Identification of Amiodarone Metabolites in Human Bile by Ultraperformance Liquid Chromatography/Quadrupole Time-of-Flight Mass Spectrometry

Pan Deng, Tiangeng You, Xiaoyan Chen, Tao Yuan, Haihua Huang, and Dafang Zhong

ABSTRACT:
Amiodarone is recognized as an effective drug in the treatment of arrhythmias. Previous experiments demonstrated that mono-N-desethylamiodarone (MDEA) was the major circulating metabolite in humans. In addition, dealkylation, hydroxylation, and deamination were minor metabolic pathways. The purpose of this study was to identify the metabolites of amiodarone in the bile obtained from patients with T-tube drainage after oral drug administration. Amiodarone metabolism in vitro was also investigated using human liver microsomes (HLMs) and S9 fraction. Ultraperformance liquid chromatography/quadrupole time-of-flight mass spectrometry (UPLC-Q/TOF MS) revealed 33 metabolites in human bile, including 22 phase I and 11 phase II metabolites. The major metabolites were MDEA (M7) and ω-carboxylate amiodarone (M12). Metabolite M12 was isolated from human bile, and the chemical structure was confirmed using UPLC-Q/TOF MS and 1H NMR. Moreover, the authentic standards of two hydroxylated metabolites, 2-hydroxylamiodarone and 3'-hydroxylamiodarone, were obtained through microbial transformation. Several novel metabolic pathways of amiodarone in human were proposed, including ω-carboxylation, deiodination, and glucuronidation. The in vitro study demonstrated that incubation of HLMs with amiodarone did not give rise to any carboxyl metabolites. In contrast, M12 and its metabolites were detected in human liver S9 incubation samples, and the production of these metabolites was inhibited almost completely by 4-methylpyrazole, an inhibitor of alcohol dehydrogenase, suggesting the involvement of alcohol dehydrogenase in the ω-carboxylation of amiodarone. Overall, UPLC-Q/TOF MS analysis leads to the discovery of several novel amiodarone metabolites in human bile and underscores the importance of bile as an excretion pathway.

Introduction
Amiodarone is a class III antiarrhythmic benzofuran derivative with extensive clinical usage in the treatment of life-threatening ventricular and supraventricular arrhythmias (Naccarelli et al., 2000). It is an amphiphilic Compound with high iodine content. Current understanding of the metabolism of amiodarone is incomplete, and only a few studies have been conducted on the human metabolism of amiodarone. Ha et al. (2005) reported that mono-N-desethylamiodarone (MDEA) was the major metabolite of amiodarone in human plasma and that further metabolism of MDEA leads to the formation of ω-carboxyl amiodarone (MDEO), di-N-desethylamiodarone (DDEA), and deaminated amiodarone (DAA). Moreover, amiodarone and its metabolites could release iodine in vivo (Broekhuysen et al., 1969), which may cause amiodarone-induced thyroid dysfunction during therapy (Marino et al., 1984, 1988; Pitsiavas et al., 1999). However, no deiodinated metabolites have ever been detected in humans. In addition, little is known about the major elimination route of amiodarone, although previous studies suggested that biliary rather than renal clearance was the major route of excretion (Broekhuysen et al., 1969; Latini et al., 1984).

The objective of the present study was to investigate the metabolism of amiodarone in human bile using ultraperformance liquid chromatography/quadrupole time-of-flight mass spectrometry (UPLC/Q-TOF MS). Human bile samples were obtained from T-tube drainage of patients suffering from hepatobiliary diseases and arrhythmia. The metabolite profiles of amiodarone in human bile were characterized after oral administration to patients enrolled in the clinical study. In addition, the formation of the major oxidized metabolite was further investigated in vitro using human liver microsomes (HLMs) and S9 fraction.

Materials and Methods
Materials. Amiodarone hydrochloride and 4-methylpyrazole (4-MP) hydrochloride were purchased from Sigma-Aldrich (St. Louis, MO). Pooled HLMs and S9 fraction were purchased from BD Gentest (Woburn, MA). Pooled HLMs and S9 fraction were purchased from BD Gentest (Woburn, MA). The microbial strain Cunninghamella blakesleean als was purchased from DSM 37671/3689563.
the Institute of Microbiology, Chinese Academy of Sciences (Beijing, China). All solvents used for UPLC/Q-TOF MS were of HPLC grade (Merck, Darmstadt, Germany). All solvents used for gel chromatography were of analytical grade (Shanghai Chemical Plant, Shanghai, China). Purified water was generated by a Milli-Q Gradient system (Millipore Corporation, Molsheim, France). Silica gel (300–400 mesh), specifically Sephadex LH-20 gel (GE Healthcare, Chalfont St. Giles, Buckinghamshire, UK), was used for column chromatography, and precoated silica gel GF254 plates (Qingdao Marine Chemical Plant, Qingdao, China) were used for thin-layer chromatography.

### In Vitro Metabolite Profiling

**Subject and sample collection.** Three patients (one male and two females, 66–89 years old) suffering from cardiac arrhythmia, and who had been surgically treated for hepatobiliary diseases, were enrolled in this study after giving informed consent. The clinical study was performed at the Shanghai East Hospital (Shanghai, China) in accordance with the Declaration of Helsinki and was consistent with State Food and Drug Administration guidelines for good clinical practice (http://www.chinadeflaw.com/laws/detail_140.html). The study protocol was approved by the hospital ethics committee. After patients had received oral doses of amiodarone hydrochloride tablet (200 mg/day) for the previous 7 days, bile was collected intermittently (approximately 10 ml) in 1-h intervals for a total of 24 h from their T-tubes. Bile samples were stored at −20°C until analysis.

**Bile sample preparation and β-glucuronidase hydrolysis.** Two hundred microliters of acetonitrile was added to a 100-μl aliquot of bile sample. After it was vortex mixed and centrifuged at 11,000g for 5 min, the supernatant was transferred into a glass tube, evaporated to dryness under a stream of air at 40°C, and reconstituted in 100 μl of acetonitrile and water (10/90, v/v). Hydrolysis of glucuronide conjugates was performed using β-glucuronidase (2000 units of Type HA-4; Sigma-Aldrich). For enzymatic incubation, a 200-μl aliquot of bile sample was mixed with 200 μl of β-glucuronidase (in 1 M carbonate buffer solution at pH 5.0). The incubation was performed at 37°C for 16 h. The effect of the glucuronidase was studied by comparing the LC/MS peak intensities for compounds of interests before and after the enzymatic incubation. The compounds of interest included glucuronide conjugates and their nonglucuronidated forms (hydrolyzed forms).

**UPLC-Q/TOF MS.** Chromatographic separation for metabolite profiling was achieved using an Acquity UPLC system (Waters, Milford, MA) on an Acquity UPLC HSS T3 column (1.8 μm, 2.1 × 100 mm; Waters). The mobile phase was a mixture of 0.05% formic acid in water (A) and 0.05% formic acid in acetonitrile (B). The gradient elution started from 5% B, increased linearly to 70% B over 15 min, increased linearly to 100% B over the next 2 min, and finally decreased to 5% B to reequilibrate the column. The column temperature was set at 40°C, and the flow rate was 0.4 ml/min. The elute was monitored by UV detection at 265 nm. The MS detection was conducted using a Synapt Q-TOF high-resolution mass spectrometer (Waters) operated in positive ion electrospray mode. Nitrogen and argon were used as the atmospheric pressure ionization and collision gas, respectively. Data were acquired from 80 to 1000 Da using a source temperature of 100°C, a desolvation temperature of 350°C, and cone voltage of 50 V. Data were centroided during acquisition using an internal reference comprising a 400-ng/ml leucine enkephalin solution infused at 5 μl/min to generate a reference ion in positive ion electrospray mode at m/z 556.2771. Data acquisition was achieved using MS², which has two separate scan functions that are programmed with independent collision energies. In this way, a low collision energy scan can be immediately followed by a scan in which the collision energy is ramped over a higher range to induce fragmentation of the ions transmitted through Q1. Acquiring data in this manner provided for collection of intact precursor ions as well as fragments.

The mass spectrometer and UPLC system were controlled by MassLynx 4.1 software (Waters). Data processing was performed using a MetaboLynx software (Waters) operated in positive ion electrospray mode at m/z 10/90. The mass spectrometer and UPLC system were controlled by MassLynx 4.1 software (Waters). The MetaboLynx software was used to acquire and process the UPLC-Q/TOF MS data. Data processing was performed using a MetaboLynx software (Waters). The MetaboLynx software was used to acquire and process the UPLC-Q/TOF MS data.

### Microbial transformation and isolation of hydroxylated metabolites.

**Frozen microbial stock culture of C. blakesleeanus AS 3.153 was incubated in 250-ml flask containing potato dextrose agar (Difco, Beijing, China) at 27°C for 7 days in a rotary shaker set to 200 rpm. At the end of this period, the seed culture (10 ml) was inoculated into 250-ml flasks containing 50 ml of bio-transformation medium, which consisted of dextrose (2.0 g), yeast extract (0.5 g), peptone (0.5 g), NaCl (0.5 g), and K₂HPO₄ (0.5 g) in 100 ml of distilled water. After incubation at 28°C and 200 rpm for 24 h, a 0.5-ml portion from the first-stage culture was used to inoculate a second-stage culture that was incubated for 24 h before the addition of amiodarone in methanol (9:1, v/v) for a final concentration of 640 μg/ml. The methanol content in the transformation system was less than 2%. After 3 days, the fermentation was harvested, and the cells were removed by centrifugation (2000g, 10 min).

The supernatant (1500 ml) was extracted three times with EtOAc (1500 ml). The EtOAc-soluble fraction was subjected to silica gel chromatography in a gradient (CH₂Cl₂/MeOH/Et₂NH, 15/1/0.1 to 0/1/0.1, v/v/v) to yield three fractions (A–C). Fraction B was purified by semi-preparative HPLC (A: MeOH; B: H₂O with 5% acetic acid and 5% Et₂NH; A/B = 80:20, 3 ml/min) to isolate the hydroxy metabolites.

The structures of the three standard compounds were characterized by high-resolution Q-TOF mass spectrometry and NMR. The NMR spectra were recorded on a Bruker AM-400 (Bruker, Newark, DE) or an INOVA 600 spectrometer (Varian, Palo Alto, CA) using tetramethylsilane as an internal standard. All compounds were dissolved in deuterated methanol. Chemical shifts are expressed as parts per million relative to tetramethylsilane.

### In Vitro Metabolite Profiling

All incubations were performed at 37°C in a water bath. A stock solution of amiodarone was prepared in dimethyl sulfoxide. The final concentration of dimethyl sulfoxide in the incubation was 0.1% (v/v). The HLMS and human liver S9 fraction were carefully thawed on ice before the experiment. Amiodarone (50 μM) was mixed with each subcellular fraction (the concentrations of microsomal protein are 1.0 mg/ml for HLM and 2.0 mg/ml for human liver S9) in 100 mM potassium phosphate buffer (pH 7.4). The total incubation volume was 200 μl. After 3 min of preincubation at 37°C, the incubation reactions were initiated by the addition of NADPH (2.0 mM). After a 60-min incubation, the reactions were terminated with an equal volume of ice-cold acetone. To determine the enzymatic pathways involved, separate incubations with human liver S9 were performed in the presence of 4-MP at the final concentration of 5 μM (Sohlenius-Sternbeck et al., 2000; Chernela et al., 2001). Control samples containing no NADPH or substrates were included. Each of the incubations was performed in duplicate. The samples were analyzed using UPLC/Q-TOF MS.

### Results

**UPLC-Q/TOF MS Analysis of Amiodarone.** To identify amiodarone metabolites, the chromatographic and MS fragmentation behaviors of the parent compound were first investigated. The retention time of amiodarone was 18.0 min under the chromatographic conditions used. In positive scan mode, amiodarone formed a protonated molecule [M + H]⁺ at m/z 646.029. Figure 1A shows the product ion spectrum of amiodarone under the high-collision energy scan. On the basis of the high-resolution mass spectral information, a tentative pathway for the formation of the most informative fragment ions of amiodarone is proposed in Fig. 1B. The fragments of amiodarone were formed predominantly by the cleavage of alkyl C-O bond, loss of the 5-keto substituent of the benzofuran moiety, and cleavage of the C-N-bond. Product ions at m/z 372.831, 276.082, 247.078, 245.956, 217.926, 201.094, 119.021, and 100.113 (100% abundance) were
observed. Detection of these ions in the high collision energy mass spectra of metabolites indicated the unmodified benzo[2][1]furan structure (m/z 201.094), hydroxybenzaldehyde moiety (m/z 372.830 and 245.956), or unchanged triethylamine (m/z 100.113). According to this fragment pattern, the structure of amiodarone was divided into three parts, A, B, and C (Fig. 1B). The high collision energy mass spectra and chromatographic behaviors of detected metabolites were compared with those of the parent compound and available authentic standards to characterize the structural modification.

Amiodarone Metabolites in Human Bile. As shown in Fig. 2A, 33 metabolites of amiodarone were detected in human bile samples. Table 1 lists the detailed information of these metabolites, including the retention times, proposed elemental compositions, and the characteristic fragment ions. The structures of metabolites were characterized by mass spectral fragmentation patterns or confirmed by comparison of chromatographic retention times and mass spectra with available reference standards. Proposed structures of the detected metabolites are shown in Fig. 3.

Parent drug M0. A chromatographic peak at 18.0 min was detected with an elemental composition of C_{25}H_{29}I_{2}NO_{3} and a protonated molecular weight of 646.032. The retention time and mass spectral fragmentation patterns were identical to the parent drug, amiodarone, indicating that this component was unmetabolized amiodarone, designated as M0.

Metabolite M1. Metabolite M1 had a retention time of 16.2 min, exhibited a protonated molecule at m/z 492.104, and had the elemental composition of C_{23}H_{25}I_{2}NO_{3}, suggesting the loss of C_{6}H_{13}I from amiodarone. M1 was consequently proposed as a deiodinated metabolite of N-desethylated amiodarone. The absence of the fragment ion at m/z 100.113 was consistent with modification on the triethylamine moiety.

Metabolite M2. Metabolite M2 was eluted at 13.1 min. It had a protonated molecular weight of 508.099, and accurate mass measurement revealed the chemical formula C_{23}H_{26}INO_{4}, suggesting monohydroxylation of molecule M1. At low collision energy scan, the fragment ions at m/z 437.024 and 419.017 were observed, which resulted from the cleavage of O-C_{14} bond (-71.075 Da, loss of C_{4}H_{9}N) and additional loss of water (-18.007 Da), indicating that hydroxylation occurred on the n-butyl side chain.

Metabolite M3. Metabolite M3 was eluted at 16.3 min with a protonated molecular weight of 546.927. The elemental composition of the metabolite was C_{19}H_{16}I_{2}O_{3}, suggesting the loss of C_{6}H_{13}N from the parent compound. The major fragment ion at m/z 372.858 was the same as that of the parent drug, whereas the fragment ion at m/z 100.113 was absent, indicating the loss of the triethylamine moiety. M3 was thus identified as the O-dealkylated metabolite of amiodarone resulting from removal of the triethylamine moiety.

Metabolite M4. Metabolite M4 had a retention time of 13.3 min, exhibited a protonated molecule at m/z 550.109, and had a derived formula of C_{25}H_{28}INO_{5}, suggesting the addition of two oxygen atoms and loss of two hydrogen atoms from deiodinated amiodarone. High collision energy analysis revealed product ions at 276.070 and 100.113 that were the same as those of the parent drug, indicating
benzofuran and triethylamine moieties were intact. Metabolite M4 was tentatively identified as deiodinated amiodarone with $\omega$-oxidation of the $n$-butyl side chain to a carboxylic acid.

**Metabolite M5.** Metabolite M5 was eluted at 21.5 min with a protonated molecular weight of 590.953. The elemental composition of the metabolite was $\text{C}_{21}\text{H}_{20}\text{I}_{2}\text{O}_{4}$, consistent with deamination and hydroxylation of amiodarone. Cleavage of the O-C$_{14}$ bond (110.023 Da, loss of $\text{C}_2\text{H}_4\text{O}$) produced the fragment ion at $m/z$ 546.930, indicating that hydroxylation occurred in part C. The fragment ions at $m/z$ 372.818, 217.927, 201.091, and 91.018 originated from intact parts A and B. Therefore, M5 was proposed to be DAA identified previously in human plasma (Ha et al., 2005).

**Metabolite M6.** Metabolites M6-1 and M6-2 were eluted at 14.4 and 18.6 min, respectively, and both displayed a protonated molecule at $m/z$ 606.948. Accurate mass measurement showed that the chemical formula of both was $\text{C}_{21}\text{H}_{20}\text{I}_{2}\text{O}_{5}$, suggesting the addition of two oxygens and loss of $\text{C}_4\text{H}_9\text{N}$ from amiodarone. The major fragment ion at $m/z$ 372.858 was the same as that of the parent drug, and $m/z$ 100.113 fragment was absent, indicating modifications of parts A and C. Other fragment ions included $m/z$ 562.924 ($\Delta m = 44.024$ Da, loss of $\text{C}_2\text{H}_4\text{O}$) and its dehydrated form at $m/z$ 544.915 ($\Delta m = 562.924$ Da, loss of $\text{H}_2\text{O}$), indicating M6-1 and M6-2 were hydroxylation metabolites of M5. Considering the readily loss of water, the sites of hydroxylation for M6-1 and M6-2 were proposed to be on the $n$-butyl side chain.

**Fig. 2.** Metabolite profiles of amiodarone in human bile after once-daily oral administration of 200 mg of amiodarone hydrochloride for 7 days (A) and extracted ion chromatograms of amiodarone metabolites M8 (B), M11 (C), and M18 (D).
Metabolite M7. Metabolite M7, eluted at 17.0 min, had a protonated molecular weight of 618,000, which is 28,031 Da lower than the parent drug. The elemental composition of the metabolite was C_{25}H_{29}I_{2}NO_{4}, indicating the loss of C_{6}H_{13} from the parent molecule. This metabolite contained fragment ions at m/z 372,858 and 201,090, indicating that parts A and B were intact. The absence of the fragment at m/z 100,113 suggested that M7 was N-desethylated amiodarone. It was shown to be one of the major metabolites in human bile on the basis of the chromatographic peak area.

Metabolite M8. The protonated molecular weight of M8 was 633,995, which is 12,036 Da less than the protonated parent drug. Its elemental composition was C_{25}H_{29}I_{2}NO_{4}, indicating the loss of C_{6}H_{13} from the parent molecule. Five peaks with a protonated ion at m/z 633,995 were detected at 13.5 min (M8-1), 13.7 min (M8-2), 14.0 min (M8-3), 14.4 min (M8-4), and 14.7 min (M8-5) (Fig. 2B). The fragment at m/z 100,113 was absent for these five metabolites, indicating that part C was modified. The fragment at m/z 372,820 suggested that the site of hydroxylation was not on part B. These metabolites were proposed to be monohydroxylated metabolites of M7. Moreover, the fragments of M8-2, M8-3, and M8-4 all included the ions at m/z 562,922 and 544,908, which were the same as those for M6, suggesting the site of hydroxylation was on the n-butyl chain.

Metabolite M9. Metabolite M9 was eluted at 13.4 min and possessed a protonated molecular weight of 647,974. The elemental composition of M9 was C_{23}H_{25}I_{2}NO_{4}, indicating the addition of two oxygen atoms and the loss of two hydrogen atoms from amiodarone to form an N-desethyl metabolite of carbocyclicarion.

Metabolite M10. Metabolites M10-1 and M10-2 eluted at 11.6 and 12.0 min, respectively, and yielded a protonated molecule at m/z 649,990. Accurate mass measurement demonstrated that the chemical formula was C_{23}H_{25}I_{2}NO_{3}, indicating the addition of two oxygen atoms to N-desethylated amiodarone. The high-energy mass spectrum of M10-1 and M10-2 revealed a characteristic fragment ion at m/z 372,823, and several fragment ions originated from part B were also observed at m/z 245,923, 217,928, 119,016, and 91,020. However, the mass spectrometry data did not reveal the site of dihydroxylation. M10-1 and M10-2 were proposed to be monohydroxylated metabolites of M8.

Metabolite M11. Metabolite M11 had a protonated molecular weight of 662,026, 15,993 Da higher than that of protonated amiodarone. The elemental composition of the metabolite was C_{25}H_{29}I_{2}NO_{4}, indicating that an oxygen atom had been introduced into the parent molecule. Fragmentation patterns and HPLC retention times for M11-1 and M11-2 were identical. The fragment at m/z 372,820, 12.0 min, respectively, and yielded a protonated molecule at m/z 372,820, 100,113, 91,020.
tion times of the isolated metabolites from in vitro incubations were identical to those detected in human bile. Proton chemical shifts for metabolites are summarized in Table 2. Comparing the $^1H$ one-dimensional spectra of M11-2 and amiodarone indicated that aromatic ring proton signals in part A were unchanged but that the $n$-butyl side chain in M11-2 might have been hydroxylated. An oxygenated methine signal at $\delta_{H} 3.69$ (m, 1H) and a doublet methyl signal at $\delta_{H} 1.15$ (d, $J = 7.2$ Hz, 1H) indicated that the hydroxyl was attached to C-3 ($\delta_{C} 66.4$). The HMBC correlations (Fig. 4) from $H_3-4$ to $C_3$, $H_2-1$, and $H_2-2$ to $C_3$ and from $H-3$ to $C-1$, $C-2$, and $C-4$ supported the above assignment. M11-2 was, accordingly, confirmed to be 3-hydroxylamiodarone. In the $^1H$ NMR spectrum of M11-5, a typical ABX proton coupling system of an aromatic ring at $\delta_{H} 6.94$ (d, $J = 1.7$ Hz, 1H), 6.78 (dd, $J = 8.5$, 1.7 Hz, 1H), and 7.23 (d, $J = 8.5$ Hz, 1H) indicated the presence of a trisubstituted phenyl ring, and the site of hydroxylation was narrowed to position C-2 or C-3. The heteronuclear single quantum correlation spectrum allowed the assignment of all protons to their bonding carbons. The hydroxylation site remained ambiguous after detailed analysis of the HMBC spectrum, however. Fortunately, the relative upfield chemical shift of $C_1$ at $\delta_{C} 97.2$ implied that the hydroxyl group in M11-5 was attached to C-2, which was caused by the electron-donating effect of the oxygen. Metabolite M11-5 was therefore identified as 2-hydroxyamiodarone. The hydroxylation site for M11-1 was tentatively proposed at C-4, which led to the formation of $\beta$-hydroxylamiodarone.

**TABLE 2**

$^1H$ NMR spectra data of amiodarone, 4'-carboxylamiodarone, 2-hydroxylamiodarone, and 3'-hydroxylamiodarone

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<th>Number</th>
<th>Amiodarone</th>
<th>4'-Carboxylamiodarone</th>
<th>2-Hydroxylamiodarone</th>
<th>3'-Hydroxylamiodarone</th>
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<tr>
<td>1</td>
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<td>15</td>
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<td>3.36 (t, $J = 6.1$ Hz, 2H)</td>
<td>3.18 (t, $J = 6.0$ Hz, 2H)</td>
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<td>1.42 (m, 2H)</td>
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<tr>
<td>4'</td>
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<td>0.95 (t, $J = 7.0$ Hz, 3H)</td>
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372.823, 245.926, 217.925, and 100.122 that originated from intact parts B and C, suggesting that part A has been oxidized. The $^1$H NMR data were obtained for M12 isolated from human bile. Compared to the spectrum of the parent compound (Fig. 5), two methylene proton signals at $\delta_H$ 4.29 (t, $J = 6.1$ Hz, 2H) and 3.36 (t, $J = 6.1$ Hz, 2H) and two N-ethyl signals at $\delta_H$ 3.04 (q, $J = 6.9$ Hz, 4H) and 1.25 (t, $J = 6.9$ Hz, 6H) were observed, supporting the idea that part C was intact. In addition, the signals of aromatic protons in M12 were in the same range as those of the parent molecule, suggesting that the two aromatic rings in parts A and B were unmodified. Together, these data indicated that the n-butyl side chain was the site of modification for M12. Further analysis of the $^1$H NMR spectrum revealed that the proton signals of CH$_2$-2 ($\delta_H$ 2.06, m, 2H) and CH$_2$-3 ($\delta_H$ 2.21, m, 2H) were shifted downfield and that the C-4 methyl signal of the parent compound disappeared, indicating the presence of an electron-withdrawing group in C-4. The structure of M12 was thus determined to be 4'-carboxylamiodarone.

Metabolite M13. Metabolite M13, eluted at 11.9 min, had a protonated molecular weight of 726.141 and a derived formula of C$_{31}$H$_{36}$INO$_{11}$. High collision energy analysis revealed a characteristic product ion at m/z 550.112 that was due to a neutral loss of 176.027 Da from protonated M13, suggesting that this metabolite was a glucuronide of M4. The position of the glucuronic acid was not determined.

Metabolite M14. Metabolite M14 was eluted at 18.1 min and had a protonated molecular weight of 766.985. The elemental composition of the metabolite was C$_{32}$H$_{25}$I$_2$O$_{10}$, consistent with the deamination, hydroxylation, and glucuronide conjugation. The fragment ion at m/z 590.954 corresponded to a neutral loss of 176.033 Da, and the other characteristic fragment at m/z 546.930 resulted from additional cleavage of the O-C$_{14}$ bond (−44.024 Da, loss of C$_2$H$_4$O). This was the same bond cleaved in DAA (M5), indicating that M14 was the glucuronide-conjugated metabolite of M5.

Metabolite M15. Metabolites M15-1 and M15-2 were eluted at 12.2 and 19.6 min, respectively, and had a precursor ion at m/z 810.027, 176.032 Da larger than M8 (m/z 633.995). Accurate mass measurement demonstrated the chemical formula to be C$_{29}$H$_{33}$I$_2$NO$_{10}$, suggesting that M15-1 and M15-2 were glucuronide conjugates of M8 (m/z 633.989, C$_{23}$H$_{25}$I$_2$NO$_4$). The fragment at m/z 633.998, observed for both M15-1 and M15-2, was formed by neutral loss of 176.036 Da. Metabolite M15-1 produced fragment ions at m/z 562.931 and 544.912, which were the same as those for M6. Therefore, the site of hydroxylation for M15-1 was proposed to be on the n-butyl side chain.
The major fragment ion for M15-2 was m/z 372.824, indicating the site of modification was not on part B.

**Metabolite M16.** Metabolite M16 was eluted at 16.3 min and had a protonated molecular weight of 822.064. The elemental composition of this metabolite was C30H23I2NO26, corresponding to the glucuronide conjugate of amiodarone. The major fragment ion at m/z 646.024 was due to a neutral loss of 176.037 Da. M16 was therefore proposed to be a glucuronide of amiodarone, and the site of conjugation was tentatively assigned at the tertiary amine group.

**Metabolite M17.** Metabolite M17 was eluted at 12.1 min and had a protonated molecular weight of 824.007, 176.032 Da larger than M1 (m/z 662.026). Under high collision energy scan, M17 produced a fragment ion at m/z 647.980 resulting from a loss of the neutral glucuronic acid moiety (176.032 Da), indicating the presence of a glucuronic moiety. M17 was proposed to be a glucuronide of M9. The site of conjugation was not established.

**Metabolite M18.** Metabolites M18-1, M18-2, and M18-3 were eluted at 12.6, 12.8, and 13.0 min, respectively (Fig. 2D), and had a precursor ion at m/z 388.059, 176.032 Da larger than M1 (m/z 662.026). Under high collision energy scan, M18-1, M18-2, and M18-3 showed the same major fragment ion at m/z 646.027 due to neutral 176.023-Da loss. The remaining fragments at m/z 372.825 and 100.113 suggested an unchanged part B and part C. Therefore, M18-1, M18-2, and M18-3 were tentatively identified as the glucuronides of the hydroxyl-amiodarone with hydroxylation in part A. After β-glucuronidase hydrolysis, the intensity of the peaks corresponding to hydroxylated metabolites of M11-1, M11-2, and M11-5 all increased significantly. Therefore, metabolites M18-1, M18-2, and M18-3 could have been produced by hydroxylation of amiodarone at C-4’, C-3’, or C-2’, followed by the glucuronide conjugation.

**Metabolite M19.** Metabolites M19-1 and M19-2 were eluted at 12.4 and 12.9 min, respectively. They showed a precursor ion at m/z 852.038 and a derived elemental composition of C31H35I2NO11. The major fragment ion at m/z 676.009 indicated a neutral loss of 176.026 Da, suggesting that M19-1 and M19-2 were glucuronide conjugates of M12; however, the sites of conjugation were not established by the mass spectral data.

**Metabolism of Amiodarone In Vitro in Human Liver Microsomes and Human Liver S9.** Incubations of amiodarone in HLMs and human liver S9 were performed to determine the hepatic contribution to the overall disposition of this drug. As shown in Fig. 6, compared with the control sample, 18 oxidized metabolites of amiodarone were detected in HLM incubations. Besides those identified in human bile (M1, M3, M6, M7, M8, M10, and M11), deiodinated amiodarone (M21, m/z 520.138) and N-oxide metabolite (M11-6, m/z 662.021) were detected. After incubation with the human liver S9 fraction, several carboxylic acid metabolites were detected aside from those observed in HLMs, including M4, M9, and M12 (Fig. 7). The amiodarone metabolite profiles in HLMs and S9 were different from the profiles observed in human bile. As indicated by LC/UV detection, N-desethylamiodarone (M7) was the only principal species found in either HLMs or human liver S9 incubation, whereas other metabolites were all detected at much lower levels.

More importantly, 4’-carboxylamiodarone (M12) was not detected in the incubations of amiodarone with HLMs, and it was a minor metabolite in human liver S9 incubation in the presence of NADPH (Fig. 7). In another experiment, the human liver S9 was preincubated with 5 μM 4-MP for 10 min before the addition of 50 μM amiodarone and further incubation for 60 min. This resulted in potent inhibition of the formation of 4’-carboxylamiodarone, and the amount of 4’-carboxylamiodarone produced was approximately 10-fold lower in human liver S9 incubations treated with 4-MP than in control samples without 4-MP as determined from the LC/MS.

**Discussion**

In general, studies of drug metabolites in human subjects focus on blood, urine, and feces; however, drugs that have high molecular weights are often excreted in the bile. The threshold molecular weight of drugs and metabolites that are preferentially excreted into human bile ranges from 500 to 600 Da (Ghibellini et al., 2006). Biliary elimination of compounds can significantly influence their systemic or hepatic exposure and pharmacological effects. Amiodarone was speculated to be excreted primarily by hepatobiliary route because of its relative large molecular weight. Indeed, hepatobiliary elimination was supported by the fact that less than 0.5% of the dose was excreted in the urine (Anastasiou-Nana et al., 1982). Feces has been traditionally used to estimate the drug and metabolites excreted via bile in humans (Ghibellini et al., 2006). However, unstable metabolites, such as glucuronides that could be hydrolyzed along the intestine, cannot be characterized properly using this method. Therefore, investigations of amiodarone metabolites in human bile allow for direct identification of metabolites, including intact glucuronides.

In the present study, human bile samples were obtained in T-tube drainage from arrhythmia patients taking amiodarone. The samples were analyzed using the UPLC/Q-TOF MS method, and a total of 33 metabolites, including 22 phase I and 11 phase II metabolites, were detected in the bile extracts. The chemical structures of the metabolites were characterized by their accurate mass, by mass spectral fragmentation patterns, and by comparison to reference standards. In particular, 4’-carboxylamiodarone (M12), a major metabolite, was isolated from human bile, and two hydroxylated metabolites, M11-2 (3’-hydroxylamiodarone) and M11-5 (2-hydroxylamiodarone), were obtained through microbial transformation.

Previous investigations of amiodarone metabolism in humans revealed that MDEA was the major metabolite in human plasma (Flanagan et al., 1982) and tissues (Storey et al., 1983; Berdeux et al., 1984). Given the known pharmacological activity of this metabolite and the high plasma and tissue concentrations in patients treated with chronic amiodarone therapy, MDEA may be considered as an independent drug. In mammals, MDEA could be transformed to 3’-hydroxyl MDEA both in vivo and in vitro (Ha et al., 1996, 2001a,b, 2005), and 3’-hydroxylaton was regarded as a primary metabolite of MDEA in humans (Ha et al., 2005). Further dealkylation and deamination of MDEA could result in low amounts of DDEA and DAA in human plasma (Freedman and Somberg, 1991; Ha et al., 2005). In human urine, only negligible amounts of amiodarone and MDEA were detectable after oral drug dosing (Harris et al., 1983). In the present study, characterization of metabolites in human bile revealed that amiodarone was extensively metabolized before excretion into bile. Metabolite M7 (MDEA) was identified as one of the major metabolites in human bile, as it is in human plasma. Subsequent oxidation of MDEA lead to several monohydroxyl and dihydroxyl metabolites (M8 and M10), and oxidative deamination resulted in the formation of DAA (M5). However, neither DDEA nor its conjugated metabolites were detected in human bile sample.

On the basis of the chromatographic peak area, the other major route of metabolism was identified as ω-oxidation and the formation of 4’-carboxylamiodarone (M12), and the content of M12 in human bile was estimated to be approximately 3-fold higher than that of the parent drug. Considering that the ionization efficiency for metabolites and the parent drug may be different, the ionization efficiency of M12...
Fig. 6. In vitro metabolism of amiodarone (50 μM) mediated by human liver microsomes (1.0 mg/ml). Top, UPLC-Q/TOF MS chromatogram of a control incubation performed in the absence of NADPH. Middle, UPLC-Q/TOF MS chromatogram of an incubation performed in the presence of NADPH. Bottom, UPLC-UV chromatogram of an incubation performed in the presence of NADPH. The inset is the expanded chromatogram in the region of 11 to 17 min.
FIG. 7. In vitro metabolism of amiodarone (50 μM) mediated by human liver S9 (2.0 mg/ml). Top, UPLC-Q/TOF MS chromatogram of a control incubation performed in the absence of NADPH. Middle, UPLC-Q/TOF MS chromatogram of an incubation performed in the presence of NADPH. Bottom, UPLC-UV chromatogram of an incubation performed in the presence of NADPH. The inset is the expanded chromatogram in the region of 11 to 17 min.
and amiodarone were compared using standard compound solutions, and they demonstrated slight differences in ionization efficiency at the same concentration, with the MS response of M12 a little lower than that of amiodarone. This supported the conclusion that carboxylation represented a major metabolic pathway of amiodarone in humans. It has been reported previously that certain compounds with alkyl side chains can be metabolized to carboxylic acids (Harvey, 1989; Samara et al., 1990; Rucker et al., 1992; Söhlenius-Sternbeck et al., 2000), and the formation of these metabolites generally involves two steps, initial \( \omega \)-hydroxylation of the alkyl side chains by cytochromes P450 and further oxidation of the \( \omega \)-hydroxylated intermediates to \( \omega \)-carboxylic acid metabolites catalyzed by cytosolic alcohol dehydrogenase (Chmela et al., 2001; Walsh et al., 2002). Therefore, a possible mechanism for the formation of 4′-carboxyamiodarone could involve oxidation of the \( n \)-butyl side chain of amiodarone by cytochromes P450 to the \( \omega \)-hydroxyl intermediate, followed by oxidation by alcohol dehydrogenase to produce M12. In vitro experiments performed using HLMs and human liver S9 revealed five hydroxylated metabolites (M11), which were the same as those detected in human bile, whereas M12 could only be detected in incubations with liver S9 fraction. This observation suggested the presence of a liver cytosolic enzyme involved in the formation of M12. To demonstrate the involvement of alcohol dehydrogenase in the metabolism of amiodarone, 4-MP, an inhibitor of alcohol dehydrogenase, was preincubated with human liver S9, and the result showed that 4-MP almost completely inhibited the formation of metabolite M12. This finding supported the hypothesis that the second step in the formation of M12 is catalyzed by alcohol dehydrogenase. Among the five monohydroxyl metabolites detected in vivo and vitro, the retention time of M11-1 was the shortest (14.3 min); together with the mass spectral data, the hydroxylation site of M11-1 was proposed to be on the \( n \)-butyl side chain rather than benzylc carbons. Steric hindrance around the heme FeO\(^{3+}\) in cytochrome P450 enzymes limits hydroxylation of sterically hindered carbons, whereas it encourages hydroxylation at the terminal (\( \omega \)) and penultimate (\( \omega-1 \)) positions of aliphatic chains (Nassar et al., 2009); M11-1 was therefore tentatively identified as \( \omega \)-hydroxylamiodarone. Additional studies to prove the presence of \( \omega \)-hydroxylamiodarone are currently underway. In addition, greater insight into the cytochrome P450 enzymes and transporters involved in the formation and elimination of M12 might explain the wide variability of amiodarone pharmacokinetics in humans.

Although the drug metabolites of toxicological concern usually are those circulating in plasma at greater than 10% of parent systemic exposure, other metabolites also can elicit safety concern. For example, a metabolite that predominantly excreted into bile may result in bile duct toxicity (February 2008, FDA Guidance for Industry, Safety Testing of Drug Metabolites. Pharmacology and Toxicology; http://www.fda.gov/cder/guidance/). Therefore, further investigation is needed to understand the importance of metabolite M12 from a safety perspective.

Amiodarone contains approximately 37% iodine by weight, and the maintenance daily dose of the drug is 200 to 600 mg. However, the recommended daily intake of iodine is only 150 \( \mu \)g (Shiraiishi et al., 2006). Excess iodine released from the parent drug and its metabolites may contribute to the amiodarone-induced thyroid dysfunction, which is a common adverse effect of this drug (Bogazzi et al., 2001). However, the deiodination of amiodarone is still unclear and is a topic of considerable debate. A previous study proposed that deiodination was one of the metabolic pathways of amiodarone in humans (Freedman and Somberg, 1991), and Young and Mehendale (1986) reported that MDEA could be deiodinated in rabbit liver microsomes. However, others claimed that no deiodinated metabolites could be found in vivo and in vitro (Ha et al., 2001a, 2005). Using UPLC-Q/TOF MS as an analytical tool, we observed several ions that could be related to the presence of deiodinated metabolites in human bile (M1, M2, M4, and M13) and in vitro (M1, M2, M4, and M21). Although deiodination is a minor metabolic pathway of amiodarone in humans, attention should be paid to the impact of the relative high amount of iodine released from amiodarone on human health during chronic drug treatment.

Glucuronide conjugation was another metabolic pathway of amiodarone identified in human bile. It was reported that amiodarone could undergo extensive enterohepatic circulation (Freedman and Somberg, 1991; Roden, 1993). Glucuronidation of the metabolites and biliary excretion was thought to be the final elimination process for amiodarone (Freedman and Somberg, 1991). However, the phase II metabolism of amiodarone had not been comprehensively studied, although there is indirect evidence (after hydrolysis) for glucuronide metabolites of amiodarone in human plasma (Ha et al., 2005). The results from the present study demonstrated that glucuronidation was the most important conjugation pathway for amiodarone and its phase I metabolites. Indeed, 11 glucuronide conjugates were identified in human bile samples. Amiodarone has a triethylamine moiety, and N-glucuronidation has proven to be a common metabolic pathway in the human metabolism of drugs with an aliphatic tertiary amine group (Hawes, 1998); therefore, glucuronide metabolites can have linkages of glucuronic acid through O or N-atoms from amiodarone or its oxidized metabolites. Amiodarone underwent \( \omega \)-oxidation to produce carboxyl acid metabolites (M4, M9, and M12), and M12 was a major metabolite on the basis of the chromatographic peak area. In addition, the corresponding glucuronide conjugates of these phase I metabolites were also detected (M13, M17, M19-1, and M19-2). These metabolites will be further investigated to unequivocally identify their structures.

In conclusion, the present study revealed that amiodarone could undergo extensive phase I and phase II metabolism in humans before being excreted into bile. In addition to N-dealkylation, O-dealkylation, deamination, and hydroxylation, novel metabolic pathways were proposed, including \( \omega \)-carboxylation, deiodination, and glucuronide conjugation. Twenty-two phase I and 11 phase II metabolites were identified in human bile; among them, 4′-carboxyamiodarone was the most abundant metabolite in humans. Further investigation is needed to understand the importance of these metabolites from both a safety and efficacy perspective. This is the first time that human bile was used for the study of amiodarone metabolism. However, caution is required in extrapolating these results to patients without T-tube bile drainage because a T-tube drain may partially block enterohepatic circulation. In addition, results were obtained from a small patient sample, and drug metabolism is known to vary significantly from patient to patient. Nevertheless, this study has increased our knowledge of the metabolic pathways of amiodarone in humans, and these findings underscore the importance of biliary excretion in the elimination of this drug in humans.

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Authorship Contributions

Participated in research design: Deng, You, Chen, Yuan, Huang, and Zhong.

Conducted experiments: Deng, You, Yuan, and Huang.

Contributed new reagents or analytic tools: Deng, Chen, Huang, and Zhong.

Performed data analysis: Deng, Chen, Yuan, Huang, and Zhong.

Wrote or contributed to the writing of the manuscript: Deng, You, Chen, Yuan, and Zhong.

Other: Chen.
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Address correspondence to: Dafang Zhong, Shanghai Institute of Materia Medica, Chinese Academy of Sciences, 501 Haoke Road, Shanghai, 201203, China. E-mail: dfzhong@mail.shcnc.ac.cn