Pharmacokinetics, Metabolism, and Excretion of the Antidiabetic Agent Ertugliflozin (PF-04971729) in Healthy Male Subjects

Zhuang Miao, Gianluca Nucci, Neeta Amin, Raman Sharma, Vincent Mascitti, Meera Tugnait, Alfin D. Vaz, Ernesto Callegari, and Amit S. Kalgutkar

Pharmacokinetics, Dynamics and Metabolism, New Chemical Entities, Groton, Connecticut (Z.M., R.S., M.T., A.D.V., E.C.) and Cambridge, Massachusetts (A.S.K.); Cardiovascular, Metabolic and Endocrine Diseases Research Unit (N.A.); Clinical Pharmacology, Cambridge, Massachusetts (G.N.); and Worldwide Medicinal Chemistry, Pfizer Inc., Groton, Connecticut (V.M.).

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ABSTRACT

The disposition of ertugliflozin (PF-04971729), an orally active selective inhibitor of the sodium-dependent glucose cotransporter 2, was studied after a single 25-mg oral dose of [14C]-ertugliflozin to healthy human subjects. Mass balance was achieved with approximately 91% of the administered dose recovered in urine and feces. The total administered radioactivity excreted in feces and urine was approximately 91% of the administered dose recovered in urine and feces. The total administered radioactivity excreted in feces and urine was 40.9% and 50.2%, respectively. The absorption of ertugliflozin in healthy human subjects. Mass balance was achieved with approximately 91% of the administered dose recovered in urine and feces. The total administered radioactivity excreted in feces and urine was approximately 91% of the administered dose recovered in urine and feces.

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bearing a dioxo-bicyclo[3.2.1]octane bridged ketal motif and is currently in development for the treatment of T2DM (Mascitti et al., 2011). The results from pharmacokinetics studies in rats and dogs suggested that ertugliflozin is well absorbed with oral bioavailability of 69% and 94%, respectively (Kalugutkar et al., 2011). The in vitro metabolic profile of ertugliflozin in liver microsomes and cryopreserved hepatocytes from rat, dog, and human was qualitatively similar; prominent metabolic pathways included monohydroxylation, O-deethylation, and glucuronidation (Kalugutkar et al., 2011). Following single oral dose administration to healthy subjects, ertugliflozin was rapidly absorbed with mean plasma concentrations occurring at 0.5 to 1.5 hours postdose. Systemic exposure as ascertained from maximal plasma concentrations ($C_{\text{max}}$), and area under the plasma concentration time curve (AUC) appeared to be dose proportional over the dose range evaluated of ertugliflozin (0.5–300 mg) in healthy human subjects (Phase I data on file). The terminal elimination half-life ($t_{1/2}$) of ertugliflozin was 11–17 hours, and oral clearance was within 1.5-fold of that predicted from allometric scaling of animal pharmacokinetics (Kalugutkar et al., 2011). The aims of the present study were (1) to quantify the levels of ertugliflozin and total radioactivity in plasma, (2) to investigate the routes of elimination of ertugliflozin, (3) to examine the biotransformation fate of ertugliflozin, and (4) to demonstrate mass balance in healthy male subjects after a single 25-mg oral dose of $^{14}$C-ertugliflozin administered as a 1-pyroglutamic acid co-crystal.

**Materials and Methods**

**Chemicals and Reference Compounds**

Ertugliflozin and $^{14}$C-ertugliflozin 1-pyroglutamic acid co-crystal (specific activity of the co-crystal and active forms were 3.09 pCi/mg and 4.18 pCi/mg, respectively, and the radiochemical purity was >99%) were synthesized at Pfizer Worldwide Research and Development (Groton, CT). The chemical structure of ertugliflozin and the position of the radiolabel are illustrated in Fig. 1. Reduced NADPH and uridine-diphosphate-glucuronic acid trisodium salt (UDPGA) were obtained from Sigma-Aldrich (St. Louis, MO). Human liver microsomes were prepared from a mixed sex pool of 50 donors (provided by BD Biosciences, Woburn, MA). All other commercially available reagents and solvents were of either analytical or HPLC grade. The syntheses of (1S,2S,3S,4R,5S)-5-[4-chloro-3-(4-ethoxybenzyl)phenyl]-, 2,3-dihydroxy-1-(hydroxymethyl)-6,8-dioxabicyclo[3.2.1]octane-2,3,4-triol (M1b), (1S,2S,3S,4R,5S)-5-(4-chloro-3-(4-ethoxybenzyl)phenyl)-1-(hydroxymethyl)-6,8-dioxabicyclo[3.2.1]octane-2,3,4-triol (M1a) and (1S,2S,3S,4R,5S)-5-[4-chloro-3-(4-ethoxybenzyl)phenyl]-1-(hydroxymethyl)-6,8-dioxabicyclo[3.2.1]octane-2,3,4-triol (M2), (1S,2S,3S,4R,5S)-5-[4-chloro-3-(4-ethoxybenzyl)phenyl]-2,3-dihydroxy-1-(hydroxymethyl)-6,8-dioxabicyclo[3.2.1]octane-2,3,4-triol (M3), (1S,2S,3S,4R,5S)-5-[4-chloro-3-(4-ethoxybenzyl)phenyl]-2,3-dihydroxy-1-(hydroxymethyl)-6,8-dioxabicyclo[3.2.1]octane-2,3,4-triol (M4a), (2S,3S,4R,5S)-5-[4-chloro-3-(4-ethoxybenzyl)phenyl]-2,3-dihydroxy-1-(hydroxymethyl)-6,8-dioxabicyclo[3.2.1]octane-2,3,4-triol (M4b), (2S,3S,4R,5S)-5-[4-chloro-3-(4-ethoxybenzyl)phenyl]-2,3-dihydroxy-1-(hydroxymethyl)-6,8-dioxabicyclo[3.2.1]octane-2,3,4-triol (M4c) have been described elsewhere (see Mascitti, 2011 and Mascitti et al., 2013). The absolute configuration of M1a and M1b was arbitrarily assigned.

**Human Study**

The study protocol, consent documents, consent procedures, and subject recruitment procedures were approved by the Independent Institutional Review Board. The study was conducted in compliance with the International Conference on Harmonization Good Clinical Practices guidelines, the ethical principles that have their origin in the Declaration of Helsinki, and the U.S. Food and Drug Administration regulations for informed consent and protection of subject rights. The study design incorporated a nonrandomized, open-label, single-period assessment of pharmacokinetics in six healthy male subjects between the ages of 20 and 55 years with a body mass index between 23.8 and 30.2 kg/m$^2$. All subjects provided written, informed consent before participation in the study. Subjects were confined to the Clinical Research Unit (Charles River Clinical Services, Tacoma, WA) under continuous observation approximately 12 hours before dose through at least 144 hours postdose or until a minimum of 90% of the radioactive dose administered was recovered or less than 1% was excreted in a 24-hour period for 2 consecutive days. After an overnight fast, subjects received a single oral dose of $^{14}$C-ertugliflozin pyroglutamate co-crystal (25-mg equivalent of ertugliflozin, $–100 \mu$Ci/subject) as a suspension in methyl cellulose (total aqueous volume administered was 240 ml). After administration, all subjects were required to refrain from eating and drinking beverages during the first 4 hours after dosing. Subjects were prohibited from consuming grapefruit or grapefruit-related citrus fruits (e.g., Seville oranges or pomelos) from 7 days prior to dosing until the collection of the final pharmacokinetics blood sample. Administration of the study drug under the supervision of medical personnel ensured adherence. Venous blood samples were collected in heparinized tubes (containing K$_2$ EDTA as an anticoagulant) from each subject and at 0.25, 0.5, 1, 2, 3, 4, 6, 9, 12, 24, 36, 48, 72, 96, 120, and 144 hours postdose. Each sample consisted of 10 ml blood for measurement of total $^{14}$C radioactivity and ertugliflozin. For analysis of ertugliflozin metabolites, venous blood samples (~30 ml) were collected from each subject at predose and at 1, 3, 6, and 12 hours postdose. All blood samples were centrifuged, and plasma samples were collected in separate tubes. Urine samples were collected at predose and at 0–12, 12–24, and then at 24–hour intervals for up to 216 hours for subjects 1001, 1002, 1003, 1005, and 1006, or up to 288 hours for subject 1004. Feces were collected as passed (1 collection per each 24-hour period) from time of dosing for up to 216 hours for subjects 1001, 1002, 1003, 1005, and 1006, or up to 288 hours for subject 1004. All samples were stored at or below –20°C until analysis.

**Measurement of Total Radioactivity in Plasma, Urine, and Feces**

The analysis of total radioactivity in urine, feces, and plasma was conducted at Charles River Laboratories Preclinical Services (Senneville, Quebec, Canada). Total radioactivity in plasma, urine, and feces was measured using a Packard 2500 liquid scintillation counter (PerkinElmer Life and Analytical Sciences, Boston, MA). The total radioactivity in plasma was expressed as nanogram-equivalents (ng-equiv)/ml ertugliflozin. For all subjects, duplicate 400 μl weighed aliquots of plasma and urine were processed for analysis of total radioactivity. Aliquots of plasma and urine were mixed directly with 10 ml of Hionic Fluor scintillation fluid, followed by liquid scintillation counting (LSC). For fecal
samples, samples were homogenized with deionized water (50% w/w, feces/water). Triplicate weighed aliquots of fecal homogenates (~400 mg) were air-dried before combustion using a PerkinElmer Model 307 sampler oxidizer. Radioactivity in the combustion products was determined by trapping the liberated $^{14}\text{CO}_2$ mixed with liquid scintillation fluid for radioactivity measurement.

**Quantitation of Ertugliflozin in Plasma**

Plasma concentrations of ertugliflozin were determined at Tandem Laboratories (West Trenton, NJ) using a validated liquid chromatography tandem mass spectrometry (LC-MS/MS) assay (Kalugutkar et al., 2011). Calibration response curves were linear over a range of 0.5 to 250 ng/ml using an weighted (l/concentration$^2$) linear least squares regression. The lower limit of quantitation for ertugliflozin was 0.5 ng/ml.

**Quantitation of Total Radioactivity in Plasma**

Plasma samples were analyzed for total radioactivity concentrations (parent drug equivalents) at Charles River Laboratories (Senneville) using a validated analytical assay in compliance with the sponsor’s standard operating procedures. Samples were assayed using a validated, sensitive, and specific liquid scintillation spectroscopy method. The lower limit of quantitation for total radioactivity in plasma was 6.7 ng-equiv/ml.

**Pharmacokinetic Analysis**

Pharmacokinetic parameters were determined using noncompartmental analysis. Maximum plasma concentrations ($C_{\text{max}}$) of ertugliflozin or total radioactivity in plasma were estimated directly from the experimental data, with $T_{\text{max}}$ defined as the time of first occurrence of $C_{\text{max}}$. Terminal elimination rate constants ($k_\text{el}$) were estimated by linear regression of the log-linear plasma concentration-time curve. AUC was calculated as $0.693 \times k_\text{el}$ from time $t$ to infinity [AUC$_{\text{from t}}$]. The residues were reconstituted in 1 ml of methanol, and aliquots were evaporated to dryness under nitrogen in a Turbo Vap LV evaporator. The residue was reconstituted in 1 ml of methanol, and aliquots (50 $\mu$l) of concentrated fecal extracts were injected onto the HPLC column for analysis.

**High-Performance Liquid Chromatography**

The HPLC system consisted of an Agilent-1100 quaternary solvent delivery system, an Agilent-1100 membrane degasser, an Agilent-1100 autoinjector, an Agilent 1100 photodiode array detector (Hewlett Packard, Palo Alto, CA), and an IN/US radioactive monitor ($\beta$-RAM). Chromatography was performed on a Phenomenex Synergi, RP column (4.6 mm × 150 mm, 4 $\mu$m) with a mobile phase comprised of 5 mM ammonium formate, pH = 3.0 (solvent A), and acetonitrile (solvent B). The mobile phase gradient was programmed as follows: initiated with 95% A, changed to 30% A over 45 minutes, followed by a short gradient to 5% A from 45 to 52 minutes, and returned to initial gradient of 95% A from 53 to 60 minutes. The system was allowed to equilibrate for 7 minutes prior to the next injection. A flow rate of 1.0 ml/min was maintained throughout the analysis. For plasma, four consecutive injections (100 $\mu$l each, 0.5 minutes apart) were made onto the column to accomplish one profiling analysis. During the first three injections, the HPLC system was operated at a flow rate of 0.2 ml/min with a mobile phase consisting of ammonium formate buffer/acetonitrile (97:3). After the fourth injection, the HPLC system resumed the normal gradient program as described above.

**LC-MS/MS**

Identification of the metabolites was performed on a Thermo LTQ (Thermo Fisher Scientific) operated with an electrospray ionization source. The effluent from the HPLC column was split, and ~50 $\mu$l/min was introduced into the API interface. The remaining effluent was directed to the flow cell of $\beta$-RAM. The $\beta$-RAM response was recorded in real time by the mass spectrometer that provided simultaneous detection of radioactivity and mass spectrometry data. The interface was operated at 4500 V, and the mass spectrometer was operated in the positive ion mode with a capillary temperature set at 240°C. Structural information was generated from the collision-induced dissociation (CID) spectra of the molecular ions (MH$^+$). Due to the lack of nitrogen atoms and/or other positively charged sites in the structural architecture of ertugliflozin, CID spectra of parent and metabolites in the mass balance study were attained from the corresponding ammonium adducts, and structure elucidation was based on these adducts.

**Identification of Ertugliflozin Metabolites**

Stock solutions of unlabeled ertugliflozin and authentic standards of M1 diastereomers, des-ethyl ertugliflozin (M2), ertugliflozin-4-β-O-glucuronide (M4a), and ertugliflozin-3-β-O-glucuronide (M4c) were prepared in methanol.

*Generation of oxidative metabolites.* The incubation volume was 1 ml and consisted of the following: 0.1 M potassium phosphate buffer (pH 7.4), human liver microsomes (P450 concentration = 0.5 $\mu$M), NADPH (1.0 mM), and ertugliflozin (10 $\mu$M). The reaction mixture was prewarmed at 37°C for 2 minutes before adding NADPH. The final concentration of methanol in the incubation media was 0.2% ($v/v$) and incubations were carried out at 37°C for 60 minutes in a shaking water bath.

*Generation of ertugliflozin glucuronide metabolites.* Human liver microsomes (protein concentration = 0.7 mg/ml) were mixed with 100 mM phosphate buffer (pH 7.4), MgCl$_2$ (5 mM), ertugliflozin (10 $\mu$M), and alamethicin (10 $\mu$g/ml). The mixture was placed on ice for 15 minutes to allow
Pharmacokinetic parameters of ertugliflozin and total radioactivity after a single 25-mg oral dose of [14C]-ertugliflozin to healthy male subjects (N=6)

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Ertugliflozin</th>
<th>Total 14C</th>
</tr>
</thead>
<tbody>
<tr>
<td>C&lt;sub&gt;max&lt;/sub&gt; (ng·ml&lt;sup&gt;-1&lt;/sup&gt;)&lt;sup&gt;a&lt;/sup&gt;</td>
<td>490.2 (14)</td>
<td>734.4 (12)</td>
</tr>
<tr>
<td>T&lt;sub&gt;1/2&lt;/sub&gt; (hours)</td>
<td>1.00 (0.500-1.05)</td>
<td>1.02 (1.00-2.00)</td>
</tr>
<tr>
<td>AUC&lt;sub&gt;0-last&lt;/sub&gt; (ng·h·ml&lt;sup&gt;-1&lt;/sup&gt;)&lt;sup&gt;b&lt;/sup&gt;</td>
<td>2787 (21)</td>
<td>6223 (19)</td>
</tr>
<tr>
<td>AUC&lt;sub&gt;0-36&lt;/sub&gt; (ng·h·ml&lt;sup&gt;-1&lt;/sup&gt;)&lt;sup&gt;b&lt;/sup&gt;</td>
<td>2802 (21)</td>
<td>6441 (19)</td>
</tr>
<tr>
<td>t&lt;sub&gt;1/2&lt;/sub&gt; (hours)</td>
<td>16.87 (43)</td>
<td>17.25 (61)</td>
</tr>
</tbody>
</table>

<sup>a</sup> Geometric mean (geometric % CV) values depicted for C<sub>max</sub> and AUC; arithmetic mean (% CV) noted for t<sub>1/2</sub> and median (range) noted for T<sub>max</sub>

<sup>b</sup> Units for radioactivity parameters are ng-equiv·ml<sup>-1</sup> (C<sub>max</sub>) or ng-equiv·h·ml<sup>-1</sup> (AUC)

Mass Balance

The excretion of radioactivity in urine and feces is summarized in Table 2. The mean (±S.D.) total recovery of administered radioactivity for the six subjects was 91.1%, of which 50.2 ± 10.1% was recovered in urine and 40.9 ± 7.1% was recovered in feces. The target recovery of >90% was achieved at ~168 hours postdose. The excretion of radioactivity in urine was rapid; at 24 hours postdose, the mean cumulative recovery was 40 ± 7.0%, which accounted for ~80% of total radioactivity recovered in urine. At 48 hours postdose, the mean cumulative recovery was 46.1 ± 8.7%, constituting approximately 92% of total radioactivity recovered in urine. At 96 and 168 hours postdose, the mean cumulative recoveries were 49.2 ± 9.7% and 50.1 ± 10.1% percent, respectively, which represented ~98% and 99.8% of total radioactivity recovered in urine. The excretion of radioactivity in feces was prolonged due to irregular bowel movement observed in some subjects. At 24, 48, 72, 96, and 168 hours postdose, the mean cumulative recoveries were 49.2 ± 9.7% and 50.1 ± 10.1% percent, respectively, which represented ~98% and 99.8% of total radioactivity recovered in urine.

Quantitative Profiles of [14C]-Ertugliflozin and Metabolites in Excreta and Circulation

Urine. A representative HPLC-radiochromatogram of urinary metabolites is shown in Fig. 3A. The mean percentages of metabolite detected in human urine, expressed as percent of administered dose, are shown Table 3. Unchanged ertugliflozin and a total of seven metabolites were detected in human urine. Unchanged ertugliflozin was a minor urinary metabolite, which represented 1.5% of the administered dose. In contrast, metabolites M4a, M4b, M4c, M5a, and

<table>
<thead>
<tr>
<th>Matrix</th>
<th>Percentage of Radioactive Dose by Subject</th>
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<tbody>
<tr>
<td>Urine</td>
<td>56.4 42.2 55.0 35.1 62.7 49.8 50.2</td>
</tr>
<tr>
<td>Feces</td>
<td>35.7 45.8 41.7 48.6 29.3 44.0 40.9</td>
</tr>
</tbody>
</table>
M5b were the major components in urine. Collectively, they accounted for 43.9% of the administered dose and 87.8% of total radioactivity excreted in the urine.

**Fig. 3.** Representative HPLC radiochromatograms of ertugliflozin and its metabolites in human urine (A), feces (B), and plasma (C) after a single 25-mg oral dose of [14C]-ertugliflozin.

**Feces.** A representative HPLC-radiochromatogram of human fecal metabolites is shown in Fig. 3B. The mean percentages of fecal metabolites, expressed as percentage of the administered dose, are shown in
Table 3. Unchanged ertugliflozin was the major component in feces, accounting for ~90% of the recovered radioactivity in feces and 33.8% of the administered dose. Minor metabolites M1, M2, and M3 were also detected in the fecal samples, which represented <2.0% of the administered dose.

**Plasma.** A representative HPLC radiochromatogram of circulating metabolites in human plasma is shown in Fig. 3C. The relative amounts of [14C]-ertugliflozin and metabolites, expressed as percentage of total radioactivity, are presented in Table 4. Ertugliflozin and a total of six metabolites were detected in circulation. The majority of circulating radioactivity was attributed to unchanged ertugliflozin (49.9%). Metabolites M1, M2, M4a, M4b, M4c, and M5a accounted for 2.5, 1.3, 12.2, 4.1, 24.1, and 6.0% of the circulating radioactivity.

**Identification of Metabolites**

Table 5 displays the proposed structures of ertugliflozin metabolites detected in humans upon administration of a single 25-mg oral dose of [14C]-ertugliflozin. Under the current experimental conditions, ertugliflozin possessed a $t_R$ of ~36.4 minutes on HPLC and showed an ammonia adduct ion [M+NH4]$^+$ at $m/z$ 454 under positive ionization conditions. The CID spectra displayed the expected fragment ions at $m/z$ 437, 419, 329, 273, 207, 155, and 135 as noted in our previous work (Kalgutkar et al., 2011). Thus, the ion at $m/z$ 437 occurred from the loss of NH3, whereas, the fragment ion at $m/z$ 329 resulted from a neutral loss of 125 Da (C6H12O2N) from the ammniated modified glucose moiety of parent compound. The fragment ions at $m/z$ 207 and $m/z$ 135 were derived from the loss of ethoxybenzene motif from the fragment ion at $m/z$ 329.

**Metabolite M1.** M1 had a $t_R$ of ~27.9 minutes on HPLC and showed an ammonia adduct ion [M+NH4]$^+$ at $m/z$ 470, an addition of 16 Da to the molecular weight of ertugliflozin, which suggested that M1 was a monohydroxylated metabolite of ertugliflozin. The CID spectrum of M1 displayed fragment ions at $m/z$ 435, 407, 299, 243 and 215. The ion at $m/z$ 435 was due to the sequential loss of NH3 and H2O. The most abundant fragment ion, which occurred at $m/z$ 407 (loss of 28 Da from $m/z$ 435) was derived from the loss of ethylene unit. The absence of fragment ions derived from benzylic cleavage (e.g., $m/z$ 207 and 135 seen in the mass spectrum of ertugliflozin) in the CID spectrum of M1 suggested the benzylic position as the most likely site of hydroxylation.

**Metabolite M2.** M2 had a $t_R$ of ~27.2 minutes on HPLC and displayed an ammonia adduct ion [M+NH4]$^+$ at $m/z$ 426, corresponding to a loss of 28 Da from the molecular weight of ertugliflozin.

Unambiguous structural characterization of M1 and M2 was obtained from an in vitro incubation of unlabeled ertugliflozin (10 μM) in NADPH-supplemented human liver microsomes. M1, which is derived from hydroxylation at the bis-benzylic position, can exist as one of the two possible diastereomeric forms, M1a and M1b, respectively (Fig. 4). As shown in Fig. 4, the HPLC $t_R$ of M1 generated in human liver microsomes (and observed in systemic circulation) suggested that both the M1a and M1b diastereomers were formed at a ratio of ~85:15 in favor of M1b. In the case of M2, the HPLC $t_R$ and MS characteristics of the enzymatically generated metabolite were identical to des-ethyl ertugliflozin. CID spectra for M1a/M1b and M2 observed in microsomal incubations and in vivo were identical to the respective synthetic standards (unpublished data).

**Metabolite M3.** M3 had a $t_R$ of ~29.8 minutes on HPLC and displayed an ammonia adduct ion [M+NH4]$^+$ at $m/z$ 470, suggestive of a monohydroxylated PF-04971729 metabolite. The CID spectrum of M3 exhibited fragment ions at $m/z$ 453, 435, 345, 327, 207, 151, and 139. The fragment ion at $m/z$ 207, which was discerned in the mass spectra of M3 and ertugliflozin, suggested that the chlorobenzyl group was not modified. The fragment ion at $m/z$ 151, which is 16 Da higher than the characteristic ion at $m/z$ 135 in ertugliflozin, suggested that the hydroxylation in M3 occurred in the aromatic portion of the ethoxyphenyl ring; a proposed structure that is consistent with the fragmentation pattern is depicted in Table 5.

**Metabolites M4a, M4b, and M4c.** M4a, M4b, and M4c were regioisomers that displayed identical ammonia adduct ions [M+NH4]$^+$ at $m/z$ 630. The molecular weights of M4a, M4b, and M4c were 176 Da higher than ertugliflozin, suggesting that they were obtained from glucuronidation of the glycoside hydroxyl groups (Table 5). Chromatographically, M4a, M4b, and M4c were well separated with $t_R$ of 29.4 minutes, 31.3 minutes, and 34.3 minutes, respectively (see Fig. 3). Additional insight into the regiochemistry of glucuronidation was obtained via separate in vitro incubations of unlabeled ertugliflozin (10 μM) in UDPGA-supplemented human liver microsomes. LC-MS analysis in the negative ion mode revealed the formation of the ertugliflozin glucuronides, M4a and M4b, with an identical molecular mass (M–H$^-$) of 611.1537 (Fig. 5A). As seen in Fig. 5, B and C, the HPLC $t_R$ of M4a and M4c generated from the microsomal incubations were identical to the authentic standards of ertugliflozin -4β-O-glucuronide and ertugliflozin -3β-O-glucuronide, respectively. The CID spectra of authentic M4a and M4c, which are shown in Fig. 5, were identical to those of enzymatically formed M4a and M4c, respectively.

**Metabolites M5a and M5b.** M5a and M5b, which eluted at $t_R$ of 21.3 minutes and 26.7 minutes, respectively, also were regioisomers that displayed identical ammonia adduct ions [M+NH4]$^+$ at $m/z$ 602. The molecular weight of M5a and M5b suggested that they were obtained from glucuronidation of M2. M5a and M5b had identical CID spectra with fragment ions at $m/z$ 459, 409, 391, 301, 283, 207, and 107. The fragment ion at $m/z$ 409 resulted from loss of glucuronic acid and ammonia, whereas the ion at $m/z$ 107, which corresponds to the benzyl-phenol carbocation (Kalgutkar et al., 2011), suggested that...
TABLE 5
Liquid chromatography tandem mass spectrometry (LC-MS/MS) characteristics and proposed structures of ertugliflozin metabolites observed in the human mass balance study

<table>
<thead>
<tr>
<th>Compound</th>
<th>Observed ([M + NH₄]⁺)</th>
<th>LC-MSⁿ Fragments, m/z</th>
<th>Structure</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ertugliflozin</td>
<td>454</td>
<td>437, 419, 329, 273, 207, 155, 135</td>
<td></td>
</tr>
<tr>
<td>M1</td>
<td>470</td>
<td>435, 407, 299, 243, 215</td>
<td></td>
</tr>
<tr>
<td>M2</td>
<td>426</td>
<td>409, 391, 373, 301, 207</td>
<td></td>
</tr>
<tr>
<td>M3</td>
<td>470</td>
<td>453, 435, 345, 327, 207, 151, 139</td>
<td></td>
</tr>
<tr>
<td>M4a</td>
<td>630</td>
<td>437, 419, 329, 301, 207, 135</td>
<td></td>
</tr>
<tr>
<td>M4b</td>
<td>630</td>
<td>437, 419, 329, 301, 207, 135</td>
<td></td>
</tr>
</tbody>
</table>
| M4c | 630 | 437, 419, 329, 301, 207, 135 | (continued)
the site of glucuronidation was not on the phenolic oxygen. Proposed structures of M5a and M5b, which are consistent with the fragmentation pattern, are shown in Table 5.

**Discussion**

In this work, we characterized the routes of elimination, metabolism, and excretion mass balance of [14C]-ertugliflozin after a single 25-mg oral dose to humans. A radioactivity dose of 100 μCi of [14C]-ertugliflozin was selected for this study based on radioactivity dosimetry estimates from the tissue distribution of [14C]-ertugliflozin in Long-Evans rats. Mass balance was achieved, with mean total recovery of ~91%. Approximately, 50.2% and 40.9% of the total administered radioactive dose was recovered in urine and feces, respectively. These results are generally consistent with the mass balance and excretion pattern of [14C]-ertugliflozin in nonclinical toxicology species (Supplemental Tables 1–8). For instance, oral administration of a 25-mg/kg dose of [14C]-ertugliflozin to Sprague-Dawley rats resulted in total radioactivity recoveries of 93.8% (mean values from male and female rats) over a time period of 0–168 hours (Supplemental Table 1). The mean radioactivity recovered in urine and feces of male and female animals accounted for ~27.5% and ~61.9% of the administered dose,

TABLE 5—Continued

<table>
<thead>
<tr>
<th>Compound</th>
<th>Observed ([M + NH4]+)</th>
<th>LC-MSn Fragments, m/z</th>
<th>Structure</th>
</tr>
</thead>
<tbody>
<tr>
<td>M5a</td>
<td>602</td>
<td>459, 409, 391, 301, 282, 207, 107</td>
<td><img src="image" alt="M5a Structure" /></td>
</tr>
<tr>
<td>M5b</td>
<td>602</td>
<td>459, 409, 391, 301, 282, 207, 107</td>
<td><img src="image" alt="M5b Structure" /></td>
</tr>
</tbody>
</table>

* Electrospray ionization source operating in the positive-ion mode.

Fig. 4. Extracted ion chromatogram of a NADPH-supplemented human liver microsomal incubation with ertugliflozin (10 μM) conducted at 37°C for 60 minutes (A). (B and C) HPLC tR of authentic standards of the diastereomers M1a and M1b, respectively.
respectively (Supplemental Tables 2, 3, and 4). Likewise, oral administration of a 10-mg/kg dose of \[^{14}C\]-ertugliflozin to beagle dogs resulted in total radioactivity recoveries of 93.4% (mean values from male and female dogs) over a time period of 0–144 hours (Supplemental Table 5). The majority of radioactivity was excreted in feces of male and female dogs and accounted for 85.5% of the dose, whereas the radioactivity recovered in urine of male and female dogs accounted for 8.0% of the administered dose (Supplemental Tables 6 and 7, respectively).

Of the total radioactivity excreted in human feces and urine, unchanged ertugliflozin constituted 35.3% of the dose. A total of 8 metabolites was identified in human excreta by LC-MS/MS (Table 4) with the primary biotransformation pathway involving glucuronidation of the glycoside hydroxyl groups in ertugliflozin to afford three regioisomeric metabolites M4a, M4b, and M4c (39.3% of the administered dose recovered in urine), of which M4c was the major regioisomer (31.7% of the dose). The structures of M4a and M4c were unambiguously identified as ertugliflozin-4-\(\beta\)-O-glucuronide and ertugliflozin-3-\(\beta\)-O-glucuronide, respectively. In vitro metabolism studies on ertugliflozin have revealed that the formation of M4a–M4c is catalyzed by UDP-glucuronosyltransferase isozyme 1A9 (Kalgutkar et al., 2011). In addition to glucuronidation, oxidative metabolism by cytochrome P450 (P450) to yield monohydroxylated metabolites (M1 and M3) and des-ethyl ertugliflozin (M2), which accounted for 5.2% of the dose in excreta. In vitro studies in human liver microsomes indicated that both diastereomers of M1, i.e., M1a and M1b, were formed, with M1b being the dominant form. The structures of M1a/M1b and M2 were unambiguously confirmed via comparison of the HPLC\(\_t_R\) and CID spectra of the metabolites generated from microsomes with the respective synthetic standards. Although, M2 possessed in vitro SGLT2 inhibitory potency (IC\(_{50}\) = 2.6 nM) comparable to ertugliflozin (IC\(_{50}\) = 0.87 nM) (Mascitti et al., 2011), it is likely that M2 will not contribute significantly toward SGLT2 inhibition in vivo due to its low circulating concentrations. In vitro P450 phenotyping studies (Kalgutkar et al., 2011) using a panel of recombinant human P450 isoforms have indicated that the formation of M1–M3 is catalyzed principally by CYP3A4/3A5. Glucuronidation of glycoside hydroxyl motif in M2 led to the glucuronide regioisomers M5a and M5b (4.6% of the dose recovered in feces). Human circulating metabolites of ertugliflozin included M1, M2, M4a–M4c, and M5a. In plasma, ertugliflozin and corresponding glucuronides M4a and M4c were the principal components, which accounted for 49.9, 12.2, and 24.1% of the circulating radioactivity, respectively. The biotransformation pathways of ertugliflozin discerned in humans (Fig. 7) are similar to the known metabolic profile of dapagliflozin (Forxiga) in humans. Like ertugliflozin, dapagliflozin (Forxiga) is metabolized via glucuronidation on the sugar moiety to yield the pharmacologically inactive dapagliflozin-3-\(\beta\)-O-glucuronide (analogous to M4c) as the major human metabolite in circulation (Kasichayanula et al., 2011a,b).

The parent drug accounted for 33.8% of the dose in feces, suggesting that the fraction of the oral dose absorbed in humans is ~66%. It is quite possible that oral absorption is significantly higher,
as inferred from corresponding mass balance studies in bile duct-cannulated rats (Supplemental Table 9) and dogs (Supplemental Table 12), wherein unchanged ertugliflozin and glucuronide M4c accounted for 2.4% and 16.5% of the dose in rat bile (Supplemental Table 10) and 9.6% and 39.2% of the dose in dog bile (Supplemental Table 13). However, in feces of intact rats and dogs (Supplemental Tables 3 and 7, respectively), unchanged ertugliflozin and oxidative metabolites (M1 and/or M2) were the major components [male/female rat feces: ertugliflozin (24.5%) and M2 (26.7%); male/female dog feces: ertugliflozin (65.1%), M1 (7.1%), and M2 (8.7%)] with little to no detectable levels of the glucuronide M4c. Similar findings were noted in feces from bile duct-cannulated rats (Supplemental Table 11) and dogs (Supplemental Table 14). These observations imply that glucuronide M4c is susceptible to hydrolysis in the intestine of animals following biliary excretion to yield parent drug ertugliflozin, which is then eliminated in the feces. The likelihood that this scenario would extend to humans is high taking into consideration the commonality in the in vitro metabolic profile of ertugliflozin in rat, dog, and humans with glucuronidation, representing a predominant biotransformation pathway (Kalgutkar et al., 2011). Ultimately, intravenous pharmacokinetic studies in humans will lead to a better understanding of the oral absorption with ertugliflozin. The carboxylic acid derivative muraglitazar, which is a dual α/γ peroxisome proliferator-activated receptor activator and is prone to acyl glucuronidation in animals and humans (Wang et al., 2006; Zhang et al., 2007), serves as an excellent example to support our hypothesis on the oral absorption of ertugliflozin.

Comparison of ertugliflozin metabolic profile in circulation and excreta of humans and preclinical toxicology species (rats and dogs) did not reveal any human-specific metabolites; each metabolite was present in at least one of the animal species used in toxicology assessments. However, some differences were noted with respect to the relative amounts of individual circulating metabolites formed in each species. For example, in rats and dogs, ertugliflozin was most abundant and accounted for ~90.3% (Supplemental Table 4) and 94.2% (Supplemental Table 8) of circulating radioactivity, respectively. In contrast with the human profile, the contribution of glucuronide metabolites (M4a and M4c) to circulating radioactivity was minor in rats (<1.0%) and dogs (~3.0%). Ertugliflozin glucuronide M4c (24.1% of the dose in systemic circulation) in humans is not anticipated to contribute to the activity of ertugliflozin in vivo. As such, the SGLT2 inhibitory potency of M4c has not been evaluated; however, existing structure-activity relationships for SGLT2 inhibition (Mascitti et al., 2011) suggest that M4c will be inactive as a SGLT2 inhibitor. This hypothesis is consistent with the lack of SGLT2 inhibition by structurally analogous glucuronide derivatives of SGLT2 inhibitors such as dapagliflozin (Forxiga) and remogliflozin (Kasichayanula et al., 2011a,b; Sigafoos et al., 2012). As an unreactive, inactive ether glucuronide, M4c does not raise any particular safety concerns (considering its disproportionate nature—humans >> animals), and in fact this type of glucuronide metabolite is specifically exempted in the Food and Drug Administration Human Metabolites in Safety Testing guidance (http://www.fda.gov/downloads/Drugs/GuidanceComplianceRegulatoryInformation/Guidances/ucm079266.pdf). In conclusion, the open-label Phase I study has shown that ertugliflozin is well absorbed and metabolized mainly via glucuronidation and to a lesser extent by oxidative metabolism. Renal excretion of unchanged ertugliflozin was deemed to be negligible.
Recovery of administered radioactivity was >90% with radiolabeled material eliminated via the fecal and urinary route. All the identified human metabolites were present in animal species used for long-term safety assessments.

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Authorship Contributions

Participated in research design: Miao, Nucci, Amin, Tugnait, Kalgutkar.

Conducted in vitro experiments: Miao, Sharma, Vaz.

Conducted clinical study: Nucci, Amin.

Contributed new reagents or analytic tools: Mascitti.

Performed data analysis: Miao, Amin, Nucci, Vaz, Sharma, Kalgutkar.

Wrote or contributed to the writing of the manuscript: Kalgutkar, Mascitti, Nucci, Callegari.

References


