Rifabutin, 4-deoxy-3,4-[2-spiro-(N-isobutyl-4-piperidyl)]-(1H)-imidazo-(2,5-dihydro)-rifamycin S, is a semisynthetic derivative of rifampycin S (1), with a broad spectrum of antimycobacterial activity in vitro (2–4). The drug has been used for the prevention of Mycobacterium avium complex in patients with AIDS (5–7) and for the treatment of tuberculosis (8–10).

Rifabutin is extensively metabolized in humans, monkeys, rabbits, and rats, and eliminated by both urinary and fecal excretion (11). The route of administration of [14C]rifabutin (po or iv) did not affect significantly the amount of total radioactivity or unchanged drug excreted in the urine or the pattern of urinary metabolites in female Sprague-Dawley rats (12). In humans, rifabutin is metabolized to >20 products (13). Several metabolites, isolated from human urine, were identified by MS and NMR as 25-O-deacetyl-rifabutin, 30-hydroxy-rifabutin, 31-hydroxy-rifabutin, 32-hydroxy-rifabutin, 32-hydroxy-27-O-deacetyl-rifabutin, and 25-O-deacetyl-rifabutin-N-oxide (13, 14). Battaglia et al. (11) reported the excretion of 31-hydroxy-rifabutin and 25-O-deacetyl-rifabutin in rat urine after administration of rifabutin, and noted that the HPLC profiles of urinary metabolites were similar in humans and rats. After a single po dose of [14C]rifabutin, the 0- to 24-hr urine of rats and humans contained 48 and 60%, respectively, of unidentified polar metabolites. These metabolites accounted for >93% of radioactivity. Major lipophilic metabolites, 25-O-deacetyl-rifabutin, 27-O-demethyl-rifabutin, 31-hydroxy-rifabutin, 32-hydroxy-rifabutin, and 20-hydroxy-rifabutin were isolated from both human and rat urine by HPLC and identified by electrospray ionization-MS, collision-induced dissociation-MS, and NMR spectrometry. In addition, two metabolites formed by the oxidation of the N-isobutyl-piperidyl group of rifabutin were found in the urine of rats, but not humans.

Materials and Methods

Chemicals. Rifabutin, 25-O-deacetyl-rifabutin, and two analogs of rifabutin bearing the spiro-piperidyl group N-substituted with an isopropyl or heptyl chain were provided by Pharmacia (Dublin, OH). Rifampicin, rifamycin SV, and rifamycin B were purchased from Sigma Chemical Co. (St. Louis, MO). Starting material for the synthesis of [14C]rifabutin, 3-amino-4-deoxy-4-aminorifamycin S, was a gift from Dr. Bruno Sardi (Pharmacia, Milan, Italy). Radiolabeled rifabutin (59.3 mCi/mmoll) was synthesized at New England Nuclear (Boston, MA) as described by Fontana et al. (16) and Marsili et al. (1). The purity of rifabutin and [14C]rifabutin was >98% and >97%, respectively. N-isobutyl-4-hydroxy-piperidine was obtained by reduction of N-isobutyl-4-piperidone with sodium borohydride. N-isobutyl-4-piperidone was produced by acetic hydrolysis of rifabutin at 60°C for 3 hr as described elsewhere (14).

Acetonitrile (HPLC grade), methanol, 1-chlorobutane, α-phosphoric acid, and liquid scintillation cocktail ScintiSafe Plus 50% were purchased from Fisher Scientific (Fair Lawn, NJ). Dowex 1, Dowex-50W, MRFA and apomorphin were purchased from Sigma. Charcoal was from MCB Manufacturing Chemists (Cincinnati, OH). Other chemicals were received from Sigma or J. T. Baker, Inc. (Phillipsburg, NJ).
HPLC Analysis. All samples were analyzed on a Hewlett-Packard HPLC system (models 1050 or 1090 M, Palo Alto, CA) equipped with a UV diode-array detector. Radioactivity was measured on-line with a Radiomatic A-500 series Flow Scintillation Analyzer (Packard, Meriden, CT) with a solid scintillation flow cell. Separation was achieved using an analytical Hypersil C18 column (250 × 4.6 mm, 5 μm; Phenomenex, Torrance, CA) at a mobile phase flow rate of 1.5 ml/min. The mobile phases A, B, C, and D contained acetonitrile and/or one of the following aqueous solutions: 3% TEA and 0.3% trifluoroacetic acid titrated with phosphoric acid to pH 2.0 (A), 0.1% TEA and phosphoric acid (pH 6.8–7.0) (B), 0.01% TEA and phosphoric acid (pH 7.0) (C), and 1.5% TEA and phosphoric acid (pH 6.0) (D).

Animals. Male Sprague-Dawley rats (Charles River Laboratories, North Wilmington, MA) weighing between 223 and 463 g, acclimated in a 12-hr light/dark cycle constant-temperature (24 ± 1°C) vivarium with free access to standard chow and water for 1 week, were prepared with the iv catheters as described previously (15).

Dosing and Sample Collection. For metabolic profiles, [14C]rifabutin was administered to rats (three in each group) iv as a single dose of 25 mg/kg (specific activity: 2.7 mCi/mmol) or 1 mg/kg (specific activity: 59.3 mCi/mmol). Dosing solutions of [14C]rifabutin (10 and 0.4 mg/ml) were prepared in saline containing 10 mM HCl. Urine and feces were collected in containers immersed in ice before dosing and at 0–24, 24–48, 48–72, and 72–96 hr, and stored at −80°C. For isolation and structural analysis of metabolites, urine was collected from 20 rats over 0–24 hr after an iv dose of 25 mg/kg of rifabutin.

Analysis of Urine. Before the analysis, urine was thawed, filtered through a 0.2-μm filter, and injected (200 μl) directly into the HPLC. Rifabutin and metabolites were separated as described previously (15) using a linear gradient of 27–42% acetonitrile in aqueous solution A over 45 min (fig. 1A). Separation of individual polar metabolites designated as PM1 and PM2 from the peak labeled P in fig. 1 was achieved by using 100% aqueous solution B as a mobile phase (fig. 2). Total radioactivity in urine was measured by liquid scintillation counting (100 μl) using scintillation cocktail Scin安心Safe Plus 50% (5 ml).

Isolation and Properties of Polar Metabolites. Chemical stability of polar metabolites was studied by incubating urine with equal volumes of 1 N HCl or 1 N KOH at 37°C for 22 hr, followed by HPLC analysis using 100% aqueous solution B as a mobile phase. PM2 was stable under these conditions while <25% of PM1 disappeared.

The following procedure was used to isolate the major polar metabolite PM2 for structural analysis. The urine (320 ml) was gently shaken twice in a separatory flask with 320 ml of 1-chlorobutane in the presence of 320 μl of isomyl alcohol. After separation of phases, the organic layer containing rifabutin and lipophilic metabolites was removed and dried under nitrogen. The aqueous phase containing polar metabolites was mixed with 5 volumes of methanol and kept overnight at 4°C to precipitate salts. After centrifugation (1200g for 10 min), the supernatant (~1.8 liters) was filtered through a 0.2-μm filter and percolated through a layer of the anion-exchange resin Dowex 1 (100 g) to remove organic acids. The eluate was adjusted to pH 2.2 with 1 N HCl and percolated through a layer of Dowex-50W (100 g) equilibrated at pH 2.2. The resin was washed with 300 ml of acidified distilled water (pH 2.2), and the metabolites were eluted with 2 liters of 2 N KOH. Activated charcoal (60 g) was shaken with the eluate over 10 min, separated by centrifugation (1200g for 10 min), and washed twice with 600 ml of 0.1 N KOH. The metabolites were eluted from the charcoal with 600 ml of a mixture consisting of methanol and acetic acid (300:1, v/v) by shaking for 10 min, and then separated by centrifugation (1200g for 10 min). The supernatant was filtered through a 0.2-μm filter and concentrated to a volume of ~3 ml using a vacuum evaporator. The recovery of polar metabolites after precipitation of salts with methanol and solid-phase extraction with Dowex-50W, and charcoal was estimated to be ~20%. These steps permitted removal of contaminants that would have interfered with further purification by HPLC. The polar metabolates had insignificant absorbance at 210 nm, indicating the absence of chromophoric interfering with further purification by HPLC. The polar metabolates had insignificant absorbance at 210 nm, indicating the absence of chromophoric

Urine (200 μl) was injected directly into the HPLC to study the chemical stability of polar metabolites resulting from hydroxylation in the N-isobutyl-piperidyl group.

Isolation of Lipophilic Metabolites. The 1-chlorobutane extract of rat urine was dried, the residue dissolved in mobile phase (40% acetonitrile and 60% aqueous solution A), and portions repeatedly injected into the HPLC. Metabolites were eluted in a linear gradient of 27–42% acetonitrile in aqueous solution A over 45 min. Fractions containing major metabolites with RTs of 20.2 (U1), 22.4 (U2), 24.0 (U3), 24.9 (U4), 26.1 (U5), and 35.4 min (rifabutin) were mixed with equal volumes of 2 M of potassium phosphate buffer (pH 7.0) and extracted with 3 volumes of 1-chlorobutane. Phases were separated by centrifugation (1200g for 10 min), and the organic phase was removed, and evaporated under nitrogen at 40°C. Each residue was reconstituted in 100–200 μl of mobile phase, injected into the HPLC, and eluted in a linear gradient of

**Fig. 1. Typical radiochromatographic profiles of rifabutin metabolites in the 0- to 24-hr (A) and 24- to 48-hr (B) rat urine after iv administration of 25 mg/kg of 14C-rifabutin.**
30–50% acetonitrile in aqueous solution B over 1 hr. Under these conditions, two metabolites were derived from each of peaks U2 (U2A and U2B) and U5 (U5A and U5B). The other three peaks (U1, U3, and U4) contained only one major metabolite each.

**Human Urinary Metabolites.** After fasting for 8 hr, 10 healthy male volunteers, aged 18–45 years, were each given a single oral dose of 300 mg of rifabutin (two 150 mg capsules of Mycobutin). Urine was collected 0–12 hr before the dose and for 0–48 hr after the dose and stored at −20°C. The protocol was approved by The Ohio State University Human Subjects Biomedical Sciences Review Committee.

For metabolic profiles, samples (0.4 ml) of predose and 0–48 hr urine from each subject were mixed with an equal volume of 0.6 M potassium phosphate buffer (pH 7.0) and extracted with 2 ml of 1-chlorobutane. The organic phase was dried under nitrogen at 40°C. The residues were redissolved in 75 μl of mobile phase, 40 μl was injected into the HPLC, and the metabolites were separated as described for the rat.

To isolate metabolites, 1.8 liters of urine pooled from all subjects was supplemented with 1.8 ml of isomyl alcohol and extracted 3 times with 200 ml of 1-chlorobutane by shaking in a separatory flask. The combined organic phase was dried under nitrogen at 40°C and the residues were redissolved in 75 μl of mobile phase, 40 μl was injected into the HPLC, and the metabolites were separated as described for the rat.

**MS.** ESI mass spectra were obtained using a TQ mass spectrometer (Finnigan MAT, San Jose, CA). Samples were dissolved in a 50% (v/v) solution of methanol in deionized water. The molecular mass of compounds was determined by scanning the first quadrupole in the profile mode from m/z 10 to m/z 1000. For the analysis of lipophilic metabolites, the ESI mass spectrometer was tuned and calibrated using MRFA and apomyoglobin tune standard. To analyze PM2, the first quadrupole was tuned with triethanolamine (Finnigan MAT, San Jose, CA). Samples were dissolved in a 50% (v/v) solution of methanol in deionized water. The molecular mass of compounds was determined by scanning the first quadrupole in the profile mode from m/z 10 to m/z 1000. For the analysis of lipophilic metabolites, the ESI mass spectrometer was tuned and calibrated using MRFA and apomyoglobin tune standard. To analyze PM2, the first quadrupole was tuned with triethanolamine.

**CID-MS.** Collision gas (argon) was set at 0.7–2 mtorr, with a collision energy of 51 eV for most metabolites. The assignment of diagnostic fragments was based on comparison of CID spectra of rifabutin and 25-O-deacetyl-rifabutin, rifampin, rifamycin SV, rifamycin B, and two analogs of rifabutin bearing the spiro-piperidyl group N-substituted with an isopropyl or heptyl chain.

**NMR Spectrometry.** Samples were dissolved in 0.5 ml of CDCl₃, transferred into NMR tubes, and analyzed on Bruker AM-500 and/or DMX-600 FT-NMR spectrometers operating at 11.75 Tesla (500 MHz) and 14.1 Tesla (600 MHz), respectively. Either internal tetramethylsilane or residual chloroform signal was used as a chemical shift reference. The structures of rifabutin metabolites were determined using one-dimensional ¹H NMR and/or two-dimensional ¹H-¹H COSY and inverse ¹H-13C HMQC.

**Results**

**Rat Urinary Metabolites. Polar Metabolites.** After administration of 25 and 1 mg/kg of [¹⁴C]rifabutin as an iv bolus, 40.1 ± 4.3% and 34.1 ± 1.8% of the dose, respectively, were excreted in urine during 96 hr (15). Polar metabolites accounted for 59.1 ± 2.5% and 88.8 ± 4.4% of the urinary radioactivity after the 25 and 1 mg/kg dose, respectively. The proportion of urinary polar metabolites was higher during 24–48 hr than 0–24 hr (fig. 1), and by 48–72 hr all radioactivity in urine consisted of polar metabolites.

ESI-MS of the major polar metabolite PM2 showed [M + H]⁺ at m/z 158. The CID spectrum of the m/z 158 ion is consistent with an assignment of a structure for the PM2 metabolite corresponding to hydroxylation of the piperidine ring, possibly forming N-isobutyl-4-hydroxy-piperidine (fig. 3). The HPLC RT of PM2 matched that of synthetic N-isobutyl-4-hydroxy-piperidine that confirmed this structural assignment.

**Lipophilic Metabolites.** Radiochemical and spectrophotometric detection (275 nm) of rifabutin and lipophilic metabolites yielded similar HPLC profiles, suggesting that rifabutin and lipophilic metabolites had similar extinction coefficients. ESI-MS of rifabutin and the metabolites U1, U2A, U2B, U3, U4, U5A, and U5B produced a protonated molecular ion [M + H]⁺ as well as sodium [M + Na]⁺ and potassium [M + K]⁺ adducts. The fragmentation of rifabutin...
Fig. 4. Chemical structure, labeling position (*), and diagnostic fragments produced by CID-MS of rifabutin.

Fragment F is the chromophore group. The ansa chain is the aliphatic moiety from carbon 15 to 29, which spans the chromophore.

could be described in terms of bond cleavage that yielded ions of the type A–G as indicated in fig. 4. Shift of the mass of any of these structurally diagnostic ions (table 1) in combination with NMR data (tables 2 and 3) provided a reasonable rationale for assigning the structure of new metabolites.

**Metabolite U1.** The $^1$H NMR spectrum of U1 showed the absence of the $H_{36}$ signal (at 2.01 ppm in the spectrum of parent drug), thus indicating the loss of the acetyl group. The HPLC RT, ESI and CID mass spectra of this metabolite matched those of the authentic standard of 25'-deacetyl-rifabutin. Thus, metabolite U1 was identified as 25'-O-deacetyl-rifabutin.

**Metabolite U3.** ESI-MS of metabolite U3 showed [M + H]$^+$ at $m/z$ 833, indicating removal of a methyl group. Otherwise, diagnostic daughter ions in the CID spectrum of U3 matched those of rifabutin (fig. 5). Furthermore, the signal of proton H$_{37}$ observed in the $^1$H NMR spectrum of rifabutin (at 3.06 ppm) was missing in the spectrum of U3. On this basis, U3 was identified as 27'-O-demethyl-rifabutin.

ESI-MS of U2A, U2B, U4, U5A, and U5B showed a [M + H]$^+$ at $m/z$ 863, indicating the presence of an additional oxygen atom in these metabolites compared with rifabutin.

**Metabolites U2A and U2B.** The daughter ions of U2A and U2B at $m/z$ 112 and 423 corresponding to the unchanged fragments G and F (table 1, fig. 4), respectively, suggest no modification on that part of the molecule for either metabolite. For U2A, the diagnostic fragments at $m/z$ 561 (545 + 16), 589 (573 + 16), and 648 (632 + 16) pointed to carbons C$_{31}$, C$_{20}$, C$_{19}$, C$_{18}$, C$_{17}$, C$_{16}$, and C$_{30}$ as possible oxidation sites (table 1, fig. 4). In an HMOC experiment, the disappearance of the C$_{31}$ signal at 17.4 ppm and correlated H$_{31}$ signal at 0.85 ppm were accompanied by the appearance of a carbon signal at 63 ppm correlated with a proton signal at 3.54–3.60 ppm (tables 2 and 3). Daughter ions of U2B at $m/z$ 545, 573, and 648 (632 + 16) implicated atoms C$_{32}$, C$_{33}$, and C$_{34}$ as possible oxidation sites (table 1, fig. 4). The signal corresponding to H$_{32}$ of parent drug (d at 1.04 ppm) disappeared, and a proton signal (3.80 and 3.98 ppm) appeared that correlated with H$_{22}$ at 1.78 ppm in $^1$H-$^1$H COSY and with C$_{32}$ at 61.9 ppm in $^1$H-$^1$C HMOC experiments (tables 2 and 3). The downfield shifts and splitting of H$_{31}$ and H$_{32}$ signals (table 2) in $^1$H NMR spectra of U2A and U2B, respectively, suggest hydroxylation of the corresponding methyl groups. Hydroxylation caused the methylene protons to become nonequivalent (appearing as an AB of ABX pattern), because they are adjacent to a chiral center. Consequently, splitting of the proton signals occurred. Downfield shifts of the corresponding C$_{31}$ and C$_{32}$ signals (table 3) confirm that hydroxylation occurred in the aforementioned positions. Thus, the metabolites U2A and U2B are 31-hydroxy-rifabutin and 32-hydroxy-rifabutin, respectively.

**Metabolite U4.** Diagnostic fragments observed in the CID spectrum of U4 at $m/z$ 423 and $m/z$ 561 (545 + 16) indicated that an oxidation site was located in the ansa chain of rifabutin between carbons C$_{15}$ and C$_{31}$ (table 1, fig. 4). In the $^1$H NMR spectrum of U4, the H$_{20}$ signal disappeared; the signals of protons H$_{19}$ and H$_{31}$ became a doublet and a singlet, respectively; and there were no changes in the chemical shifts and multiplicities of H$_{17}$ and H$_{18}$ (table 2). In an $^1$H-$^1$H COSY experiment, signals of coupling interactions between protons H$_{30}$ and H$_{31}$, H$_{30}$ and H$_{19}$, and H$_{30}$ and H$_{31}$ disappeared (fig. 6). Also, no signal was observed for C$_{30}$ in an HMOC experiment, confirming that there is no attached proton, and C$_{31}$ shifted downfield.

<table>
<thead>
<tr>
<th>Compound</th>
<th>[M + H]$^+$</th>
<th>A</th>
<th>B</th>
<th>C</th>
<th>D</th>
<th>E</th>
<th>F</th>
<th>G</th>
</tr>
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<td>847</td>
<td>815</td>
<td>755</td>
<td>632</td>
<td>573</td>
<td>545</td>
<td>423</td>
<td>112</td>
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<tr>
<td>U4</td>
<td>805</td>
<td>773</td>
<td>755</td>
<td>632</td>
<td>573</td>
<td>545</td>
<td>423</td>
<td>112</td>
</tr>
<tr>
<td>U2A</td>
<td>863</td>
<td>831</td>
<td>771</td>
<td>648</td>
<td>589</td>
<td>561</td>
<td>423</td>
<td>112</td>
</tr>
<tr>
<td>U2B</td>
<td>863</td>
<td>831</td>
<td>771</td>
<td>648</td>
<td>573</td>
<td>545</td>
<td>423</td>
<td>112</td>
</tr>
<tr>
<td>U3</td>
<td>833</td>
<td>815</td>
<td>755</td>
<td>632</td>
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<td>589</td>
<td>561</td>
<td>423</td>
<td>112</td>
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</table>

$^a$ ND, not detected.

$^b$ NA, no data available.
to 30 ppm (table 3). Thus, it is concluded that hydroxylation occurred at carbon C20, and metabolite U4 is assigned the structure of 20-hydroxy-rifabutin.

**Metabolites U5A and U5B.** There was a 16 mass units increase in the mass of all characteristic fragments observed in the CID spectra of U5A and U5B, compared with the parent drug (table 1), thus indicating that these metabolites contained an additional oxygen atom in the \( N \)-isobutyl-piperidyl moiety (fig. 4). The lack of authentic standards and difficulties in interpretation of the CID and NMR spectra did not permit a more complete structural characterization of these metabolites.

**Human Urinary Metabolites.** Figure 7A shows a typical HPLC profile of lipophilic metabolites of rifabutin extracted with 1-chlorobutane from 0- to 48-hr human urine. Individual peaks were collected and rechromatographed in a gradient of 30–50% acetonitrile in aqueous solution D (see Materials and Methods) for 1 hr. This demonstrated that HU1, HU3, and HU4 consisted of one major metabolite each, whereas HU2 was composed of two compounds designated as HU2A and HU2B. Chemical identity of the metabolites HU1, HU2A, HU2B, HU3, and HU4 with the corresponding rat metabolites U1, U2A, U2B, U3, and U4 was established by comparison of HPLC RTs, NMR, and/or mass spectra. Thus, the major lipophilic metabolites were identified as 25-O-deacetyl-rifabutin, 31-hydroxy-rifabutin, 32-hydroxy-rifabutin, 27-O-demethyl-rifabutin, and 20-hydroxy-rifabutin.

ESI-MS of metabolite HU0 showed a \([M + H]^+\) at \(m/z\) 821 suggesting the loss of the acetyl group and the presence of an additional oxygen atom. The loss of the acetyl group was confirmed by the absence of the \(H_{36}\) signal in the \(^1H\) NMR spectrum of HU0. The unchanged fragment F at \(m/z\) of 423 in the CID spectrum of HU0 indicated that oxidation occurred in the ansa chain. However, the amount of HU0 was insufficient for complete characterization by NMR and MS.

**Discussion**

Our results showed that radiolabeled polar metabolites PM1 and PM2 (figs. 1 and 2) accounted for most of the radioactivity excreted in rat urine after iv administration of \([^{14}C]\)rifabutin. The retention of radiolabel indicated that these polar metabolites were derived from the \(N\)-isobutyl-piperidyl group of rifabutin (fig. 4) and, possibly, its lipophilic metabolites. PM2 was identified as \(N\)-isobutyl-4-hydroxy-piperidine. Similarity of physiochemical properties of PM1 and PM2 (chemical stability, binding to a strong cation exchanger and activated charcoal, and the absence of chromophoric groups) suggested that the more polar metabolite PM1 is a hydroxy derivative of PM2. The

<table>
<thead>
<tr>
<th>Atom</th>
<th>Rifabutin</th>
<th>U2A</th>
<th>U2B</th>
<th>U4</th>
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<tr>
<td>C17</td>
<td>132.7</td>
<td>133</td>
<td>133</td>
<td>134</td>
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<td>33.9</td>
<td>41</td>
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</tr>
<tr>
<td>C23</td>
<td>20.5</td>
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</tr>
<tr>
<td>C24</td>
<td>17.4</td>
<td>63</td>
<td>18.1</td>
<td>30</td>
</tr>
<tr>
<td>C25</td>
<td>11.9</td>
<td>12.5</td>
<td>61.9</td>
<td>14.5</td>
</tr>
</tbody>
</table>

\^a\ ND, not detected.

\^b\ These hydroxymethylene protons have become nonequivalent because they are adjacent to a chiral center. \(J_{AB}\) \(= 11\) Hz for both U2A and U2B.
metabolite PM1 could not be identified conclusively because of the lack of essential synthetic standards.

The proportion of different urinary metabolites of rifabutin in the rat was dose-dependent. The fraction of the dose excreted in urine as polar metabolites was lower at a higher (25 mg/kg) dose than at a lower (1 mg/kg) dose apparently due to saturation of enzymatic and/or transport systems involved in the formation and excretion of these metabolites. This is in agreement with our previous findings (15) that first-pass metabolism of rifabutin was more significant at the lower dose (bioavailability after po administration of 25 mg/kg and 1 mg/kg of rifabutin was >90% and 44%, respectively).

The proportion of polar metabolites was higher in urine collected at later times; unchanged drug and lipophilic metabolites were not detected in 48- to 96-hr urine. Large amounts of polar metabolites in urine and an increase in their percentage at later times were observed previously after po administration of [14C]rifabutin to humans and rats (11) and after iv administration to rats (12). The predominant urinary excretion of radioactivity as polar metabolites indicates that the cleavage of the N-isobutyl-piperidyl group plays a major role in renal elimination of rifabutin after iv and po administration of the drug.

The mechanism of PM2 formation in vivo is unclear. We hypothesize that it is a two-step process that includes oxidative N-dealkylation of rifabutin by cytochrome P450 to form N-isobutyl-4-piperidone and subsequent reduction of N-isobutyl-4-piperidone to N-isobutyl-4-hydroxy-piperidine by alcohol dehydrogenase or carbonyl reductase.

It has been shown that polar metabolite(s) of rifabutin are present in human urine (11) and also in incubations of the drug with human liver and enterocyte microsomes (17). However, the identity of these metabolites remains to be established conclusively.

In previous work (11), two rat urinary metabolites were identified as 25-O-deacetyl-rifabutin and 31-hydroxy-rifabutin by comparison of their HPLC RTs with those of authentic standards. In addition to these metabolites, we found in rat urine 32-hydroxy-rifabutin, 27-O-demethyl-rifabutin, 20-hydroxy-rifabutin, and two products that resulted from oxidation of the N-isobutyl-piperidyl group.

Five rifabutin metabolites were isolated from human urine and identified in this study as 25-O-deacetyl-rifabutin, 31-hydroxy-rifabutin, 32-hydroxy-rifabutin, 20-hydroxy-rifabutin, and 27-O-demethyl-rifabutin. The first three have been described previously (13, 14),
Table 4

<table>
<thead>
<tr>
<th>Rifabutin</th>
<th>HU1</th>
<th>HU2</th>
<th>HU3</th>
<th>HU4</th>
</tr>
</thead>
<tbody>
<tr>
<td>100 ± 29</td>
<td>29 ± 16</td>
<td>9.4 ± 3.3</td>
<td>6.0 ± 2.0</td>
<td>36 ± 10</td>
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</table>

Urinary metabolites of rifabutin and unchanged drug were extracted with 1-chlorobutane and separated by HPLC in a gradient of 27–42% acetonitrile in aqueous phase A over 45 min as described in Materials and Methods.

a Values are means ± SD for 10 subjects.

About 5% of the dose is excreted in urine as rifabutin (11).

whereas 20-hydroxy-rifabutin and 27-O-demethyl-rifabutin are newly identified. 20-Hydroxy-rifabutin and 25-O-deacetyl-rifabutin seem to be the major urinary lipophilic metabolites of rifabutin in humans (fig. 7, table 4). Previously reported 30-hydroxy-rifabutin and 25-O-deacetyl-rifabutin-N-oxide (13, 14) were not found in this study, possibly because of their low quantities in human urine. Although several common major lipophilic metabolites of rifabutin have been identified in human and rat urine, there is a difference in the metabolism of the drug in these species. The metabolites USA and USB excreted in rat urine were not found in significant amounts in human urine.

References