiwara et al., 2001; Dresser et al. 2002
ОАТР-В	SLC21A9	11	Small intestine, Liver, Placenta	BL	pravastatin	Tamai <i>et al.</i> , 2000, 2001; Kullak- Ublick <i>et al.</i> , 2001
OATP-C	SLC21A6	12	Liver	BL	pravastatin, MTX, rifampin, thyroid hormones	Abe et al., 1999; Hsiang et al., 1999; König et al., 2000a; Kullak-Ublick e al., 2001; Nakai et al., 2001; Tirona et al., 2001, 2003
OATP-D	SLC21A11	15	Ubiqutous	?	?	Tamai et al., 2000
OATP-E	SLC21A12	20	Ubiqutous	AP	thyroid hormones	Tamai et al., 2000; Fujiwara et al., 2001; Sato et al., 2003
OATP-F	SLC21A14	12	Brain, Testis	?	thyroid hormones	Pizzagalli et al., 2002
OATP8	SLC21A8	12	Liver	BL	digoxin, MTX, rifampin, thyroid hormones	König et al., 2000b; Abe et al., 2001 Kullak-Ublick et al., 2001
OATI	SLC22A6		Kidney	BL	MTX, probenecide, furosemide, benzylpenicillin, salicylate, indomethacin, losartan, tetracycline, oxytetracycline, minocycline, cephalosporin ab., acyclovir, ganciclovir, zidovudine, adefovir, cidofovir	Cihlar et al., 1999; Race et al., 1999; Hosoyamada et al., 1999; Ho et al., 2000; Sun et al., 2001; Babu et al., 2002b; Khamdang et al., 2002; Takeda et al., 2002a, 2002c
OAT2	SLC22A7	6	Kidney, Liver	BL	MTX, probenecid, PGF _{2a} , tetracycline, oxytetracycline, minocycline, zidovudine	Simonson et al., 1994; Sekine et al., 1998; Babu et al., 2002b; Enomoto et al., 2002; Takeda et al., 2002c
OAT3	SLC22A8	11	Kidney	BL	MTX, probenecide, furosemide, indomethacin, ibuprofen, diclofenac, cimetidine, quinidine, tetracycline, cephalosporin ab., valacyclovîr, zidovudine	Race et al., 1999; Cha et al., 2001; Sun et al., 2001; Babu et al., 2002b; Khamdang et al., 2002; Takeda et al. 2002a, 2002c
OAT4	SLC22A9	11 .	Kidney, Placenta	AP	MTX, probenecid, furosemide, indomethacin, ibuprofen, diclofenac, piroxicam, tetracycline, cephalosporin ab., zidovudine	Cha et al., 2000; Babu et al., 2002a, 2002b; Enomoto et al., 2002; Khamdang et al., 2002; Takeda et al. 2002a, 2002c
OCTI	SLC22A1	6	Liver	BL	acyclovir, ganciclovir	Gorboulev et al., 1997; Zhang et al., 1997; Motohashi et al., 2002; Takeda et al., 2002c
OCT2	SLC22A2	6	Kidney, Brain	BL	amantadine	Gorboulev et al., 1997; Busch et al., 1998; Motohashi et al., 2002
ОСТ3	SLC22A3	6	Kidney, Liver, Placenta, Skeletal muscle	?	?	Wu et al., 2000a
OCTN1	SLC22A4	5	Kidney, Bone marrow	AP	carnitine, verapamil, pyrilamine, quinidine	Tamai et al., 1997; Yabuuchi et al., 1999
OCTN2	SLC22A5	5	Kidney, Brain, Heart, Skeletal muscle, Placenta	AP	carnitine, verapamil, pyrilamine, quinidine, cephalosporin ab.	Wu et al., 1998, 1999; Tamai et al., 1998; Ohashi et al., 1999, 2001; Ganapathy et al., 2000

a) Basolateral; BL, Apical; AP.

b) MTX; Methotrexate, ab.; antibiotics, PG; Prostagrandin.

(haplotypes) have been found to date (Table 2 and 3). Among the 17 non-synonymous variants, N130D appeared in all ethnic populations. As shown in Table 2, G488A and E667G are more common mutations in African-Americans than other populations. In contrast, P155T and V174A are found at higher frequency in European-Americans. These results indicate that genotypic frequencies of OATP-C variants appeared to be dependent on race. However, the interethnic difference in haplotypes of the OATP-C allele has not been well documented.

In vitro experiments with cultured cells expressing the wild type and mutations revealed that the allelic variants of OATP-C*2, *3, *5, *6, *9, *12 and *13 significantly reduced estrone-3-sulfate and estradiol 17 β -D-glucuronide transport activity [Tirona et al., 2001]. The F73L (*2 or *12), V82A (*3 or *13), V174A (*5), I353T (*6), G488A (*9) and L193R (unidentified allele) mutations decreased cellular surface membrane expression of OATP-C protein but did not change the expression of total cellular protein

[Tirona et al., 2001; Michalski et al., 2002]. Interestingly, almost all these mutations localize to the putative transmembrane domains, suggesting an important role for these regions in the trafficking or sorting of mature transporter protein at the cellular membrane.

Rifampin, an antibiotic drug, is broadly used in the treatment of tuberculosis, and is a substrate of OATP-C [Vavricka et al., 2002; Tirona et al., 2003]. Using the recombinant vaccinia virus expression method, Tirona et al. have reported that rifampin transport is robustly reduced by the *1b, *2, *3, *5, *6, *7, *9, *12 and *13 allelic variants [Tirona et al., 2003]. Interestingly, they also reported that OATP-C*1b (N130D) and *7 (N432D) did not affect the capacity for transporting estrone-3-sulfate and estradiol 17 β -D-glucuronide [Tirona et al., 2001]. In contrast, uptake of cholyltaurine but not estradiol 17 β -D-glucuronide is found to be decreased by the OATP-C*1b allele [Michalski et al., 2002]. Taken together, these results suggest that at least two variants, N130D and N432D located at putative N-

Table 2. Summary of Current Genetic Variants in OATP-C.

						All	ele Frequency	0/0		
Allele	Allele		Effect	E-A b)	A-A b)	A-A ()	CA b)	CA ()	Jpn ^{b)}	Jpn b)
Geneti	Genetic	Cellular *)		(N=42) Tirona et al., 2001	(N=22) Tirona <i>et</i> <i>al.</i> , 2001	(N=104-150)	(N=81) Michalski <i>et</i> <i>al.</i> , 2002	(N=150)	(N=267) Nozawa et al., 2002	(N=120) Nishizato <i>et</i> <i>al.</i> , 2003
T217C	Exon 2	TM 2	F73L	2	0	n.d.	n.d.	n.d.	n.d.	0
T245C	Exon 3	TM 2	V82A	. 2	0	n.d.	n.d.	n.d.	n.đ.	0
A388G	Exon 4	EL 2	N130D	30	74	77	n.d.	46	53.7	63
A452G	Exon 4	EL2	N151S	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	4
G455A	Exon 4	EL 2	R152K	0	0	n.d.	n.d.	n,d.	0	0
C463A	Exon 4	EL 2	P155T	16	2	n.d.	n.d.	n.d.	n.d.	0
A467G	. Exon 4	EL 2	E156G	2	0	n.d.	n.d.	n.d.	n.d.	0
T521C	Exon 5	TM 4	V174A	14	2	1	n.d.	12	0.7	16
T578G	Exon 5	TM 4	L193R	n.d.	n.d.	n.d.	< 0.3	n.d.	n.d.	0
G721A	Exon 6	EL 3	D241N	0	0	n.d.	n.d.	n.d.	0	0
C1007G	Exon 8	TM 7	P336R	n.d.	n.d,	n.d.	n.d.	n.d.	n.d.	1
T1058C	Ехоп 8	TM 7	I353T	2	0	n.d.	n.d.	n.d.	n.d.	0
A1294G	Exon 9	EL 5	N432D	1	0	n.d.	n.d.	n.d.	n.d.	0
A1385G	Exon 10	EL 5	D462G	1.	0	n.d.	n.d.	n.d.	n.d.	0
G1454T	Exon 10	EL 5	C485F	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	1
G1463C	Exon 10	EL 5	G488A	0	9	n.d.	n.d.	n.d.	n.d.	0
A1964G	Exon 14	C-terminus	D655G	2	0	n.đ.	n.d.	n.d.	n.d.	0
A2000G	Exon 14	C-terminus	E667G	2	34	n.d.	n.d.	n.đ.	n.d.	0

a) TM: Transmembrane, EL: Extracellular loop, n.d.; not determined

b) E-A; European-American, A-A; African-American, CA; Caucasian, Jpn; Japanese

c) our recent unpublished data.

Table 3. The Influence of OATP-C Variants on Expression or Transport Activity.

Haplotype	Variant	Functional	consequence	Reference
		Transport activity *)	Protein expression	Reference
*1b	NI30D	rifampin ↓	_	Tirona et al., 2003
*lc	R152K	-	-	
*2	F73L	estrone-sulfate↓, estradiol-Glu↓, total cellular and membrane expression↓		Tirona et al., 2001, 2003
*3	V82A, E156G	estrone-sulfate↓, estradiol-Glu↓, rifampin↓		
*4	P155T	_	_	
*5	V174A	1) estrone-sulfate↓, estradiol-Glu↓, rifampin↓ 2) estrone sulfate→	1) membrane expression_, total cellular expression→ 2) protein expression→	1) Tirona et al., 2001, 200 2) Nozawa et al., 2002
*6	1353T	estrone-sulfate↓, estradiol-Glu↓, rifampin↓	membrane expression↓, total cellular expression→	Tirona et al., 2001, 2003
*7	N432D	rifampin↓	_	Tirona et al., 2003
*8	D462G	-	-	
* 9	G488A	estrone-sulfate↓, estradiol-Glu↓, rifampin↓	membrane expression↓, total cellular expression→	Tirona et al., 2001, 2003
*10	D655G	estrone-sulfate↓	_	Tirona et al., 2001
*11	E667G		_	
*12	F73L, D655G	estrone-sulfate↓, rifampin↓	-	Tirona et al., 2001, 2003
*13	V82A, E156G, E667G	estrone-sulfate↓, rifampin↓	_	Tirona et al., 2001, 2003
*14	N130D, P155T	-	_	
*15	N130D, V174A	n.d.	n.d.	
unidentified	N130D, P155T, L193R	estradiol-Glu↓↓	retained intracellularly	Michalski et al., 2002

a) Estrone sulfate; Estrone-3-sulfate, Estradiol-Glu; Estradiol 17β-D-Glucuronide

glycosylation sites in the predicted extracellular loops (2 and 5, respectively) [Abe *et al.*, 1999], exhibit an altered transport capability dependent on substrate.

1.2.2. Influence of OATP-C Polymorphisms on Drug Disposition

Human OATP-C is predominantly expressed on the basolateral membrane in hepatocytes [Abe et al., 1999; Hsiang et al., 1999; König et al., 2000a]. It has been reported that the hepatocellular uptake of bilirubin and its glucronide conjugates is mediated via OATP-C [Cui et al., 2001]. Thus, it seems likely that OATP-C plays an important role in the hepatocellular elimination, metabolism and conjugation of clinical drugs as well as various endogenous compounds.

Pravastatin, one of the 3-hydroxy-3-methylglutaryl coenzyme A reductase inhibitors (statins), is widely used in the treatment of hypercholesterolaemia. Recently, we have

investigated the contribution of the polymorphism of the OATP-C gene to the pharmacokinetics of pravastatin, a substrate for OATP-C [Nishizato et al., 2003]. Among 23 healthy Japanese volunteers, four non-synonymous variants (N130D, N151S, V174A and P336A) and more than five haplotypes (OATP-C*1a, *1b, *15, *16, and unidentified) were observed in the OATP-C gene. Subjects with the *15 allele (D130A174) had a reduced total and non-renal clearance compared to those with the *1b allele; non-renal clearance in *1b/*1b (n = 4), *1b/*15 (n = 9), and *15/*15(n = 1) subjects was 2.01 ± 0.42 , 1.11 ± 0.34 and 0.29(L/hr/kg), respectively. These results suggest that the OATP-C*15 allele is likely to be associated with altered pharmacokinetics of pravastatin. As the hepatic clearance of pravastatin is rate limited by uptake [Hsiang et al., 1999], low transport activity of OATP-C may lead to a reduction of hepatocellular uptake of pravastatin, resulting in lower total clearance. The target organ of pravastatin is the liver. In

^{-;} unchanged when compared to OATP-C*1a, n.d.; not determined

addition, although pravastatin is generally well tolerated in patients with hypercholesterolaemia, it is not free of serious adverse effects, such as skeletal muscle abnormalities (e.g., benign myalgias and rhabdomyolysis). The mechanism of statin-induced rhabdomyolysis is not clearly known, though high serum concentrations of pravastatin have been linked to it. Since certain variants of OATP-C may reduce hepatoselective uptake of pravastatin and be associated with high serum concentrations, patients who carry the mutated alleles would theoretically be expected to have both a loss of pharmacological effects and an increased risk of adverse events. These theoretical but important hypotheses should be tested further.

1.2.3. Influence of OATP-C Polymorphisms on Drug Interaction

Drug-drug interactions are clinically important because of alterations in the metabolism and elimination of certain drugs. Rifampin is well known as an inducer of drug metabolizing enzymes and drug transporters such as CYP2A6, 2B6, 2C8, 2C9, 3A4, 3A5, 3A7, UDPglucuronosyltransferase-1A (UGT1A) [Rae et al., 2001], Pglycoprotein [Greiner et al., 1999; Westphal et al., 2000], and MRP2/cMOAT [Formm et al., 2000]. As described above, Tirona et al. demonstrated that the human liverspecific transporter OATP-C mediates the hepatocellular uptake of rifampin and that several naturally occurring OATP-C variants were found to have markedly reduced rifampin transport activity. Furthermore, they indicated that expression of OATP-C enhances rifampin-mediated pregnane X receptor (PXR) activation as a result of increased intracellular substrate retention. The above-mentioned induction of drug-metabolizing enzymes and drug transporters by rifampin is known to depend upon the activation of the adapted nuclear receptor PXR [Lehmann et al., 1998; Geick et al., 2001]. Although there is no clinical evidence to support this hypothesis, certain genetic variants of OATP-C would be expected to contribute to rifampin-mediated drug interactions.

2. HUMAN OCT / OCTN FAMILY

2.1. Tissue Distribution and Functional Characterization

(a). OCT Family

The mRNA transcript of human OCT1 is predominantly expressed in the liver, and weakly expressed in kidney, whereas OCT1 protein is detected only in the liver, not in the kidney [Gorboulev et al., 1997; Zhang et al., 1997, Motohashi et al., 2002]. Rat Octl is localized at the sinusoidal membrane of hepatocytes in the liver [Meyer-Wentrup et al., 1998]. In Oct1 knockout mice, the accumulation of substrate drugs (metformin, TEA, metaiodobenzylguanidine and MPP+) in liver is diminished compared to that in wild-type mice [Jonker et al., 2001; Wang et al., 2002]. Therefore, it seems that OCT1 plays a predominant role in the transport of substrates across the sinusoidal membrane of human liver. On the other hand, human OCT2 mRNA and protein are expressed in the kidney [Gorboulev et al., 1997; Motohashi et al., 2002], and localized mainly at the basolateral membrane in the distal tubules [Gorboulev et al., 1997]. However, a recent report suggests that OCT2 protein is localized to the basolateral

membrane in the proximal tubules like OAT1, OAT2 and OAT3 but not in the glomeruli, distal tubules or collection ducts [Motohashi et al., 2002]. Therefore, OCT2 likely plays a more important role in the renal disposition of organic cations in human kidney than other members of the OCT family. The mRNA of OCT3 is broadly expressed in human tissues including the liver, kidney and placenta [Wu et al., 2000a]. In mouse kidney, Oct3 mRNA is expressed in proximal and distal convoluted tubules, but not in the glomerulus [Wu et al., 2000a]. However, little is known about the intracellular localization of OCT3 as well as OCT1 in human tissues.

Aciclovir and ganciclovir, antiviral drugs, are predominantly eliminated from kidney, with approximately 63% and 91% of the administered dose recovered unchanged in the urine, respectively [Morse et al., 1993]. In a current study using cells stably expressing human organic anion and cation transporters, these drugs were transported by OAT1 and OCT1 [Takeda et al., 2002c]. However, these drugs might be mainly excreted through a renal mechanism via OAT1 transport, since OAT1 protein but not OCT1 protein is expressed in the kidney [Motohashi et al., 2002]. Although NSAIDs are not transported by OCT1 and OCT2, the transporting of an organic cationic substrate via OCT1 and OCT2 is inhibited by some NSAIDs [Khamdang et al., 2002].

(b). OCTN Family

OCTN1 and OCTN2 transport organic cations such as TEA in a pH-dependent or an Na⁺-independent manner [Yabuuchi et al., 1999; Wu et al., 1999]. On the other hand, OCTN2 mediates carnitine transport in a Na⁺-dependent manner [Tamai et al., 1998]. OCTN1 and OCTN2 have similar substrate specificity. In human tissues, OCTN1 mRNA is expressed predominantly in kidney, trachea, bone marrow and fetal liver [Tamai et al., 1997]. The expression of OCTN2 mRNA in human tissues is detected strongly in kidney, placenta, heart and skeletal muscle, and weakly in brain, lung and liver [Wu et al., 1998, Tamai et al., 1998]. In the kidney, rat Octn1 and Octn2 mRNA are expressed in the absorptive cells in both proximal and distal tubules [Wu et al., 1999, 2000b]. Although the functional characterization of OCTNs in human body has not been well documented. human OCTNs may influence the disposition of various drugs in the kidney. Subcellular localization and in vitro functional characterization suggest that OCTN1 contributes to the active secretion of organic cations across the renal brush-border membrane [Tamai et al., 1997], and OCTN2 exhibits properties as an exchange transporter in Na+dependent carnitine reabsorption in the kidney and Na+independent secretion of organic cations [Ohashi et al., 2001]. Some cephalosporin (β-lactam) antibiotics such as cephaloridine, cefoselis, cefepime and cefluprenam are substrates for OCTN2 [Ganapathy et al., 2000].

2.2. Impact of OCT1 Variants on Pharmacokinetics and Pharmacodynamics

2.2.1. Frequency and In Vitro Transport Activity of OCT1 Variants

The human OCT1 contains 554 amino acids and is predicted to have 12 putative transmembrane domains (TMs) with the extracellular localization of the large hydrophilic

oop between TM1 and 2 [Zhang et al., 1997]. A current eport has identified several synonymous and nonynonymous variants in the human OCT1 gene [Kerb et al., 002]. By systematic screening of the OCT1 gene in a ealthy Caucasian population, 10 mutations were detected in he coding region, of which 8 variants caused non-synonynous amino acid changes (Table 4). Among those, R61C. 160L, and M429del are often observed in the Caucasian opulation, with the respective allele frequencies of 9.1, 22, nd 16%, respectively. In a functional characterization using Kenopus oocytes with OCT1 point mutations, three variants R61C, C88R, and G401S) reduced the transport activity ompared with the wild-type. Interestingly, C88R and 3401S are found to exhibit altered substrate selectivity. The 161C and C88R variants localize to the large extracellular pop, and G401S variant occurs in the intracellular loop etween TM 8 and 9 that is highly conserved in major ansport proteins [Zhang et al., 1997].

.2.2. Influence of OCT1 Polymorphisms on Drug **Visposition**

In full Octl-deficient mice, the accumulation in liver and xcretion into small intestine of the model agent TEA are ound to be reduced compared with the wild-type mice, ecause Oct1 knockout mice exhibit a reduced hepatic uptake nd subsequently direct intestinal excretion of the cationic ubstrate [Jonker et al., 2001]. Interestingly, the hepatic ptake of metformin after intravenous injection is dramatically educed in Oct1 gene-knockout mice [Wang et al., 2002]. letformin belongs to the family of biguanide anti-diabetic rugs, and leads to a reduction of gluconeogenesis through n inhibition of complex I of the mitochondrial respiratory

chain in hepatocytes [Owen et al., 2000; Hundal et al., 2000]. In humans, metformin is extensively eliminated from kidney via glomerular filtration and tubular secretion and recovered in urine at approximately 80 % of the administered dosage [Sirtori et al., 1978; Tucker et al., 1981]. However, since the liver, which expresses human OCT1 protein, is one of the main therapeutic targets of metformin, patients with polymorphisms involved with functional change in the OCT1 gene might exhibit a decrease or lack of pharmacological efficacy for the drug. At the moment, little is known about the specific substrates for OCT1 among therapeutic drugs except antiviral agents [Takeda et al., 2002c].

2.3. Impact of OCT2 Variants on Pharmacokinetics and Pharmacodynamics

2.3.1. Frequency and In Vitro Transport Activity of OCT2 Variants

Members of the organic cation transporter family share a predicted 12 TM structure with a large extracellular loop between TM1 and 2. Genetic variations of human OCT2 have been recently identified in ethnically diverse populations [Leabman et al., 2002]. Eight variable sites including non-synonymous amino acid changes occur in the coding region that distributes throughout the loops and transmembrane domains (Table 5). In vitro studies using oocytes expressing various variants showed that M165I and R400C have significantly reduced uptake activity for the prototypical organic cation MPP+ compared with the OCT2 wild-type, although these variants are present only in the African-American population. A single-nucleotide insertion at position 134 leads to a prematurely terminated protein that might abolish the transporter function. Furthermore, K432Q,

lable 4.	Summary of OCT1 Gene Polymorphisms in Caucasians	[Kerb et al., 2002]	١.
	The state of the s	,	

Aliele	Locali	Localization		Transport activity b)	Genotype	Frequency % (N	i=217-243)
	Genetic	Cellular *)	Effect	Transport activity	Wt/Wt	Wt/Mut	Mut/Mut
G-1795A	Promoter			n.d.	74.5	23.7	1.8
G-1685A	Promoter			n.d.	98.1	1.9	0
G-1672C	Promoter			n.d.	98.1	1.9	0
C181T	Exon 1	EL I	R61C	MPP+↓	83.2	15.6	1.2
T262C	Exon 1	EL 1	C88R	MPP+↓, TEA↓, serotonin↓	98.8	1.2	0
C8237G	Exon 2	TM 2	F160L	-	61.4	34	4.6
G17857A	Exon 7	IL 4	G401S	MPP+↓, TEA↓, serotonin↓	93.5	6.5	0
A17878G	Exon 7	TM 9	M408V	n.d.	17.7	45.2	35.1
G17897C	Exon 7	TM 9	G414A	n.d.	99.6	0.4	0
17914 ATG del	Exon 7	TM 9	M420del	-	71.1	26.3	2.6
G32870A	Exon 9	IL 5	G465R	n.d.	97	3	0

⁾ TM: Transmembrane, EL: Extracellular loop, IL; Intracellular loop

⁾ MPP+; 1-methyl-4-phenylpyridinium, TEA; Tetraethylammonium.

^{-;} unchange when compared to wild type of OCT1, n.d.; not determined

present in both the African-American and Mexican-American population, has an increased affinity for MPP+. These variants may be involved in the altered transport function of organic cations, but occur at low frequency. In contrast, the high-frequency variant, A270S (haplotypes *3D and *3E), is less sensitive to hydrophobic inhibitors [Leabman et al., 2002].

2.3.2. Influence of OCT2 Polymorphisms on Drug Disposition

At the moment, it is not clear whether the polymorphisms in the OCT2 gene are associated with interindividual differences of drug disposition. In addition to the kidney, OCT2 is expressed in neurons of widespread brain regions including the hippocampus and various subcortical nuclei [Gorboulev et al., 1997; Busch et al., 1998]. Monoamine neurotransmitters such as dopamine, serotonin, norepinephrine, histamine and choline are transported by OCT2 [Busch et al., 1998, Sweet et al., 2001]. Interestingly, amantadine and memantine, anti-Parkinsonian drugs, are substrates and competitive inhibitors of OCT2 [Busch et al., 1998]. It has been suggested that amantadine exhibits a pharmacological effect through increased extracellular concentrations of neurotransmitters by inhibition of dopamine uptake via OCT2.

2.4. Impact of OCTN2 Variants on Pharmacokinetics and/or Pharmacodynamics

2.4.1. Polymorphisms of OCTN2 and Systemic Carnitine Deficiency (SCD)

Primary systemic carnitine deficiency (SCD; MIM 212140) is a rare autosomal recessive disorder caused by defective carnitine transport and characterized by hypoketotic

hypoglycemia, cardiomyopathy and myopathy. Carnitine is essential factor for the transfer of long-chain fatty acids from cytosol to mitochondrial matrix where β -oxidation takes place for the production of ATP.

Recently, it has been clarified that SCD is caused by mutations in human OCTN2 which undergoes sodiumdependent carnitine transport in heart, skeletal and renal tissues for \(\beta \)-oxidation. All SCD patients are hetero- or homozygous for various OCTN2 mutant alleles creating a disruption of carnitine transport. The mutations in the OCTN2 gene involved with the functional deficiency of carnitine transport are shown in Table 6. Notably, the mutations causing a missense or a frameshift (a partial nucleotide deletion or insertion) creating a truncated protein have been reported in numerous papers. OCTN2 encodes a polypeptide of 557 amino acids with twelve putative transmembrane domains [Tamai et al., 1998; Wu et al., 1998]. The single missense mutation, C844T in exon 5. converts the arginine at amino acid position 282 into a stop codon (R282X), leading to the production of a truncated protein (by 275 amino acids) compared with the wild-type [Vaz et al., 1999; Wang et al., 1999]. Wang et al. [1999] have reported an SCD patient who is a compound heterozygote for a paternal 1-bp insertion in exon 7 and a maternal 1-bp deletion in exon 8. The paternal mutation changes the codon for the tyrosine at amino acid position 401 to a STOP codon (Y401X). Also, the maternal mutation causes a frameshift starting at the codon for the glycine at position 435 and then creates a stop codon at position 458 (458X), resulting in the production of premature truncated protein. On the other hand, the 113-bp deletion including the initial ATG codon in exon 1 shifts the next available ATG codon at amino acid position 177 (Nezu et al., 1999).

Table 5. Summary of OCT2 Gene Polymorphisms [Leabman et al., 2002].

A 11-1-	Localization		T	money and the bi		Allele frequency %					
Allele	Genetic Cellular **) Effect Transport activity **)	CA c) (N=200)	A-A c) (N=200)	A-S*) (N=60)	ME °) (N=20)	PA ^{c)} (N=14					
134 Ins A	Exon 1	TM 1	45	prematured protein (47 AA)	0.5	0	0	0	0		
C160T	Exon 1	ELI	P54S	n.d.	0	0.5	0	0	0		
T481C	Exon 2	TM 2	FI6IL	n.d.	0.5	0	0	0	0		
A493G	Exon 2	TM 2	M165V	n.d.	0	0.5	0	0	0		
G495A	Exon 2	TM 2	M165I	MPP+↓	0	1	0	0	0		
G808T	Exon 4	TM 6	A270S	sensitive to TBA inhibition↓	15.7	11	8.6	15	7		
C890G	Exon 5	IL 4	A297G	n.d.	0.5	0	0	0	0		
C1198T	Exon 7	IL 5	R400C	MPP+↓ sensitive to TBA inhibition7	0	1.5	0	0	0		
A1294C	Exon 8	EL 5	K432Q	affinity for MPP+ ↑ sensitive to TBA inhibition↑	0	1	0	5	0		

a) TM; Transmembrane, EL: Extracellular loop, IL; Intracellular loop,

b) MPP+; 1-methyl-4-phenylpyridinium, TBA; Tetrabutylammonium.

c) CA; Caucasian, A-A; African-American, A-S; Asian-American, ME; Mexican-American, PA; Pacific Islander

Ins; Insertion, AA; Amino acid, n.d.; not determined

Table 6. Summary of OCTN2 Gene Polymorphisms.

Position *)	Local	ization		Effect	Transport fo	unction	Reference
	Genetic	Cellular b)			Carnitine transport	TEA transport	
113-bp Del	Exon 1			shift ATG at codon 177	n.d.	n.d.	Nezu et al., 1999
226 Ins C	Exon 1			truncating	n.d.	n.d.	Nezu et al., 1999
255-22851 Del (255-1649 Del)	Exon 1-8	TM 11		truncating	n.d.	n.d.	Lamhonwah and Tein, 1998
15591 Ins 19-bp (874 Ins 19 -bp)	Exon 4	TM 4		truncating	n.đ.	n.d.	Lamhonwah and Tein, 1998
15592-17283 Del (875-1046 Del)	Exon 4-5	TM 4-6	-	truncating	n.d.	n.đ.	Lamhonwah and Tein, 1998
G 8639 A	Exon 2	ELI	W132X	truncating	no activity	n.d.	Koizumi et al., 1999; Tang et al., 1999; Nezu et al., 1999
C 14417 T	Ехоп 2	JL 2/3 *	R169W		no activity	n.d.	Wang et al., 2000c
A 14447 T	Exon 3	TM 3	M179L		activity↓	n.d.	Koizumi et al., 1999
A 14544 G	Exon 3	TM 4	Y211C		no activity	-	Seth et al., 1999; Vaz et al., 1999
G 15663 T	Exon 4	TM 5	G242V		no activity	n.d.	Wang et al., 2000c
C 17302 T	Exon 5	IL 6/7	R282X	mRNA level↓	no activity	n.d.	Vaz et al.,1999; Wang et al., 1999
G 17307 T	Exon 5	IL 6/7	W283C		no activity	n.d.	Koizumi et al., 1999
	Exon 5	IL 6/7	W283R		no activity	n.d.	Mayatepek et al., 2000
C 17360 A	Exon 5	IL 6/7	A301D		no activity	n.d.	Wang et al., 2000c
T 19278 C	Exon 6	TM 7	W351R		no activity	n.d.	Wang et al., 2000c
	Exon 7	TM 7	M352R	protein level→	no activity	no activity	Seth et al., 1999; Wu et al., 1999
21098 Ins A	Exon 7	TM 9	Y401X	mRNA level↓	no activity	n.d.	Wang et al.,1999
G 22759 T	Exon 8	IL 10/11	V446F		no activity	n.d.	Mayatepek et al., 2000
G 22777 A	Exon 8	IL 10/11	E452K		no activity	n.d.	Wang et al., 2000a, 2000b
22727 Del G	Exon 8	IL 10/11	458 X	mRNA level↓	no activity	n.d.	Wang et al.,1999
C 22823 G	Exon 8	тм н	S467C		no activity	-	Koizumi et al., 1999; Ohashi e al., 2002
C 22856 T	Exon 8	TM 11	P478L	protein level→	no activity	activity T	Seth et al., 1999; Tang et al., 1999; Wu et al., 1999
G 23934 A	Intron 8			truncating	n.d.	n.d.	Nezu et al., 1999

a) Position of nucleofide substitution, accession number AB016625 (NM_00306) Ins; Insertion, Del; Deletion

Moreover, previous studies have shown OCTN2 mutations causing a production of truncated protein in SCD patients (Table 6). These mutations lead to the loss of several putative transmembrane domains. The lack of several predicted transmembrane domains would likely result in the production of OCTN2 protein that either is rapidly degraded or not functional.

2.4.2. Influence of OCTN2 Polymorphisms on Drug Disposition

Several drugs such as verapamil, quinidine and some cephalosporin antibiotics are recognized by human OCTN2 [Ohashi et al., 1999; Ganapathy et al., 2000]. Most of the mutations in the OCTN2 gene are identified in SCD patients

b) TM: Transmembrane, EL: Extracellular loop, IL; Intracellular loop.

 $[\]ensuremath{\text{\#}}$ Location in the intracellular loop between transmembrane domains 2 and 3

^{-;} unchanged when compared to wild type of OCTN2, n.d.; not determined

(Table 6). Heterozygotes for the OCTN2 mutations (e.g., W132X, S467C, W283C and M179L) with impaired carnitine transport are also identified in healthy subjects who are characterized by low levels of serum carnitine [Koizumi et al., 1999]. It is considered that the truncating mutations containing a deletion of the coding region or change of the conserved splice acceptor site in the OCTN2 gene fail to transport organic cations as well as carnitine. However, the S467C mutant of OCTN2 elicits a loss of carnitine transport without interference in OCTN2-mediated TEA transport [Ohashi et al., 2002]. Similar results are reported in P478L and Y211F [Seth et al., 1999]. Carnitine has an anionic and cationic moiety within the molecule and exists as a zwitterion under physiological conditions. OCTN2 recognized both anionic and cationic charges, and transported carnitine or organic cations in an Na⁺-dependent or Na⁺-independent manner, Mutations in S467C and P478L are located in transmembrane domain 11 which is the anion recognition site and is closely related to the Na⁺-binding site on OCTN2 protein [Seth et al., 1999; Ohashi et al., 2002]. On the other hand, E452K is located in the intracellular loop between predicted transmembrane domains 10 and 11 [Wang et al., 2000b]. Therefore, these variants might influence the pharmacokinetic or pharmacodynamic properties of zwitterionic drugs but not cationic drugs. In future studies, it will be important to clarify whether these mutations in the OCTN2 gene influence the transport function of organic cations.

3. FUTURE OF DRUG TRANSPORT RESEARCH IN HUMANS

Drug transporters are widely distributed in human tissues and have an important role in regulating the absorption, distribution, and excretion of many clinically useful drugs. Although it is obvious that additional studies with regard not only to drug transporters but also drug metabolizing enzymes and functional target proteins (receptors and converting enzymes) are necessary to facilitate the translation of pharmacogenomics into clinical practice (i.e., tailoring drug therapy), some critical issues must be considered.

In order to establish a genotype-phenotype correlation, a specific probe drug(s) for each objective protein is essential. In drug transport studies, digoxin and fexofenadine are often used as probe drugs for P-glycoprotein. However, recent studies have clearly indicated that these drugs are dual substrates for P-glycoprotein and other polymorphic drug transporters: digoxin for OATP-8 and fexofenadine for OATP-A [Suzuki et al., 2002; Dresser et al, 2002]. Thus, the contribution of at least two transporters with regard to genetic variations needs to be considered in order to describe the pharmacokinetics, and then the clinical outcome of each drug treatment more accurately. The involvement of multi transporters in the pharmacokinetics of these drugs is one possible reason for the controversial and conflicting findings on genotype-phenotype correlations of P-glycoprotein (MDR1) [Kim, 2002]. Nevertheless, it is clear that the identification of specific probe drugs for each drug transporter is required.

Most drug effects are determined by the interplay of several proteins (gene products) that regulate the pharmacokinetics and pharmacodynamics of medications.

The synergistic action of intestinal CYP3A and P-glycoprotein is a typical interplay for detoxication [Zhang and Benet, 2001]. The majority of initial data on the importance of polymorphisms with regard to drug transporters are focused on a single SNP or a single gene. Currently, strategies for genotype-phenotype studies have been extended from a single SNP analysis to haplotype analysis [Tang et al., 2002; 12:437-50; Nishizato et al., 2003]. In addition, candidate-gene(s) analysis based on the knowledge of the mechanism of drug action and pathways of metabolism and disposition has been introduced with the development of powerful molecular diagnostic methods. We believe these evolving strategies will lead to the accurate elucidation of genetically determined drug responses.

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ABBREVIATIONS

CYP = Cytochrome P450

SNP = Single-nucleotide polymorphism

PM = Poor metabolizer

EM = Extensive metabolizer

MRP2 = Multidrug resistance associated protein-2

OAT = Organic anion transporter

OATP = Organic anion transporting polypeptide

OCT = Organic cation transporter

PG = Prostagrandin

PAH = p-aminohippurate

NSAID = Nonsteroidal anti-inflammatory drug

UGT1A = UDP-glucuronosyltransferase-1A

PXR = Pregnane X receptor
TEA = Tetraethylammonium

MPP+ = 1-methyl-4-phenylpyridinium

TM = Transmembrane

SCD = Primary systemic carnitine deficiency

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