Paraoxonase 1 as a Major Bioactivating Hydrolase for Olmesartan Medoxomil in Human Blood Circulation: Molecular Identification and Contribution to Plasma Metabolism

Tomoko Ishizuka, Izumi Fujimori, Atsuko Nishida, Hidetaka Sakurai, Yasushi Yoshigae, Kaori Nakahara, Atsushi Kurihara, Toshihiko Ikeda, and Takashi Izumi

Drug Metabolism and Pharmacokinetics Research Laboratories (T.Is., I.F., Y.Y., A.K., T.Iz.), Biologics Research Laboratories (A.N.), and Translational Medicine and Clinical Pharmacology Department (H.S.), Daiichi Sankyo Co., Tokyo, Japan; Daiichi Sankyo RD Associe Co., Tokyo, Japan (K.N.); and Yokohama College of Pharmacy, Yokohama, Japan (T.Ik.)

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ABSTRACT:

Olmesartan medoxomil (OM) is a prodrug-type angiotensin II type 1 receptor antagonist. The OM-hydrolyzing enzyme responsible for prodrug bioactivation was purified from human plasma through successive column chromatography and was molecularly identified through N-terminal amino acid sequencing, which resulted in a sequence of 20 amino acids identical to that of human paraoxonase 1 (PON1). Two recombinant allozymes of human PON1 (PON1\textsubscript{192QQ} and PON1\textsubscript{192RR}) were constructed and were clearly demonstrated to hydrolyze OM; hydrolysis by the latter allozyme was slightly faster than that by the former. In addition, we evaluated the contribution of PON1 to OM bioactivation in human plasma. Enzyme kinetic studies demonstrated that OM was hydrolyzed more effectively by the recombinant PON1 proteins than by purified albumin. The OM-hydrolyzing activities of the recombinant PON1 proteins and diluted plasma were greatly reduced in the absence of calcium ions. Immunoprecipitation with anti-PON1 IgG completely abolished the OM-hydrolyzing activity in human plasma, whereas the activity was partially inhibited with anti-albumin IgG. The distribution pattern of the OM-hydrolyzing activity in human serum lipoprotein fractions and lipoprotein-deficient serum was examined and showed that most of the OM-hydrolyzing activity was located in the high-density lipoprotein fraction, with which PON1 is closely associated. In conclusion, we identified PON1 as the OM-bioactivating hydrolase in human plasma on a molecular basis and demonstrated that PON1, but not albumin, plays a major role in OM bioactivation in human plasma.

Introduction

Several prodrug strategies have been developed to enable drugs to exhibit optimal pharmacokinetics and pharmacological actions by overcoming a number of barriers to drug-like properties. In particular, an esterification strategy has been used historically to increase transcellular absorption of poorly permeable drugs administrated orally. Esterases, which are involved in the prodrug bioactivation process, are widely distributed in the blood, liver, intestine, and many other biological fluids and tissues (Testa and Mayer, 2003). In most cases, intestinal esterases serve as the major enzymes in bioactivation of prodrugs during the first pass through the gut after absorption. In some cases, however, prodrug molecules escape the activation process catalyzed by intestinal esterases, enter the blood circulation as the prodrug, and then are activated by serum (plasma) and liver esterases. Several esterases in human plasma have been investigated as key enzymes responsible for prodrug bioactivation (Ettmayer et al., 2004; Testa, 2004; Li et al., 2005; Satoh and Hosokawa, 2006), including paraoxonase/arylesterase 1 (PON1), cholinesterase, and albumin. For example, human PON1, which is localized predominantly in plasma and is associated with high-density lipoprotein (HDL), was reported to be a major bioactivating enzyme for the antibacterial agent prulifloxacin (Tougou et al., 1998).

Olmesartan medoxomil (OM) is a prodrug-type angiotensin receptor blocker that is prescribed throughout the world as monotherapy and in combination with a thiazide diuretic and/or a calcium channel blocker (Chrysant, 2008; Scott and McCormack, 2008; Rump and Sellin, 2010; Ram, 2011). As shown in Fig. 1, OM is one of the exemplary cases of bioavailability improvement through derivatization into the (5-methyl-2-oxo-1,3-dioxol-4-yl)methyl ester (medoxomil ester) prodrug (Scott and McCormack, 2008). It was reported that multiple enzymes are capable of OM bioactivation in humans, including plasma albumin (Ma et al., 2005) and an intestinal and liver hydrolase carboxymethylenebutenolidase homolog (CMBL) (Ishizuka et al., 2010).

The identification and characterization of enzymes responsible for prodrug bioactivation are important because their properties become...
Materials and Methods

Materials. OM, olmesartan, and 2-buty1-4-(1-hydroxy-1-methylethyl)-1-
[2'-(1H-tetrazole-5-yl)-4-biphenyl]-1H-imidazole-5-carboxylic acid (RNH-
6272; a structural analog of olmesartan) used as the internal standard for
olmesartan determination, were synthesized at Daiichi Sankyo (Tokyo, Japan).
Phenyl acetate and paraoxon were purchased from Sigma-Aldrich Japan (To-
kyo, Japan). Benzoyl choline was purchased from Nakalai Tesque (Kyoto,
Japan). Human plasma or serum was prepared from blood collected from
healthy subjects by using a protocol approved by the institutional human
ethical committee of Daiichi Sankyo. Animal plasma was prepared from blood
collected in-house from Wister-Imamichi rats, ddY mice, Japanese white
rabbits, cynomolgus monkeys, and beagle dogs, in accordance with the
guidelines of the institutional animal care and use committee of Daiichi
Sankyo. Purified human serum albumin and anti-human albumin rabbit
polyclonal IgG were purchased from Sigma-Aldrich.

Hydrolase Activity Measurement. OM-hydrolyzing activity was deter-
mined as follows. Animal and human plasma for the species difference
examination and each eluent fraction obtained from successive column
chromatography for purification of our target hydrolase were appropriately diluted (final dilutions, 50–400-fold and 10–100-fold, respectively) with 10 mM
potassium phosphate buffer. The diluted protein solutions were incubated at
37°C for 5 to 10 min with OM as a substrate (final solvent concentration, 2%
acetonic acid). After reaction termination through addition of ice-cold acetoni-
carboxylic acid, the concentration of the active metabolite olmesartan was determined with a high-performance liquid chromatography-tandem mass spectrometry system consisting of a Prominence LC-20A system (Shimadzu) and an API 3200 mass spectrometer (AB Sciex, Foster City, CA). Olmesartan was separated with a reverse-phase C18 column (Atlantis T3, 5 μm, 2.1 mm i.d. × 150 mm; Waters) and a mobile phase of 64% methanol containing 0.2% for-
ic acid, at a flow rate of 0.2 ml/min, and was determined through monitoring of the ion transition of m/z 447 to m/z 207 with multiple-
reaction monitoring in the positive electrospray ionization mode. The lower limit of quantitation was set at 20 nM. The enzymatic activity was ex-
pressed as a metabolite formation rate (in nanomoles per minute per milligram of protein) on the basis of the production of olmesartan for the
reaction by the recombinant protein, which was subtracted from that in the
buffer control (nonenzymatic hydrolysis).

Phenyl acetate-hydrolyzing activity was determined as follows. Over the
process of protein purification from human serum, 20 to 40 μl of each fraction
was incubated at 37°C for 10 to 20 min with 0.2 ml of 10 mM phenyl acetate
solution in 50 mM Tris-HCl buffer (pH 8). After reaction termination through addition of 1 ml of 0.04% 4-aminoantipyrine in acetonic acid and then color
development with addition of 2 ml of 0.08% potassium ferricyanide with 50
Mm Tris-HCl buffer (pH 8) in acetonic acid, the absorbance at 510 nm was
measured. After column purification, the activity of the purified protein was
measured as reported previously (Gan et al., 1991), with slight modification.
Twenty microliters of the purified esterase solution were incubated at room
temperature with 1.5 ml of 1 mM phenyl acetate solution in 50 mM Tris-HCl
buffer (pH 8) containing 1 mM CaCl2. Formation of the metabolite phenol was
determined through monitoring of absorbance changes at 270 nm. The activity
was expressed with units of change in absorbance at 270 nm per minute per
milligram of protein.

Paraoxon-hydrolyzing activity was measured as reported previously (Gan et
al., 1991), with slight modification. Twenty microliters of the appropriately
diluted purified protein solution were incubated at room temperature with 0.8
ml of paraoxon solution (1 mM) in 50 mM Tris-HCl buffer (pH 8) containing
1 mM CaCl2 and 1 M NaCl. Formation of the metabolite p-nitrophenol was
determined through monitoring of absorbance changes at 412 nm. The activity
was expressed with units of change in absorbance at 412 nm per minute per
milligram of protein.

Benzoyl choline-hydrolyzing activity was measured as follows. One hun-
dred twenty microliters of the appropriately diluted purified protein solution
were incubated at 37°C for 10 min with benzoyl choline (final concentration,
1 mM). After reaction termination through addition of ice-cold acetonic acid, the concentration of the metabolite benzonic acid was determined with a high-
performance liquid chromatography system (SLC-10A system; Shimadzu).
The metabolite was separated from the benzoyl choline peak with a reverse-
phase C18 column (YMC-Pack ODS-A A-312, C18, 5 μm, 4.6 mm i.d. × 150 mm; YMC) and a mobile phase of 55% acetone containing phosphoric acid for
pH adjustment (pH 3.0), at a flow rate of 1.0 ml/min. UV detection was per-
formed at 225 nm. The activity was expressed with units of nanomoles per minute per milligram of protein.
against the purified protein, which was later identified as human PON1, was raised in female Japanese white rabbits. The animals received three boosts with equal volumes of the purified protein as an antigen in complete Freund's adjuvant, with 2-week intervals. The antisera was obtained from the animals, and the IgG was purified from the antisera by using 50% saturated ammonium sulfate precipitation, followed by DEAE-Sepharose column chromatography. The IgG was further purified with an Econo-Pac serum IgG purification column kit (Bio-Rad Laboratories), to remove components with OM-hydrolyzing activity.

The plasma proteins in each purification step that were separated with SDS-PAGE and then blotted on a PVDF membrane were detected with the purified anti-PON1 IgG described above, followed by enhanced chemiluminescence, horseradish peroxidase-linked, donkey anti-rabbit IgG (GE Healthcare, Little Chalfont, UK), as primary and secondary antibodies, respectively. These immunoblots were observed through chemiluminescence with an enhanced chemiluminescence detecting reagent (GE Healthcare).

Inhibitory effects of the purified IgG against PON1 and albumin on the OM-hydrolyzing activity in human plasma were investigated to estimate the contribution of each protein. Diluted human plasma at an appropriate dilution ratio was incubated overnight at 4°C with the respective IgG fractions at various IgG fraction/plasma volume ratios. After separation of the antigen-antibody complex through centrifugation, the supernatant was used as an enzyme source for OM-hydrolyzing activity measurements.

Expression of Human PON1 in Mammalian Cell Line. The open reading frame of the full-length human PON1 (amino acids 1–355) and that of the Q192R mutant were subcloned into a vector plasmid (pcDNA6-myc-His; Invitrogen, Carlsbad, CA) providing a C-terminal myc-polyhistidine-epitope tag, confirmed with DNA sequencing, and expressed in mammalian FreeStyle 293-F cells (Invitrogen). The transfected cells were cultured for 7 days in FreeStyle 293 expression medium (Invitrogen), and the conditioned media from the cells overexpressing human PON1(192QG) and PON1(192RR) were filtered with polyethersulfone membrane filters (0.45 μm; Thermo Fisher Scientific, Waltham, MA). After dialysis against 20 mM Tris-HCl buffer (pH 7.5), the overexpressed histidine-tagged proteins were purified with a two-stage purification process involving anion chromatography with a HiTrap Q- XL column (GE Healthcare) and Ni- affinity chromatography with a HisTrap FF column (GE Healthcare). The eluates were collected and desalted with PD-10 columns (GE Healthcare), and then the resultant proteins were stored frozen at −80°C until use. The protein concentration was determined by using a micro-bicinchoninic acid Pierce protein assay (Thermo Fisher Scientific), with bovine serum albumin as the standard.

Kinetic Analysis. The enzyme kinetics for OM hydrolysis by human plasma, recombinant PON1 proteins, and purified human serum albumin were evaluated with substrate concentrations ranging from 3.125 to 400 μM. For reactions with purified serum albumin, 100 mM potassium phosphate buffer (pH 7.4) was used instead of 100 mM Tris-HCl buffer (pH 7.5) containing 1 mM CaCl2. Kinetic parameters, namely, the Michaelis constant (Km) and the maximal velocity (Vmax), were estimated from the data on substrate concentrations ([S]) and initial velocities (v) with WinNonlin Professional (version 5.2.1; Pharsight, Mountain View, CA), by using nonlinear least-squares regression analysis fitted to the Michaelis-Menten equation, v = Vmax × [S]/(Km + [S]).

Distribution of OM-Hydrolyzing Activity in Serum Lipoprotein Fractions. The lipoprotein fractions, namely, very-low-density lipoprotein (VLDL) including chylomicron, low-density lipoprotein (LDL), and HDL, were separated from human serum through sequential ultracentrifugation in continuous-density gradients (Havel et al., 1955) (CS150GXL ultracentrifuge with S120AT2 rotor; Hitachi Koki, Tokyo, Japan), desalted (PD-10 desalting columns; GE Healthcare), and concentrated through centrifugation (Amicon Ultra filters; molecular weight cutoff, 10,000; Millipore Corporation, Billerica, MA). The lipoprotein-deficient serum (LPDS) fraction obtained after the lipoprotein separation, which was thought to include serum albumin, was also desalted with PD-10 columns and was used for activity measurements. The OM-hydrolyzing activity was measured at a substrate concentration of 10 μM, as described above. Incubations with the LPDS fraction in 100 mM KPB (pH 7.4) also were performed, because purified serum albumin showed higher OM-hydrolyzing activity in KPB than in Tris-HCl buffer containing CaCl2.

Other Methods. Protein concentrations were determined by using the Bradford (Bradford, 1976) protein assay (Bio-Rad Laboratories), with bovine serum albumin as the standard, unless indicated otherwise.
Results

Characteristics of Plasma OM Hydrolase. In plasma fractions from six different species including humans, OM was substantially hydrolyzed and converted into the active metabolite olmesartan. The OM-hydrolyzing activities in human and animal plasma are shown comparatively in Fig. 2. Rabbit plasma demonstrated the highest activity, followed by dog and human plasma. The hydrolysis in rat plasma was much slower than that in human plasma.

Purification of OM Hydrolase from Human Plasma. The OM hydrolyase was purified from human plasma through successive column chromatography. As shown in Table 1, the purification resulted in a 386-fold increase in specific activity of OM hydrolysis, in accordance with those of phenyl acetate hydrolyase and paraoxon hydrolysis activities, which were monitored as markers of PON1 activity, whereas the marker activity for choline esterase, the benzoyl choline-hydrolyzing activity, was completely removed during the purification process. The fractions containing the OM hydrolyase were separated through SDS-PAGE and stained with Coomassie Brilliant Blue, which showed a highly purified enzyme preparation with a molecular mass of 48.5 kDa (Fig. 3A, lane 5). After transfer onto the PVDF membrane, the immunoblot membrane showed a highly purified enzyme preparation with a molecular mass of 48.5 kDa. As shown in Fig. 3B, the anti-PON1 IgG immunostained the targeted protein in active fractions of each column purification step as a single band with the same migration point, whose intensity increased in accordance with the proceeding purification step.

N-Terminal Amino Acid Sequencing. The automated Edman degradation procedure provided the N-terminal sequence of the first 20 amino acids of the column-purified OM hydrolyase from human plasma. The following sequence was obtained: Ala-Lys-Leu-Ile-Ala-Leu-Thr-Leu-Leu-Gly-Met-Gly-Leu-Ala-Leu-Phe-Arg-Asn-His-Gln. A Basic Local Alignment Search Tool search of a human protein database (the National Center for Biotechnology Information RefSeq database) demonstrated that PON1, which was postulated to be our target protein in plasma, is the only human protein that shows a perfect match to the determined 20-amino acid sequence.

OM Hydrolysis by Recombinant PON1 Proteins. To confirm the protein identification results from N-terminal amino acid sequencing, we overexpressed recombinant human PON1 in FreeStyle 293-F cells, a mammalian cell line derived from human embryonic kidney 293 cells, and the OM-hydrolyzing activity of the recombinant protein was measured. Because residue 192 is a well investigated polymorphic site of human PON1 that accounts for marked qualitative differences (Harel et al., 2004; Ginsberg et al., 2009), two types of allelic homozygotes at residue 192, PON1192QQ and PON1192RR, were generated. To confirm the recombinant proteins produced, we examined tryptic fragments by mass spectrometry and achieved 78% and 95% amino acid sequence coverage of PON1192QQ and PON1192RR, respectively, with covering of the Q192R mutated sequence. Both recombinant PON1 allozymes rapidly hydrolyzed OM, converted it into the active metabolite olmesartan, and showed calcium ion dependence of the enzymatic activity (Table 2).

Immunoblotting of Plasma OM Hydrolase. Specific immunoreactivity of the IgG fraction against the PON1 protein was confirmed with Western blotting (Fig. 3B). The anti-PON1 IgG immunostained the targeted protein in active fractions of each column purification step as a single band with the same migration point, whose intensity increased in accordance with the proceeding purification step.

Metal Ion Requirements. In Table 2, the OM-hydrolyzing activities of several plasma esterases in incubation buffer containing Ca2+ ions are compared with those in buffer in which Ca2+ ions were replaced by either Zn2+ or Mg2+ ions. The enzymatic activities of the diluted plasma and recombinant PON1 proteins were greatly reduced in the absence of Ca2+ ions. In contrast, the purified serum albumin hydrolyzed OM equally in all incubations, regardless of the metal ions contained.

Kinetic Analysis. The OM hydrolysis activity in human plasma, the recombinant proteins PON1192QQ and PON1192RR, and purified serum albumin exhibited single-enzyme Michaelis-Menten kinetics, as shown in Fig. 4. The parameters of enzyme kinetics are summarized in Table 3. Higher estimated Km values for the recombinant proteins PON1192QQ and PON1192RR (157 and 102 μM, respectively) were found in human plasma, whereas the recombinant proteins in buffer were reduced by 3.5- and 2.2-fold, respectively.

<table>
<thead>
<tr>
<th>Enzyme Source</th>
<th>+Ca2+</th>
<th>+Mg2+</th>
<th>+Zn2+</th>
</tr>
</thead>
<tbody>
<tr>
<td>Plasma</td>
<td>7.91 (100)</td>
<td>0.266 (3.4)</td>
<td>0.0918 (1.2)</td>
</tr>
<tr>
<td>Recombinant PON1192QQ</td>
<td>9.50 (100)</td>
<td>0.650 (6.8)</td>
<td>0.250 (7.9)</td>
</tr>
<tr>
<td>Recombinant PON1192RR</td>
<td>20.6 (100)</td>
<td>2.25 (10.9)</td>
<td>1.75 (8.5)</td>
</tr>
<tr>
<td>Serum albumin</td>
<td>0.0102 (100)</td>
<td>0.0106 (103.9)</td>
<td>0.0164 (160.8)</td>
</tr>
</tbody>
</table>
Lipoprotein Fractions. Less than 30% of the control activity was observed at IgG fraction/plasma ratios of more than 2-fold, was added (data not shown). The maximal inhibition magnitude, which activity in purified albumin with the same volume of IgG fraction plasma ratio (Fig. 5B), despite showing complete inhibition of the plasma OM-hydrolyzing activity even at the highest IgG fraction/plasma ratio. In contrast, the IgG hydrolyzing activity in human plasma and completely abolished the human PON1 showed concentration-dependent inhibition of the OM-hydrolyzing activity displayed only incomplete inhibition of the natural protein in plasma. A comparison of V_max/K_m, representing enzymatic efficiency, between the two recombinant PON1 proteins showed that PON1_192RR was more active with OM as a substrate than was PON1_192QQ. The V_max/K_m value for serum albumin was considerably lower than those of the recombinant PON1 proteins.

Immunoprecipitation of Plasma OM Hydrolyase. The contribution of PON1 and albumin to OM bioactivation in human plasma was estimated through immunoprecipitation with specific antibodies against the respective proteins. As shown in Fig. 5A, the IgG against human PON1 showed concentration-dependent inhibition of the OM-hydrolyzing activity in human plasma and completely abolished the activity at a 4-fold IgG fraction/plasma ratio. In contrast, the IgG against human serum albumin displayed only incomplete inhibition of the plasma OM-hydrolyzing activity even at the highest IgG fraction/plasma ratio (Fig. 5B), despite showing complete inhibition of the activity in purified albumin with the same volume of IgG fraction added (data not shown). The maximal inhibition magnitude, which was observed at IgG fraction/plasma ratios of more than 2-fold, was less than 30% of the control activity.

Distribution of OM-Hydrolyzing Activity in Human Serum Lipoprotein Fractions. The distribution of the OM-hydrolyzing activity in lipoprotein fractions (VLDL including chylomicron, LDL, HDL) and LPDS separated from human serum is summarized in Table 4. Most of the activity (more than 93%) was located in the HDL fraction, whereas fairly low enzymatic activity was observed in LPDS, which is thought to include serum albumin.

**TABLE 3**

<table>
<thead>
<tr>
<th>Enzyme Source</th>
<th>K_m (µM)</th>
<th>V_max (nmol min⁻¹ mg⁻¹ protein⁻¹)</th>
<th>V_max/K_m (mL min⁻¹ mg⁻¹ protein⁻¹)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Human Plasma</td>
<td>6.71</td>
<td>18.6</td>
<td>2.77</td>
</tr>
<tr>
<td>Recombinant PON1_192QQ</td>
<td>157</td>
<td>124</td>
<td>0.79</td>
</tr>
<tr>
<td>Recombinant PON1_192RR</td>
<td>102</td>
<td>140</td>
<td>1.37</td>
</tr>
<tr>
<td>Serum albumin</td>
<td>354</td>
<td>2.61</td>
<td>0.00737</td>
</tr>
</tbody>
</table>

**Discussion**

Although several reports stated that some human plasma esterases are capable of bioactivation of the prodrug OM (Laët et al., 2001; Ma et al., 2005), we found no reports that presented evidence of the molecular identification of enzymes responsible for the hydrolytic reaction. In this report, we directly identified the OM hydrolyase purified from human serum as human PON1 through N-terminal peptide sequencing and we demonstrated significant OM-hydrolyzing activities of recombinant PON1 proteins. In our previous work (Ishizuka et al., 2010), the OM-hydrolyzing activity in human plasma was strongly inhibited by p-chloromercuribenzoic acid (a free thiol modifier) and EDTA (a divalent cation chelator), which are both PON1 inhibitors, but was not sensitive to diisopropyl fluorophosphate (an organophosphatase), which inhibits cholinesterases and carboxylesterases. The cross-species difference in plasma OM-hydrolyzing activities (abundant in rabbits and limited in rats, as shown in Fig. 2) also suggested the involvement of PON1 (Costa et al., 1990; Kuo and La Du, 1995) in OM bioactivation in plasma, rather than other plasma esterases. Therefore, we purified this OM-hydrolyzing activity according to the method historically used for PON1 purification (Gan et al., 1991). The N-terminal sequence (20 amino acids) of the extruded 48.5-kDa protein was, as we expected, identical to the N-terminal region spanning Ala2 to Gln21 of human PON1 (EC 3.1.8.1/EC 3.1.1.2).

In an attempt to confirm the OM-hydrolyzing activity of human PON1, we constructed recombinant human PON1 proteins, PON1_192QQ and PON1_192RR, in a mammalian cell line. We compared their enzyme characteristics with those of diluted human plasma and purified serum albumin, which was reported as another OM-hydrolyzing enzyme in human plasma. Consistent with the well known feature of paraoxonases as calcium-dependent metalloenzymes, both recombinant PON1 allosymes and diluted plasma showed calcium ion-dependent OM-hydrolyzing activities, whereas the activity of purified serum albumin was hardly affected by the metal ion replacements (Table 2).

OM was hydrolyzed slightly faster by recombinant PON1_192RR than by PON1_192QQ (Table 2). Genetic variability in human PON1 activity has been of interest and has been widely studied over the years. PON1 has two common coding-region polymorphisms, M55L and Q192R; more attention has been paid to the latter because it accounts for marked qualitative differences between the two allosymes in their...
concentration was 10-fold faster by PON1192R, floxacin-hydrolyzing activity was positively correlated with the para-
prodrug-type antibacterial agent with a medoxomil moiety (like OM), whereas most organophos-
phabetes at approximately equivalent rates, whereas most organophos-
pheres at approximately equivalent rates, whereas most organophos-
phases are hydrolyzed by the PON1 192Q and 192R allo-
ness et al., 1998a,b; Costa et al., 2003). Some ester substrates, such as

affinity for and catalytic activity with a number of substrates (Mack-
ness et al., 1998a,b; Costa et al., 2003). Some ester substrates, such as

phenyl acetate, are hydrolyzed by the PON1 192Q and 192R allo-
zymes in prodrug activation, in the same manner as OM
bioactivation. When these results are considered together with the result regarding
the paraoxon-hydrolyzing activity was 9-fold (Tougou et al., 1998).
The authors showed that the prulifloxacin-hydrolyzing activity was positively correlated with the para-
noxon-hydrolyzing activity (which is catalyzed faster by PON1102Q), which suggests that the PON1092R
zyme in prodrug activation, in the same manner as OM
bioactivation. The interindividual variation in the prulifloxacin-hydro-
lyzing activity was reported to be only 2-fold, whereas the variation in the para-
noxon-hydrolyzing activity was 9-fold (Tougou et al., 1998). When these results are considered together with the result regarding
OM, the effects of the PON1 Q192R polymorphism on the bioacti-
vation of prodrugs with a medoxomil moiety is not considered to be
significant. As another example, the latest research on PON1 involve-
ment in the hydrolysis of pilocarpine, which is used as a treatment for
xerostomia, demonstrated higher activity of the R/R genotype, com-
pared with the Q/R and Q/Q genotypes, by using 50 individual human
plasma samples (Hioki et al., 2011). The analogy of this polymorphic
phenomenon in the pilocarpine lactone ring-opening reaction to those
of the medoxomil prodrugs described above seems to be attributable
to the structural similarity in the hydrolyzed groups of these drugs.

Next, we evaluated the contribution of the two plasma hydrolases,
PON1 and albumin, to OM bioactivation in human plasma. In a com-
parison of kinetic parameters between these two proteins (Table 3), a significantly lower $K_m$ and higher $V_{max}$, resulting in a higher
$V_{max}/K_m$ for recombinant PON1 demonstrated a larger capacity of
PON1 for OM hydrolysis, compared with albumin. Because albumin is the most abundant protein in plasma, however, it is still possible
that albumin plays a certain role in OM bioactivation in human plasma. Indeed, a several hundred-fold difference in PON1 (~0.2 mg
protein/ml) (Garin et al., 1997; Connelly et al., 2008) and albumin (~40 mg protein/ml) concentrations in human plasma numerically
offset the difference in the in vitro catalytic efficiencies of these
purified proteins. Therefore, we directly examined the contributions of
PON1 and albumin by using human plasma in immunoprecipitation
assays with specific IgG fractions against these two proteins. The
anti-PON1 IgG completely abolished the OM-hydrolyzing activity in human
plasma, whereas maximal inhibition of only 30% was observed with the antialbumin IgG (Fig. 5), which suggests a predom-
ine contribution of PON1 rather than albumin. Similar to the find-
ings for OM, Tougou et al. (1998) reported that human serum albumin
had prulifloxacin-hydrolyzing activity but the contribution of albumin
to the total activity in human serum was <5%, and the authors

TABLE 4

<table>
<thead>
<tr>
<th>Fraction</th>
<th>Incubation Buffer</th>
<th>Velocity</th>
<th>Protein Content</th>
<th>Distribution of OM-Hydrolyzing Activity</th>
</tr>
</thead>
<tbody>
<tr>
<td>VLDL and chylomicron</td>
<td>Tris-HCl/Ca$^{2+}$</td>
<td>13.9</td>
<td>0.174</td>
<td>2.42 (0.4)</td>
</tr>
<tr>
<td>LDL</td>
<td>Tris-HCl/Ca$^{2+}$</td>
<td>12.6</td>
<td>0.323</td>
<td>4.07 (0.6)</td>
</tr>
<tr>
<td>HDL</td>
<td>Tris-HCl/Ca$^{2+}$</td>
<td>277</td>
<td>2.15</td>
<td>596 (93.4)</td>
</tr>
<tr>
<td>LPDS</td>
<td>Tris-HCl/Ca$^{2+}$</td>
<td>0.516</td>
<td>69.0</td>
<td>35.6 (5.6)</td>
</tr>
<tr>
<td>LPDS</td>
<td>KPB</td>
<td>0.131</td>
<td>69.0</td>
<td>9.04 (N.C.)</td>
</tr>
</tbody>
</table>

N.C., not calculated.

concluded that PON1 is mainly responsible for the hydrolysis of prulifloxacin.

Furthermore, the distribution pattern for the OM-hydrolyzing ac-
tivity in serum lipoprotein fractions and LPDS, with most of the activity
located in the HDL fraction (Table 4), brings us evidence showing the practically exclusive involvement of PON1 in plasma
OM hydrolysis. PON1 is an enzyme secreted into the blood, where it
resides on HDL particles. Studies showed that both the activity and
stability of PON1 are highly dependent on the HDL components (La
Du et al., 1993; Sorenson et al., 1999). Gaidukov and Tawfik (2005)
demonstrated that the stability and lactonase activity of recombinant
PON1 were dramatically stimulated by treatment with apolipoprotein
A-1-containing HDL; in addition, the paraoxonase and arylesterase
activities were stimulated with HDL particles regardless of the apo-
lipoprotein content. The association of PON1 with human phosphate-
binding protein, a HDL component with a molecular weight similar to
that of PON1, is highlighted to be essential for preserving active
conformations of the enzyme (Rochu et al., 2007; Renault et al.,
2010). Lacking these HDL components as chaperones might explain
the considerably lower affinity for OM of our recombinant PON1
proteins, compared with that of natural PON1 in diluted human
plasma in the enzyme kinetic analysis (Table 3).

OM is an orally administered prodrug. After oral administration of
the prodrug, first-pass bioactivation may occur in the intestine, fol-
lowed by the portal blood and liver, before the prodrug reaches the
systemic circulation. We discovered the involvement of an unknown
human protein, CMBL, in OM bioactivation in the intestine and liver
(Ishizuka et al., 2010). High metabolic clearance of intestinal CMBL
suggests that the intestinal bioactivation firstly and predominantly
contributes to the quick onset of drug action after oral administration
of OM. For reference, the intestinal first-pass availability in the
prodrug form was estimated to be several percent in QClaw
model predictions (Yang et al., 2007) using the in vitro clearance for intes-
tinal CMBL and a permeability estimate for OM (see Supplemental
Method 1). However, the plasma esterase PON1, presumably in the
portal blood, may play a supplemental role to complete the bioacti-
vation of prodrug molecules that escape hydrolysis by CMBL in the
intestine. Although the transit time through portal blood is quite short,
the possibility of a significant contribution of plasma PON1 was
indicated in our previous publication (Kobayashi et al., 2000), which
showed that OM hydrolysis proceeds in human plasma with a half-life
of less than several seconds. This multiple-enzyme contribution at
multiple sites is considered to effectuate the minimal risk of signifi-
cant interindividual variation regardless of possible inhibition by
concomitantly administered drugs or genetic polymorphisms in
CMBL that may cause varied production of the pharmacologically
active metabolite. No components other than the active metabolite
olmesartan were detected in plasma after oral administration of ra-
References


Supplemental Method 1

The intestinal first-pass availability ($F_G$) of OM after oral administration was estimated using the $Q_{Gut}$ model (Yang et al., 2007) with the equation (1):

$$F_G = \frac{Q_{Gut}}{Q_{Gut} + fu_{Gut} \cdot CL_{int \ Gut}}$$  

where $F_G$ represents intestinal availability, $CL_{int \ Gut}$ represents unbound intestinal intrinsic clearance, and $fu_{Gut}$ represents the fraction unbound in the enterocytes. $Q_{Gut}$ is a hybrid parameter of the two more fundamental parameters, $CL_{perm}$ representing permeability through the enterocyte membrane and $Q_{villi}$ representing villous blood flow:

$$Q_{Gut} = \frac{Q_{villi} \cdot CL_{perm}}{Q_{villi} + CL_{perm}}$$  

Here, $Q_{Gut}$ was simulated by simCYP software (version 11, Symcyp Ltd.) based on the equation (2) using the topological polar surface area of OM molecule 154, to estimate the membrane permeability, and $Q_{villi}$ of 18 l/h. To calculate $CL_{int \ Gut}$ of 7290 ml/min/man, in vitro metabolic intrinsic clearance of OM in human intestinal cytosol (Ishizuka et al., 2010), experimentally determined the unbound fraction of OM in the incubation mixture, 0.953, by ultrafiltration method, and published scaling factors (Cubitt et al., 2011; Davies and Morris, 1993) were used. With the $fu_{Gut}$ values ranging 1 to 0.1, $F_G$ resulted in 0.01 to 0.08.

Reference

