IDENTIFICATION OF THE ACTIVE COMPONENTS IN SHENMAI INJECTION THAT DIFFERENTIALLY AFFECT CYP3A4-MEDIATED 1'-HYDROXYLATION AND 4-HYDROXYLATION OF MIDAZOLAM

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Running Title: Active components in SMI differentially affected MDZ metabolism

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Abbreviations: SMI, Shenmai injection; MDZ, midazolam; 1′-OH MDZ, 1′-hydroxymidazolam; 4-OH MDZ, 4-hydroxymidazolam; TG, total ginsenoside; OTS, ophiopogon total saponins; OTF, ophiopogon total flavone; RLM, rat liver microsomes; HLM, human liver microsomes; rCYP3A4, recombinant CYP3A4; rCYP3A5, recombinant CYP3A5; RILD, Research Institute for Liver Disease Co; SPE, solid phase extraction; HPLC, high performance liquid chromatography; LC-MS, liquid chromatography mass spectrometry.
Abstract

*Shenmai injection (SMI)* is a popular herbal preparation that is widely used for the treatment of atherosclerotic coronary heart disease and viral myocarditis. In our previous study, *SMI* was shown to differentially affect CYP3A4-mediated 1’-hydroxylation and 4-hydroxylation of midazolam (MDZ). The present study was conducted to identify the active components in *SMI* responsible for the differential effects on MDZ metabolism, using *in vitro* incubation systems (rat and human liver microsomes, and a recombinant CYP3A4 system) to measure 1’-hydroxylation and 4-hydroxylation of MDZ. Firstly, different fractions of *SMI* were obtained by gradient elution on an SPE (solid phase extraction) system, and individually tested for their effects on MDZ metabolism. The results demonstrated that lipid-soluble constituents were likely to be the predominant active components of *SMI*. Secondly, the possible active components were gradually separated on an HPLC (high performance liquid chromatography) system under different conditions, and individually tested *in vitro* for their effects on MDZ metabolism. Thirdly, the active component obtained in the above experiment was collected and subjected to structural analysis, and identified as panaxytriol (PXT). Finally, it was validated that PXT had significant differential effects on 1’-hydroxylation and 4-hydroxylation of MDZ, in various *in vitro* systems, that were similar to those of *SMI*. We conclude that PXT is the constituent of *SMI* responsible for the differential effects on CYP3A4-mediated 1’-hydroxylation and 4-hydroxylation of MDZ.
Introduction

CYP3A4 is the most important member of the cytochrome P450 superfamily of enzymes, and is involved in the majority of P450-mediated reactions (Guengerich, 1996). Drug interactions involving substrates, inhibitors, activators or inducers of CYP3A4 are more prevalent and complex than those of other members of the P450 family (Pal et al., 2006; Kim et al., 2006). It is becoming evident that many CYP3A4-mediated reactions proceed with atypical Michaelis-Menten kinetics, including substrate activation (Shou et al., 1999), substrate inhibition (Lin et al., 2001; Wu, 2011) and differential kinetics (Shou et al., 2001; Zhang et al., 2008; Xia et al., 2009). These phenomena are thought to be due to the binding of multiple substrates within the active site of the enzyme (Kenworthy et al., 2001; Galetin et al., 2003; Zhou et al., 2010).

Midazolam (MDZ) is a drug that is commonly used as a probe to estimate CYP3A4 activity (Galetin et al., 2005), and is mainly metabolized to 4-hydroxymidazolam (4-OH-MDZ) and 1’-hydroxymidazolam (1’-OH-MDZ) in reactions catalyzed by CYP3A4 (Rogers et al., 2003; Link et al., 2007). Studies have demonstrated that CYP3A4-mediated metabolism of MDZ may be altered to favor the formation of either 1’-OH-MDZ or 4-OH-MDZ. For example, Zhang and colleagues reported that citral, 6-gingerol and d-limonene (compounds found in spices) enhance 1’-hydroxylation of MDZ but inhibit 4-hydroxylation of the drug (Zhang et al., 2008).

Shenmai injection (SMI) is one of the most widely used herbal medicines in traditional Chinese medicine, and is made from red ginseng and Ophiopogon. It is
used to treat atherosclerotic coronary heart disease and viral myocarditis, and is often concomitantly administered with other prescribed medications, including certain cardiovascular drugs with a narrow therapeutic window (Janetzky et al., 1997; Gurley et al., 2002; Donovan et al., 2003; Jiang et al., 2004; Yuan et al., 2004). In our previous study (Xia et al., 2009), we demonstrated that SMI could significantly enhance 1’-hydroxylation of MDZ but inhibit 4-hydroxylation of this compound, in human liver microsomes (HLM), rat liver microsomes (RLM) and recombinant human CYP3A4. Furthermore, total ginsenoside (TG), Ophiopogon total saponins (OTS), Ophiopogon total flavones (OTF), ginsenoside Rd and ophiopogonone A (important constituents of SMI) were all found to significantly inhibit both 1’-hydroxylation and 4-hydroxylation of MDZ in HLM and RLM. Interestingly, no activation of MDZ hydroxylation was observed in the presence of these major SMI constituents, applied either alone or in combination. This contrasts with the actions of SMI, raising a question about which components of SMI are responsible for the differential effects on MDZ metabolism.

The aim of the present study was to identify the active components present in SMI that differentially affect 1’-hydroxylation and 4-hydroxylation of MDZ, using gradual separation of the constituents of SMI with a solid phase extraction (SPE) column and high performance liquid chromatography (HPLC), combined with in vitro incubation systems (RLM, HLM and recombinant human CYP3A4).
Materials and Methods

Chemicals

SMI was provided by Hebei Shenwei Pharmaceutical Co. Ltd (Hebei, China). Each milliliter volume of SMI was comprised of the extract of 0.1 g red ginseng and 0.1 g *radix ophiopogonis*, and contained 76.2 μg ginsenoside Rg1, 69.7 μg ginsenoside Re, 68.1 μg ginsenoside Rd, 178.4 μg ginsenoside Rb1, 15.7 μg ophiopogonin D and 1.7 μg ophiopogonione A (Xia *et al.*, 2009). Glucose-6-phosphate, NADP⁺, glucose-6-phosphate dehydrogenase, MDZ, 1’-OH-MDZ and 4-OH-MDZ were purchased from Sigma Chemical Co. (St. Louis, MO, USA). All other reagents and solvents were of analytical or chromatographic grade. De-ionized water, obtained from a Milli-Q water purification system (Millipore, Billerica, MA, USA), was used throughout the study.

Enzymes

Human liver microsomes (HLM) and rat liver microsomes (RLM) used in this study were provided by the Research Institute for Liver Diseases (RILD) Co. Ltd (Shanghai, China). The microsomes had been previously characterized for CYP3A activity by RILD. Recombinant CYP3A4 (rCYP3A4, Cat. CYP/EZ005), co-expressed with NADPH-CYP oxidoreductase and cytochrome b₅, was also purchased from RILD. The cytochrome c reductase activity in the recombinant CYP3A4 system was 5000 nmol/min/mg protein. The microsomes and recombinant CYP3A4 system were stored at -80°C until use.

Incubation systems
The 1'- and 4-hydroxylations of MDZ, a specific substrate for CYP3A4, were determined using HPLC, as described previously (Xia *et al.*, 2009). A reaction mixture (200 μL), containing MDZ (5 μM for the HLM and recombinant CYP3A4 systems, 10 μM for the RLM system), 100 mM phosphate buffer (pH 7.4), 0.2 mg/mL liver microsomal protein or 20 nM recombinant CYP3A4, and an NADPH-generating system (0.5 mM NADP⁺, 10 mM glucose-6-phosphate, 10 mM magnesium chloride and 1.0 unit of glucose-6-phosphate dehydrogenase), was equilibrated at 37°C for 5 min. Incubation with MDZ alone was used as a negative control, and incubation with 5% SMI (10 μL SMI added to a final reaction mixture volume of 200 μL) was used as a positive control. All experiments were conducted in triplicate.

**Fractions of SMI separated using a solid phase extraction (SPE) system**

Ten SPE C₁₈ cartridges (Supelco Co., Bellefonte, USA) were each loaded with 1 mL SMI, and the fractions collected were separated using different concentrations of methanol. In detail, an initial eluate was collected from each cartridge as the sample (SMI) passed through the stationary phase. Then, each cartridge was washed with 1 mL water, and the eluate was collected as a water-soluble eluate. Finally, ten cartridges were respectively washed with 1 mL of a different concentration of methanol (10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or 100%) and the eluates collected. These fractions were all evaporated to dryness, and reconstituted in 1 mL 20% methanol. The effects of these different fractions on the metabolism of MDZ were evaluated by adding 10 μL of each reconstituted fraction to the RLM incubation system.
Fractions of SMI separated using an HPLC system

HPLC analysis was performed using a Diamosil C18 column (150 mm × 4.6 mm, I.D. 5 μm, Dikma Technologies Inc., Beijing, China). A gradient elution, using solvent A (water) and solvent B (acetonitrile), was used as follows: 0-10 min, 10%→20% (B); 10-30 min, 20%→20% (B); 30-60 min, 20%→40% (B); 60-90 min, 40%→85% (B); 90-100 min, 85%→10% (B); 100-110 min, 10%→10% (B) (condition 1). The flow rate was set at 1 mL/min, and the column was run under room temperature. The eluate was monitored by the absorption at 203 nm, and fractions were collected as follows, based on the HPLC chromatogram and the retention times of the peaks: SM-1 (0-15 min), SM-2 (15-30 min), SM-3 (30-45 min), SM-4 (45-60 min), SM-5 (60-72 min), SM-6 (72-87 min) and SM-7 (87-97 min). Then, each fraction was evaporated under a stream of nitrogen, and each residue dissolved in 20% methanol. Finally, the effect of each residue on the metabolism of MDZ was investigated using the RLM system, to determine which fraction had differential effects on the metabolism of MDZ.

The SM-5 fraction (60-72 min), eluted under HPLC condition 1 (described above), was further separated using different HPLC conditions. HPLC analysis was performed with a Synergi C18 column (250 mm × 4.6 mm, I.D. 4 μm, Phenomenex, Inc., Torrance, CA, USA), using gradient elution with solvent A (water) and solvent B (acetonitrile), as follows: 0-60 min, 35%→43% (B) (condition 2). All other HPLC conditions were the same as those described for condition 1. Using this HPLC separation, the following fractions were collected: SM-5-1 (0-10 min), SM-5-2 (10-24...
min), SM-5-3 (24-32 min) and SM-5-4 (32-45 min). The effects of each of these residues on the metabolism of MDZ were also investigated. The fraction that demonstrated a differential effect on the metabolism of MDZ was defined as the active component.

Preparation and structural identification of the active component

The active component, fraction SM-5-3 (24-32 min), was collected by preparative liquid chromatography performed with a YMC-Pack Pro C$_{18}$ column (250 mm × 10 mm, I.D. 5 μm, HanKing Instrument Equipment Co., Shanghai, China). The eluate was freeze-dried, and the residue dissolved in a small volume of methanol and subjected to structural analysis. The $^1$H- and $^{13}$C-NMR spectra were measured using a Bruker AV-600 spectrometer (Bruker Corp., Billerica, MA, USA), with the residual CHCl$_3$ as an internal standard. Chemical shifts were recorded as δ values. The mass spectra were obtained using an Agilent-6430 Triple Quadrupole LC/MS system (Agilent Technologies Inc., Santa Clara, CA, USA). The optical rotations were measured using a JASCO DIP-4 automatic polarimeter (JASCO Co., Tokyo, Japan) at 25°C. In addition, the chromatographic behavior, spectra of MS and $^1$H-NMR of the active component collected by preparative liquid chromatography was compared with that of a panaxytriol(PXT) standard (Kaimi Co., Shanghai). A trace of standard PXT spiked into the extracted component to show co-chromatography was also conducted under the same HPLC conditions (condition 2).

Validation of the differential effect of panaxytriol (PXT) on MDZ metabolism

First, the concentration of PXT in $SM$ was quantified using an HPLC method (this
was found to be approximately 20 μg/mL. Then, the differential effects of PXT on
the metabolism of MDZ in RLM, HLM and recombinant CYP3A4 systems were
assessed. The production of 1’-OH-MDZ and 4-OH-MDZ was simultaneously
determined in the presence of varying concentrations of isolated PXT (2.0 μg/mL, 1.0
μg/mL and 0.5 μg/mL), standard PXT (2.0 μg/mL, 1.0 μg/mL and 0.5 μg/mL) and
SMI (10%, 5% and 2.5%, v/v); PXT concentrations of 2.0, 1.0 and 0.5 μg/mL are
equivalent to 10%, 5% and 2.5% SMI, respectively. All experiments were conducted
in triplicate.
Results

Effects of the SMI fractions, separated using SPE, on the metabolism of MDZ

To investigate which components of SMI are responsible for the differential effects on CYP3A4-mediated metabolism of MDZ, SMI was loaded onto SPE cartridges and separated using different concentrations of methanol. The effects of all collected fractions on the metabolism of MDZ are presented in Fig. 1. The initial eluate, the water-soluble eluate, and the residues eluted with 10 - 40% methanol, did not affect the metabolism of MDZ in RLM. In contrast, after pretreatment with the residues eluted using 50 - 100% methanol, 1'-hydroxylation of MDZ in RLM was increased to 108.7±9.8%, 149.7±4.5%, 187.9±12.7%, 186.8±7.1%, 213.9±13.4% and 223.7±8.1% compared with that of the control, while the formation of 4-OH MDZ was reduced to 79.6±8.7%, 72.7±4.4%, 76.6±3.8%, 64.1±12.7%, 61.6±9.8% and 70.4±8.6% of that in the control. These results indicate that the possible active components responsible for the differential effects on MDZ metabolism may predominantly be the lipid-soluble constituents of SMI; this is in good agreement with our previous study (Xia et al., 2009).

Effects of the SMI fractions, separated by HPLC, on the metabolism of MDZ

A representative HPLC chromatogram of SMI is shown in Fig. 2. Seven fractions were collected, according to the HPLC chromatogram and the retention times of the peaks, and the effect of each fraction on the metabolism of MDZ was investigated. Of these seven fractions, only fraction SM-5 (60-72 min) showed clear differential effects on the metabolism of MDZ, as shown in Fig. 3. Fraction SM-5 (60-72 min)
was further separated using different HPLC conditions (condition 2, described in the Materials and Methods). As shown in Fig. 4, several peaks were identified in fraction SM-5 (60-72 min). Of these, only fraction SM-5-3 (24-32 min), which was isolated as a single peak, demonstrated clear differential effects on the metabolism of MDZ that were similar to those of SMI (Fig. 5).

**Identification of the chemical structure of the active component of SMI**

The isolated compound, SM-5-3 (24-32 min), was subjected to structural analysis using liquid chromatography-mass spectrometry, $^1$H-NMR, $^{13}$C-NMR and optical rotation. The physical data (Supplemental Fig. 1) obtained are shown below: [$\alpha$]$_D$ -18.6° (CHCl$_3$); LC-MS: $m/z$ 301(M+1)$^+$; $^1$H-NMR (400 MHz, CDCl$_3$) δ 5.94 (ddd, $J = 5.3, 10.1, 15.7$ Hz, 1H-2), 5.47 (d, $J = 17.0$ Hz, 1H-1a), 5.25 (d, $J = 10.1$ Hz, 1H-1b), 4.92 (brs, 1H-3), 3.36 (brs, 1H-9), 3.60 (brs, $J = 1H$-10), 2.58 (brd, $J = 3.8$ Hz, 2H-8), 2.44 (brs, 3-OH-3), 2.10 (brs, 2-OH-9,10), 1.50 (m, 2H-11), 1.1~1.4 (10H-12~16), 0.87 (t, $J = 6.8$ Hz, 3H-17); $^{13}$C-NMR (400 MHz, CDCl$_3$) δ 117.15 (C-1), 136.04 (C-2), 63.48 (C-3), 78.11 (C-4), 70.90 (C-5), 66.51 (C-6), 74.77 (C-7), 24.98 (C-8), 73.08 (C-9), 72.13 (C-10), 31.78 (C-11), 25.55 (C-12), 29.52 (C-13), 29.19 (C-14), 35.58 (C-15), 22.62 (C-16), 14.06 (C-17). Based on the comparison to the known components’ stereochemistry structure in SMI, it can be found these spectral data coincide with those of PXT. In addition, the chromatographic behavior of isolated PXT was the same as that of standard PXT under the same HPLC conditions (the retention time of PXT was 27.5 min). The co-chromatography of standard PXT spiked into isolated PXT was also in good agreement with that of standard PXT and isolated
PXT alone (Fig. 6). Moreover, the spectra of MS and $^1$H-NMR of the isolated PXT were also in coincidence with that of the standard PXT. From these results, it may be concluded that the active component of $SMI$ corresponding to SM-5-3 (24-32 min) was PXT, which has the structure:

$$(3R,9R,10R)$-heptadec-1-ene-9,10-isopropylidenedioxy-4,6-diyn-3ol$ \quad$ (Fig. 7) 

(Matsunaga et al., 1989; Satoh et al., 2001).

**Validation of the differential effects of PXT on the metabolism of MDZ**

The effects of isolated PXT, standard PXT and $SMI$ on 1’-hydroxylation and 4-hydroxylation of MDZ were investigated and compared using different incubation systems. The effects of various concentrations of isolated PXT, standard PXT and $SMI$ on the metabolism of MDZ are shown in Table 1. In all the incubation systems used, isolated PXT, standard PXT and $SMI$ all caused a concentration-dependent inhibition of 4-hydroxylation of MDZ, as well as a significant activation of 1’-hydroxylation of MDZ.
**Discussion**

In our previous study (Xia et al., 2009), we found that *SMI* could significantly enhance CYP3A4-mediated 1'-hydroxylation of MDZ, but inhibit its 4-hydroxylation. *SMI*, extracted from red ginseng and *radix ophiopogonis*, contains a large number of chemical compounds, raising the possibility that several of these components could affect the catalytic activity of CYP3A4. To explore the possible active components, various fractions of *SMI* obtained by gradient elution on an SPE column were individually tested for their effects on MDZ metabolism. The fraction collected initially showed no effect on the metabolism of MDZ in RLM, excluding the possibility that the effect of *SMI* on CYP3A4 resulted from the adjuvant used in the preparation of *SMI*. The water-soluble eluate and the residues eluted with methanol at low concentrations (<50%, v/v) were also without effect on the metabolism of MDZ. In contrast, the residues eluted with higher concentrations of methanol (≥60%, v/v) showed significant differential effects on 1'-hydroxylation and 4-hydroxylation of MDZ in RLM, indicating that the lipid-soluble components of *SMI* may predominantly underlie these differential actions on MDZ metabolism. Further investigation of the components in *SMI*, that may be responsible for the differential effects on the metabolism of MDZ, were therefore carried out.

To further explore the possible active constituents, an HPLC system was used to separate the complex components in *SMI*. Seven fractions were obtained, according to the HPLC chromatogram and the retention times of the peaks, and the effects of each fraction were investigated on the metabolism of MDZ. It was found that only fraction
SM-5 (60-72 min) showed obvious differential effects on the metabolism of MDZ. As a result, the SM-5 (60-72 min) fraction was further separated using different HPLC conditions, until the main components were isolated as individual peaks on the HPLC chromatogram. Fraction SM-5-3 (24-32 min), which displayed only one peak, demonstrated differential effects on MDZ hydroxylation, and was subsequently identified as PXT by spectral analysis. This structural identification was supported by the observation that SM-5-3 (24-32 min) exhibited the same chromatographic behavior and spectra of MS and $^1$H-NMR as a PXT standard.

To further validate these data, the differential effects of isolated PXT, standard PXT and $SMI$ on the metabolism of MDZ were compared in RLM, HLM and recombinant CYP3A4 systems, with the synthesis of 1'-OH-MDZ and 4-OH-MDZ simultaneously determined in the presence of varying concentrations of PXT and $SMI$. It was found that isolated PXT and standard PXT behaved in a similar manner to $SMI$ in all these incubation systems, significantly enhancing MDZ 1'-hydroxylation and inhibiting MDZ 4-hydroxylation.

In many cases, CYP3A4 exhibits non-Michaelis-Menten kinetics, as well as homo- and heterotropic activation for numerous substrates. Recent advances have demonstrated that CYP3A4 co-operativity involves the binding of multiple (at least 2) substrate molecules to the binding pocket, and represents a case of true allostery characterized by effector-induced conformational transitions (Dmitri et al., 2008). Based on the above theory and our results, the differential effects of PXT on the metabolism of MDZ, similar to the effectors of citral, 6-gingerol and d-limonene...
(Zhang et al., 2008), can be explained by a two-site model (Korzekwa et al., 1998; Schrag et al., 2001; Domanski et al., 2001) or a multi-site model (Kenworthy et al., 2001; Manoj et al., 2010; Smirnov et al., 2011) of CYP3A4. It can be hypothesized that PXT can bind to one defined site that is also occupied by MDZ in the position required for 4-hydroxylation (or 1’-hydroxylation), and that both substrates can displace each other. The binding of PXT to one site causes an allosteric effect on the other MDZ-binding site that is required for its 1’-hydroxylation (or 4-hydroxylation). Alternatively, it can be hypothesized that, in addition to substrate binding sites, an activator binding site also exists that is closely related to the substrate binding sites. PXT can bind to the activator binding site, leading to conformational transitions in CYP3A4, and ultimately to differential effects on the substrate binding sites.

In summary, we have successfully isolated the active component of SMI that is responsible for the differential effects on CYP3A4-mediated 1’-hydroxylation and 4-hydroxylation of MDZ, and identified this constituent as PXT. SMI and PXT both had the potential to inhibit MDZ 4-hydroxylation but activate its 1’-hydroxylation. MDZ is mainly metabolized to 4-OH MDZ and 1’-OH MDZ mediated by CYP3A, but the preferential metabolic pathway of MDZ is 1’-hydroxylation in humans and 4-hydroxylation in rats (Rogers et al., 2003). After pretreatment with SMI or PXT, therefore, a predominant inhibitory effect on MDZ metabolism in rats would be observed (Xia et al., 2009). But it is possible to obtain an activation effect of SMI or PXT on MDZ metabolism in humans. The potential interactions between SMI, PXT
and other CYP3A4 substrates in clinical practice are likely to be more complex and its underlined mechanism is needed to be explored in the coming work.
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Authorship Contributions

Participated in research design: C.H. Xia, Y.Q. Xiong

Conducted experiments: C.W. Zeng, F. He, H Zhang

Performed data analysis: C.W. Zeng, F. He, C.H. Xia

Wrote or contributed to the writing of the manuscript: C.W. Zeng, C.H. Xia
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Footnotes

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Legends for Figures

Fig. 1. Effects of SMI fractions, separated by SPE, on 4-hydroxylation and 1'-hydroxylation of MDZ in RLM. *P < 0.05, vs control.

Fig. 2. HPLC chromatogram of SMI, obtained under condition 1.

Fig. 3. Effects of SMI fractions, separated by HPLC under condition 1, on 4-hydroxylation and 1'-hydroxylation of MDZ in RLM. *P < 0.05, vs control.

Fig. 4. HPLC chromatogram of SM-5 (60-72 min), obtained under condition 2.

Fig. 5. Effects of the fractions, separated from SM-5 (60-72 min) by HPLC under condition 2, on 4-hydroxylation and 1'-hydroxylation of MDZ in RLM. *P < 0.05, vs control.

Fig. 6. HPLC chromatograms of 20 μg/ml isolated PXT (A), 20 μg/ml standard PXT (B), 20 μg/ml isolated PXT + 10 μg/ml standard PXT (C) obtained under condition 2.

Fig. 7. Chemical structure of panaxytriol (PXT).
TABLE 1

Effects (percentage of control activity) of various concentrations of SMI, isolated PXT and standard PXT on 4-hydroxylation and 1'-hydroxylation of MDZ in RLM, HLM and recombinant CYP3A4 (rCYP3A4) systems, compared with the corresponding control groups.

<table>
<thead>
<tr>
<th>Groups</th>
<th>4-OH MDZ</th>
<th>1'-OH MDZ</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>RLM</td>
<td>HLM</td>
</tr>
<tr>
<td>Control (%)</td>
<td>100</td>
<td>100</td>
</tr>
<tr>
<td>10% SMI /2.0 μg/ml isolated PXT</td>
<td>34.8</td>
<td>36.9</td>
</tr>
<tr>
<td>10% SMI /2.0 μg/ml standard PXT</td>
<td>45.3</td>
<td>39.2</td>
</tr>
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<td>5% SMI /1.0 μg/ml isolated PXT</td>
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<td>54.8</td>
</tr>
<tr>
<td>5% SMI /1.0 μg/ml standard PXT</td>
<td>42.4</td>
<td>39.3</td>
</tr>
<tr>
<td>2.5% SMI /0.5 μg/ml isolated PXT</td>
<td>65.9</td>
<td>64.5</td>
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<tr>
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<td>74.4</td>
<td>70.4</td>
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<tr>
<td>0.5% SMI /0.5 μg/ml isolated PXT</td>
<td>70.5</td>
<td>71.2</td>
</tr>
</tbody>
</table>
FIG 2

SM-5 (60-72 min)
FIG 3

% of control activity

Control  SMI  SM-1  SM-2  SM-3  SM-4  SM-5  SM-6  SM-7

4-OH MDZ

1'-OH MDZ
Supplemental Material

Drug Metabolism and Disposition

IDENTIFICATION OF THE ACTIVE COMPONENTS IN SHENMAI INJECTION THAT DIFFERENTIALLY AFFECT CYP3A4-MEDIATED 1’-HYDROXYLATION AND 4-HYDROXYLATION OF MIDAZOLAM

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Supplemental Fig.1 $^1$H-NMR spectrum (A), $^{13}$C-NMR spectrum (B), DEPT135°spectrum (C), two-dimensional proton-proton chemical shift correlation spectrum (D) and LC-MS scan spectra (E) of the active components (panaxytriol) isolated from Shenmai Injection (SMI). The data well supported the structure identification of panaxytriol which was a known component in Ginseng and was proved differential effect on 4-hydroxylation and 1’-hydroxylation metabolism of midazolam mediated CYP3A4 in our study.
SM-5b, CDC13, 400MHz.

A

B
ESI Scan (13.857-14.200 min, 46 scans) Frag=135.0V 20.d

Counts (%) vs. Mass-to-Charge (m/z)