Metabolism and Pharmacokinetics of 3-n-Butylphthalide (NBP) in Humans: The Role of Cytochrome P450s and Alcohol Dehydrogenase in Biotransformation

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ABSTRACT

3-n-Butylphthalide (NBP) is a cardiovascular drug currently used for the treatment of cerebral ischemia. The present study aims to investigate the metabolism, pharmacokinetics, and excretion of NBP in humans and identify the enzymes responsible for the formation of major metabolites. NBP underwent extensive metabolism after an oral administration of 200 mg NBP and 23 metabolites were identified in human plasma and urine. Principal metabolic pathways included hydroxylation on alkyl side chain, particularly at 3-, ω-1-, and ω-carbons, and further oxidation and conjugation. Approximately 81.6% of the dose was recovered in urine, mainly as NBP-11-oic acid (M5-2) and glucuronide conjugates of M5-2 and mono-hydroxylated products. 10-Keto-NBP (M2), 3-hydroxy-NBP (M3-1), 10-hydroxy-NBP (M3-2), and M5-2 were the major circulating metabolites, wherein the areas under the curve values were 1.6-, 2.9-, 10.3-, and 4.1-fold higher than that of NBP. Reference standards of these four metabolites were obtained through microbial biotransformation by Cunninghamella blakesleae. In vitro phenotyping studies demonstrated that multiple cytochrome P450 (P450) isoforms, especially CYP3A4, 2E1, and 1A2, were involved in the formation of M3-1, M3-2, and 11-hydroxy-NBP. Using M3-2 and 11-hydroxy-NBP as substrates, human subcellular fractions experiments revealed that P450, alcohol dehydrogenase, and aldehyde dehydrogenase catalyzed the generation of M2 and M5-2. Formation of M5-2 was much faster than that of M2, and M5-2 can undergo β-oxidation to yield phthalide-3-acetic acid in rat liver homogenate. Overall, our study demonstrated that NBP was well absorbed and extensively metabolized by multiple enzymes to various metabolites prior to urinary excretion.

INTRODUCTION

3-n-Butylphthalide (NBP) [(±)-3-butyl-1(3H)-isobenzofuranone] is a potent and widely used drug for the treatment of ischemic stroke in clinic. Racemic NBP was approved for marketing in 2004 by the State Food and Drug Administration (SFDA) of China in the form of soft capsule and infusion drip. The recommended dose of NBP is 200 mg, taken three times a day. Previous pharmacological studies have demonstrated that NBP exhibits neuroprotective effects by increasing the release of glutamate and 5-hydroxytryptamine (Yan and Feng, 1998; Yan et al., 1998; Chong and Feng, 1999; Xu and Feng, 2001). Recent studies have revealed that NBP displays beneficial effects in attenuating amyloid-induced cell death in neuronal cultures, improving cognitive impairment in an animal model of Alzheimer’s disease and preventing neuronal cell death after focal cerebral ischemia in mice via the c-Jun N-terminal kinase pathway (Peng et al., 2008, 2010; Li et al., 2010).

Although the pharmacological properties of NBP were intensively investigated, its absorption, distribution, metabolism, and excretion are not well understood; only a few studies have investigated its metabolism in rats (Peng and Zhou, 1996; Wang et al., 1997). On the basis of the fragmentation of tentative metabolites and their tetramethylsilane derivatives, four hydroxylated metabolites were observed in the urine after an oral administration in rat. In another in vivo study of radiolabeled 3H-NBP, NBP was absorbed rapidly and metabolized extensively. The metabolites were mainly excreted in urine. One of the urinary metabolites was confirmed as 10-hydroxy-NBP, whereas the other metabolite was proposed to be 3-hydroxy-NBP without robust structure elucidation. To date, few studies have investigated the biotransformation of NBP in humans. Thus, a clear understanding of the metabolism of NBP in humans and the identification of the enzymes involved in its biotransformation would provide solid evidence for the safety evaluation of NBP, avoidance of potential drug-drug interaction, and inspiration for further discovery of new anti-stroke drugs (Li et al., 2011).

In light of these concerns, the present study aims to (1) investigate the metabolism of NBP in humans after an oral administration of 200 mg NBP soft capsules via ultraperformance liquid chromatography-UV/quadruple time-of-flight mass spectrometry (UPLC-UV/Q-TOF MS); (2) characterize the pharmacokinetic and elimination profiles of NBP in humans; and (3) evaluate the roles of cytochrome P450s (P450), alcohol dehydrogenase (ADH), and aldehyde dehydrogenase (ALDH) in NBP biotransformation.
Materials and Methods

Materials

NBP was kindly provided by the China Shijiazhuang Pharmaceutical Group Co., Ltd. (Shijiazhuang, Hebei, China). Phthalic acid-3-acetic acid was purchased from Alfa Aesar (Heysham, UK). Proadifen (SKF525A), 1-aminobenzotriazole (ABT), 4-methylpyrazole (4-MP), 17-octadecynoic acid (17-ODYA), and 4-phenytoxic acid (4-PA) were provided from Sigma-Aldrich Co. (St. Louis, MO). 11-Hydroxy-NBP, d4-NBP, d4-3-hydroxy-NBP, d4-10-hydroxy-NBP, d4-10-keto-NBP, and d4-11-ic acid were synthesized in our laboratory using previously described methods with minor modifications (Brenstrom et al., 1994; Brimble et al., 1996; Yang et al., 2007). Pooled human liver microsomes (HLMs) and human liver cytosol from both sexes; reconstituent human P450 isoenzymes CYPIA2, B1, 2D6, and 4A11 without cytochrome b5 reductase; and CYP2A6, 2B6, 2C8, 2C9, 2C19, 2E1, 3A4, 3A5 with cytochrome b5 reductase were supplied by BD Gentest (Woburn, MA). The microbial strain C. blakesleeanus ATCC29244 was obtained from the Institute of Microbiology, Chinese Academy of Sciences (Beijing, China). All solvents for LC-MS analysis were of high-performance liquid chromatography grade (Merck, Darmstadt, Germany). Other reagents were of analytical grade (Shanghai Chemical Plant, Shanghai, China). Ultrapure water was generated using a Milli-Q Gradient system (Millipore Corporation, Molsheim, France).

Study Protocol and Sample Collection

This study is an open-labeled, nonrandomized single-dose study. Four healthy Chinese male volunteers, aged 22 years to 26 years, with a mean body mass index of 21.65 kg/m² (ranging from 20.76 to 22.72), were enrolled in this study. The study protocol was approved by the Ethics Committee of the First Affiliated Hospital of Lanzhou University (Lanzhou, Gansu, China) and conducted in accordance with the Declaration of Helsinki and the principles of Good Clinical Practice. Written informed consents were obtained from all subjects prior to the study.

After an overnight fast, the four healthy volunteers received an oral administration of 200 mg NBP soft capsules (China Shijiazhuang Pharmaceutical Group Co., Ltd., 100 mg/capsule, product lot: 11060211). Blood samples were collected predose and at 0.25, 0.5, 1, 1.5, 2, 3, 4, 5, 8, 12, 24, 36, 48, and 72 hours postdose. The plasma samples were separated and stored at −20°C until analysis. Urine and feces samples were collected predose and at 0–12, 12–24, 24–48, 48–72, and 72–96 hours postdose. The total volume of the urine and total weight of the feces were recorded after each sample collection. The urine and feces samples were stored frozen at −20°C until analysis.

Metabolite Profiling and Identification

Preparation of Plasma and Urine Samples. Human plasma and urine samples were pooled for metabolite profiling. Plasma samples were segregated by the sample collection time (0 hour, 1 hour, and 8 hours), and equal volumes (150 μl) from each subject were pooled. Urine samples (0, 0–24, 24–48, 48–72, and 72–96 hours) were pooled by combining the volumes proportional to the bioavailability of NBP in urine and determined for each sample collection interval. For every 150 μl aliquot of pooled plasma (or urine) samples, 450 μl of acetonitrile was added. The mixture was mixed for 1 minute and centrifuged for 5 minutes at 11,000 g. The supernatant was then evaporated to dryness under nitrogen stream at 40°C and reconstituted in 75 μl (150 μl for urine samples) of methanol and water (10:90, v/v). A 10-μl aliquot of the resulting solution (2 μl for urine samples) was injected for analysis.

Preparation of Feces Samples. Each feces sample was thawed and placed in 5 parts (1 g:5 ml) methanol. The mixture was blended by a motor-driven homogenizer, and then the sample was vibrated by ultrasound wave for 15 minutes. A 20-ml aliquot of the mixture was removed and centrifuged at 3,500 g for 10 minutes. The 300-μl supernatant was transferred into another tube, evaporated to dryness under nitrogen stream at 40°C, and then reconstituted in 100 μl of methanol and water (10:90, v/v). A 10-μl aliquot of the solution was injected for metabolite identification.

UPLC-UV/Q-TOF MS Analysis. Chromatographic separation for the metabolite profiling and identification was conducted on an Acquity UPLC HSS T3 column (100 mm × 2.1 mm id., 1.8 μm) using an Acquity UPLC system (Waters, Milford, MA). The mobile phase was a mixture of 5 mM ammonium acetate (A) and methanol (B). The gradient elution was maintained at 5% B for 3 minutes, increased linearly to 55% B over 15 minutes to 100% B over the next 2 minutes, and maintained for 1 minute and finally to 5% B for 3 minutes to re-equilibrate the column. The flow rate was set at 0.4 ml/min, and the column temperature was set at 45°C. The eluted fractions were monitored by UV detection at 230 nm.

MS detection was achieved using a Synapt Q-TOF high-resolution mass spectrometer (Waters) operated in both positive and negative ion electrospray (ESI) modes. The desolvation gas was set to 700 l/h at 350°C, with the source temperature set at 100°C. Data were collected from 80 Da to 1000 Da during acquisition using an internal reference (400 ng/ml of leucine enkephalin solution infused at 20 μl/min to generate a reference ion in ESI (+) mode at m/z 556.2771 and in ESI (−) mode at m/z 554.2615). MS² function was programmed with independent low and high collision energies so that a low collision energy scan can be immediately followed by a high collision energy scan to induce the fragmentation of the ions transmitted through the quadrupole. Both intact precursor and fragment ions can be collected in a single run.

The UPLC and MS control were performed using the MassLynx 4.1 software (Waters). The blank and actual samples were processed using MetaboLynx, a subroutine of the MassLynx software integrated with the mass defect filtering technology and dealkylation tool to remove interferences from the matrix and facilitate the characterization of metabolites (Zhu, 2006; Zhang et al., 2009; Xie et al., 2012).

Isolation of Metabolites from Microbial Transformation.

Frozen microbial stock culture of C. blakesleeanus ATCC29244 was first incubated in 250-ml flasks containing potato dextrose agar at 28°C for 7 days in a rotary shaker set to 220 rpm (Asha and Vidhyavathi, 2009; Deng et al., 2011). The seed culture (5.0 ml) was then inoculated into 250-ml flasks containing 50 ml of biotransformation medium consisting of dextrose (1.0 g), yeast extract (0.25 g), peptone (0.25 g), NaCl (0.25 g), and K₂HPO₄ (0.25 g). After incubation at 28°C and 220 rpm for 24 hours, NBP in methanol (10 mg/ml) was added for a final concentration of 100 μg/ml. After 5 days of incubation, the fermentation was collected and the cells were removed by centrifugation at 3,500 for 10 minutes.

The supernatant (1000 ml) was first acidified with 75 ml HCl (1.0 M) and then extracted three times with n-hexane/dichloromethane/isopropanol (2/1/0.1, v/v/v). The upper organic layer was combined and subjected to a rotary evaporator under vacuum. The residue was reconstituted in methanol. The metabolites were isolated using a Gilson 281 Liquid Handler (Gilson, Paris, France) equipped with a Gilson 322 pump and a Gilson 156 UV detector. Synergi MAX-RP Prep ODS column (150 mm × 30 mm id., 4 μm, Phenomenex, Torrance, CA) was employed. Acetonitrile (A) and 10 mM ammonium acetate (B) were used as the mobile phase. The flow rate was set to 25 ml/min and detection was conducted at 230 nm. The gradient elution program was as follows: 0 minutes, 10% A; 1.5 minutes, 10% A; 21.8 minutes, 40% A; 22 minutes, 100% A; 25 minutes, 100% A; 25.2 minutes, 10% A. Several major chromatographic peaks (retention times at 6.2, 6.8, 9.1, 12.8, 19.1, and 22.0 minutes) were collected using an automatic fraction collector. All fractions of the same peak were combined and evaporated to dryness via lyophilization. The structures of these compounds were confirmed by UPLC-Q/TOF MS, 1H NMR, and carbon-13 (13C) NMR. The NMR spectra were recorded on a Bruker AVANCE III-400 (Newark, DE) or a Varian INOVA 600 spectrometer (Palo Alto, CA) at standard conditions. Standard compounds were dissolved in deuterated methanol or chloroform. Chemical shifts were expressed as parts per million relative to tetramethylsilane.

Pharmacokinetics of NBP and its Four Major Metabolites in Human Plasma

The concentrations of NBP and its major metabolites, M2, M3-1, M3-2, and M5-2, in human plasma were simultaneously quantified using a sensitive and selective LC-MS/MS method, validated according to FDA guidance, including selectivity, linearity, precision and accuracy, matrix effect, recovery, and stability. Briefly, the analytes and the corresponding synthesized deuterium-labeled internal standards were separated on a Zorbax Eclipse XDB C18 column (50 mm × 4.6 mm i.d., 1.8 μm, Agilent, Santa Clara, CA) on an Agilent 1200 high-performance liquid chromatography system (Agilent). The mobile phase
contained methanol-acetonitrile and 5 mM ammonium acetate with the flow rate of 0.6 ml/min. A 6460 triple-quadruple mass spectrometer (Agilent) operated with an electrospray ionization source was used for mass detection in both negative (for M3-1 and M5-2) and positive (for NBP, M2, and M3-2) modes. The MS parameters were as follows: capillary voltage, +5.0 kV and charging voltage, +40.5 kV; nebulizer gas pressure, 25 psi; carrier gas, 10 l/min and 280°C; and sheath gas, 6 l/min and 280°C. Multiple reaction monitoring was employed with the following transitions: NBP, m/z 191→145; m/z M2, 205→145; M3-1, m/z 205→161; M3-2, m/z 207→128; M2, m/z 219→175. Calibration curves for NBP and its four major metabolites were fitted via linearly weighted (1/x²) least-squares regression. The standard curves ranged from 3.00 ng/ml to 800 ng/ml for NBP and M2 and 3.00 ng/ml to 2400 ng/ml for M3-1, M3-2, and M5-2 in human plasma. The pharmacokinetic parameters were calculated by noncompartmental method using the WinNonlin software (V5.3, Pharsight, Mountain View, CA). The maximum plasma concentration (Cmax) and the time to reach Cmax (Tmax) were taken directly from the quantification data. The area under the plasma concentration versus time curve (AUC0→inf) was calculated from 0 to the last measurable time point (t) based on linear trapezoidal approximation. The terminal elimination rate constant (kT) was evaluated using the log-linear regression of the plasma concentration during the terminal phase of elimination. Corresponding elimination half-time (t1/2) was calculated at 0.693/kT. The area under the plasma concentration versus time curve from 0 to infinity (AUC0→inf) was estimated as the sum of (AUC0→Tmax) and C/T, where C is the concentration at the last quantified time point.

Excretion of Metabolites in Human Urine

The concentrations of M3-1 and M5-2 in human urine were determined by UPLC with UV detection at 230 nm. The chromatographic condition for quantification was similar to that for metabolite profiling and identification. Propranolol was selected as internal standard at a concentration of 22.6 µM. Calibration curves for M3-1 and M5-2 were also fitted via linearly weighted (1/x²) least-squares regression, and the dynamic curve ranged from 4.85 µM to 388 µM and 4.55 µM to 364 µM for M3-1 and M5-2, respectively, in human urine. Mono-hydroxylated metabolites and their glucuronide conjugates and M8 were semiquantified using M3-1 as pseudoreference standard. The other urinary products were semiquantitatively analyzed using the M5-2 calibration curve.

Metabolism of NBP, M3-2, and 11-Hydroxy-NBP in HLMs

The HLMs were carefully thawed on ice prior to the experiment. All analytes were dissolved in methanol and diluted with phosphate-buffered saline (PBS, pH 7.4) to the desired concentrations. The final methanol concentration did not exceed 0.1%. The analytes (50 µM) were mixed with HLMs (1.0 mg of protein/ml) in 100 mM PBS, and the total incubation volume was 200 µl. After 3 minutes of preincubation at 37°C, NADPH (2.0 mM) was added to initiate the reactions. After 1 hour incubation, the reactions were terminated with an equal volume of ice-cold acetonitrile. NBP was separately incubated in HLMs with P450 inhibitors, SKF525A (10 µM) and ABT (1.0 mM), to identify the enzymatic pathways involved (Solheimsen-Sternbeck et al., 2000; Furnes and Schlenk, 2005). For M3-2, subsequent experiments were conducted in the presence of ABT (1.0 mM). For 11-hydroxy-NBP, inhibition tests were carried out in the presence of ABT (1.0 mM) and 17-ODYA (10 µM), a potent inhibitor for CYP4A and CYP4F subfamilies (Lasker et al., 2000; Nithipatikom et al., 2004; Jin et al., 2011). Each of the inhibitors was preincubated with HLMs and NADPH for 5 minutes at 37°C before the reactions were started by the addition of the analytes. The solutions were allowed to react for 1 hour and quenched thereafter with ice-cold acetonitrile (200 µl).

Human P450 Isoenzymes Phenotyping

The general incubation conditions of NBP with 12 major commercially available human recombinant P450 isoforms (50 pM), CYP1A2, 1B1, 1A6, 2B6, 2C8, 2C9, 2C19, 2D6, 2E1, 3A4, 3A5, or 4A11, were essentially identical to those for HLMs, except that HLMs was replaced by P450 individual isoforms. In each P450 isoform incubation system, the UPLC-UV peak areas of the detected metabolites were recorded to determine the contributions of the selected P450 enzymes to the NBP metabolite formation. The peak areas of the metabolites detected in each P450 isoform were normalized with the nominal specific content of the corresponding P450 in native HLMs (Rodrigues, 1999). The sum of the normalized peak areas of one specific metabolite was regarded as 100%. The metabolite formed in each P450 isoform was expressed as the percentage of the summed area. The effect of individual P450 enzyme-specific inhibitors on the formation of hydroxylated metabolites was also evaluated using HLMs. The incubation medium contained NBP (50 µM), HLMs (1.0 mg protein/ml), and chemical inhibitors. P450-specific inhibitors, α-naphthoflavone (2.0 µM), diethylidithiocarbamate (50 µM), tioctopride (24 µM), clomethiazole (24 µM), and ketoconazole (2.0 µM), were employed to determine the involvement of CYP1A2, 2A6, 2B6, 2C19, 2E1, and CYP3A4/5 in the process. Incubations were preincubated for 3 minutes at 37°C before the addition of NADPH (2 mM) and then stopped after 1 hour by ice-cold acetonitrile (200 µl).

Metabolism of M3-2 and 11-Hydroxy-NBP in Human Liver Cytosol

Human liver cytosol catalyzed oxidation was conducted in duplicate at 37°C in a total volume of 200 µl. The incubation medium contained analytes (50 µM) and human liver cytosol (1.0 mg protein/ml) in 100 mM PBS (pH 7.4). The mixture was preincubated for 3 minutes. The reactions were then started by adding NAD (2.0 mM), and allowed to proceed for 1 hour before being stopped by ice-cold acetonitrile (200 µl). Inhibition experiments were performed in the presence of an ADH specific inhibitor, 4-MP, with four concentration levels (5 µM, 50 µM, 250 µM, and 1 mM), and ALDH inhibitor disulfiram (50 µM). The inhibitors were preincubated with NAD-supplemented human liver cytosol for 5 minutes at 37°C before the reactions were started by adding the analytes. The reactions were quenched as mentioned previously.

Trapping of 11-Aldehyde-NBP in Human Liver Cytosol and HLMs

The 11-hydroxy-NBP (50 µM) was incubated with 1.0 mg/ml of human liver cytosol supplemented with NAD (2.0 mM). Methoxylamine was added at the start of the incubation into a final concentration of 5 mM. The reaction was conducted at 37°C in duplicate and stopped with ice-cold acetonitrile (200 µl) after 1 hour of incubation. Similarly, 11-aldehyde-NBP was captured in HLMs in the same manner as in human liver cytosol, except that NAD was replaced by NADPH.

Incubation of NBP and M5-2 in Rat Liver Homogenate

Fresh rat liver homogenate was prepared from male Sprague-Dawley rats as described previously (Bjorge and Baillie, 1991). The incubation mixture in a 50-ml Petri dish contained freshly prepared homogenate (2.5 ml), NAD (2.0 mM). Methoxylamine was added at the start of the incubation into a final concentration of 5 mM. The reaction was conducted at 37°C in duplicate and stopped with ice-cold acetonitrile (200 µl) after 1 hour of incubation. Similarly, 11-aldehyde-NBP was captured in HLMs in the same manner as in human liver cytosol, except that NAD was replaced by NADPH.

Results

UPLC-Q/TOF MS Analysis of NBP

The chromatographic and MS fragmentation behaviors of the parent drug were first studied to identify NBP metabolites. The NBP retention time was 18.0 minutes under the chromatographic conditions employed. In ESI (+) mode, NBP provided a protonated molecule [M + H]+ and sodium adduct ion [M + Na]+ at m/z 191.109 and 213.093, respectively. The product ion spectrum of NBP under high collision energy scan was shown in Fig. 1A. Fragment ions at m/z 173.098 (−H2O), 145.103 (−HCOOH, 100% abundance), 135.047 (−C6H4), 131.052 (−H2O −C6H4), 117.072 (−HCOOH −C6H4), 105.074 (C6H4), 103.057 (C7H7), and 91.057 (−CO2 −C6H4, C7H7) were observed. A tentative fragmentation profile was proposed based on the high-resolution mass spectral information (Fig. 1B). Therefore, the
NBP fragments were formed predominantly by cleavage on the n-butyl side chain and the lactone moiety.

Unfortunately, NBP did not show any response in ESI (−) mode, making the interpretation of some metabolites challenging, which gave more informative fragment ions in ESI (−) than in ESI (+) mode. Thus, plasma, urine, and feces samples were detected in both positive and negative modes. On the basis of the fragmentation patterns, high collision energy mass spectra, and chromatographic behaviors, the

Fig. 1. Mass spectra of the reference substances: NBP (A and B), M2 (C and D), M3-1 (E and F), M3-2 (G and H), and M5-2 (I and J) under high collision energy in positive detection mode and their tentative fragmentation profiles.
detected metabolites were compared with those of the parent compound and available reference standards to elucidate their structures.

NBP Metabolite Profiling and Identification

After being processed using the mass defect filtering and dealkylation techniques, 6 and 13 metabolites of NBP were detected in human plasma in the ESI (+) and ESI (−) modes, respectively (Fig. 2, A and B); whereas 10 and 17 metabolites of NBP were observed in urine samples in the ESI (+) and ESI (−) modes, respectively (Fig. 3, A and B). Metabolite profiles in pooled human feces as well as urine samples beyond 24 hours postdose were not shown because only trace amount of metabolites were detected. The MS response alone cannot reflect the relative quantity of the metabolites because metabolic modification of the parent drug changes the polarity and their tendency to form ions in the ESI source, resulting in different ionization efficiency and diverse mass responses. Moreover, several metabolites predominantly displayed sodium adducts ([M + Na]+), making the MS response of protonated molecule ([M + H]+) less reliable for relative quantity comparison among the metabolites. Common metabolic conversions, such as hydroxylation and dealkylation, do not cause sharp changes to the chromophoric groups of the parent compound. Thus, the UV absorbance, rather than MS response, can roughly reflect the relative quantity of the metabolites. Figs. 2C and 3C display the corresponding UPLC-UV chromatograms of the plasma and urine samples. Comparing the plasma UV chromatogram with that of blank plasma (Fig. 2D), predominant circulating metabolites were eluted at 7.8 (M5-2), 11.5 (M2), 11.8 (M3-1), and 12.1 minutes (M3-2). NBP was not detected because of sensitivity. Likewise, the major urinary metabolites were those with the retention times of 7.8 (M5-2), 8.0 (M10), 8.5 (M9-1), 8.7 (M9-2), and 11.3 minutes (M9-6) compared with corresponding blank urine (Fig. 3D).

Table 1 lists the detailed information of these metabolites, including the pseudomolecular ion, proposed elemental composition, retention time, and the characteristic fragment ions. Speculated structures of the metabolites are shown in Fig. 4. The metabolites were named in the order of molecular weight; metabolites with the same molecular weight were named in sequential order of retention time. The identification of the metabolites is as follows.

Parent Drug M0. A chromatographic peak at 18.0 minutes, with an elemental composition of C12H14O2, was detected in human plasma. Its protonated molecular weight was 191.106 Da in ESI (+) mode. The retention time and mass spectral fragmentation patterns were identical to the parent drug, indicating that this component was unmetabolized NBP, designated as M0. M0 was not found in human urine and feces.

Metabolite M1. M1, detected only in urine, was much more hydrophilic than other metabolites, being eluted at an early retention time of 4.2 minutes. M1 displayed [M + H]+/[M + Na]+ ions at m/z 193.050/215.033 in ESI (+) and [M − H]− ion at 191.035 in ESI (−). The elemental composition of M1 was C10H14O2, suggesting that two carbon units were removed in M1 compared with the parent drug. In ESI (+), a predominant fragment ion at m/z 133.029 was yielded by neutral loss of CH3COOH from the precursor ion. In ESI (−), consecutive neutral losses of CO2 molecules were observed, resulting in m/z 147.045 (−CO2) and m/z 103.056 (−2CO2). M1 was confirmed as phthalide-3-acetic acid by comparing its chromatographic and MS behaviors with the commercially available reference standard.

Metabolite M2. M2 was a major circulating metabolite eluted at 11.5 minutes. M2 exhibited [M + H]+/[M + Na]+ ions at m/z 205.087/227.071 in ESI (+); no MS response was observed in ESI (−). The chemical formula of M2 was C12H12O3, indicative of mono-oxidation with dehydrogenation compared with NBP. The high energy mass spectrum of M2 revealed fragment ions at m/z 187.074 (−H2O), 145.063 (−H2O − CH3CO), and 117.071 (−CH3CHO − CO2). Among them, m/z 117.071 was the same as that of NBP, demonstrating that the n-butyl side chain was modified. M2 was further confirmed by comparing its retention time and mass spectrum with the reference standard obtained via microbial transformation as described in Materials and Methods. The 1H NMR and 13C NMR data of M2 are listed in Table 2. Comparing the chemical shifts of M2 with NBP, aromatic H and C, C-1, and CH3 were unchanged; however, those of the n-butyl side chain shifted downfield. The phenomenon was especially obvious on CH2-11, where the H and C signals moved downfield from 0.90 to 2.13 and 13.9 to 30.4, respectively, indicating a carbonyl moiety next to CH2-11. The appearance of a new carbonyl signal in 13C NMR spectrum (i.e., δC 210.6) and the disappearance of two H signals of the n-butyl side chain further strengthened the assumption. Therefore, M2 was confirmed as 10-keto-NBP. Fragmentation profile of M2 is proposed in Fig. 1D.

Metabolite M3. M3 exhibited [M + H]+/[M + Na]+ ions at m/z 207.104/229.080 in ESI (+). The elemental composition was C12H14O3, indicating mono-oxidation products of NBP. M3 contained four isomers, eluted at 11.8 (M3-1), 12.1 (M3-2), 13.1 (M3-3), and 13.8 minutes (M3-4). M3-1 and M3-2 were major circulating components and apt to lose one (m/z 189.094) and two (m/z 171.082) H2O in ESI (+), illustrating that the aliphatic hydroxyl group was introduced in either C-3 or the n-butyl side chain rather than the benzene ring. The reference standards of M3-1 and M3-2 were isolated and purified from microbial incubations to pinpoint the exact hydroxylation site. The 1H NMR and 13C NMR spectra data of M3-1 and M3-2 are summarized in Table 2. The comparison of chemical shifts between M3-1 and NBP indicated that the aromatic ring and n-butyl side chain signals were intact, whereas the H-3 signal of NBP (i.e., δH 5.47) was missing in M3-1. Meanwhile, C-3 signal moved downfield from 81.4 to 107.5, suggesting that the C-3 of M3-1 was connected to two oxygen atoms. Therefore, M3-1 was confirmed to be 3-hydroxy-NBP, which was also reported as one metabolite of ligustilide, a bioactive ingredient from Rhizoma Chuanxiong, in rat plasma (Yan et al., 2008). The tentative fragmentation pattern of M3-1 is shown in Fig. 1F. The NMR spectra between NBP and M3-2 were significantly different, as listed in Table 2. The H-10 signal of M3-2 moved downfield from 1.42 to 3.80 and the C-10 signal moved downfield from 22.4 to 67.9, indicating that one hydrogen atom of CH2-10 was substituted by a hydroxy group. Stepping downfield of both the C and H signals of CH2-11 further supported the assumption. Thus, M3-2 was elucidated as 10-hydroxy-NBP. The proposed fragmentation profile of M3-2 is displayed in Fig. 1H. M3-3 and M3-4, two minor metabolites in human plasma, displayed no signal in ESI (−). In ESI (+), almost the same fragment ions were observed for both metabolites, including m/z 189.092 (−H2O), 171.081 (−2H2O), 153.070 (−3H2O), 149.061 (−C6H4OH), 131.050 (−C5H3OH − H2O), and 103.055 (C4H5). The fragment ions m/z 131.050 and 103.055 were the same as those of NBP, indicating that the hydroxy group was not attached to the aromatic ring. On the basis of the fact that the positions of C-3, C-10, and C-11 were occupied by M3-1, M3-2, and 11-hydroxy-NBP, respectively, the hydroxyl groups in M3-3 and M3-4 were exclusively attached in positions C-8 or C-9.

Metabolite M4. M4 was detected in human plasma and urine at trace level. M4 was eluted at 11.1 minutes and exhibited [M − H]− ion at 207.101 in ESI (−), but none in the ESI (+). The chemical formula of M4 was C12H16O3, suggesting that an H2O molecule was added to
NBP. In ESI (−), a single fragment ion at \( m/z \) 163.110 was observed, which was generated from the neutral loss of CO\(_2\) (−43.992 Da). When NBP was incubated in basic aqueous solutions (pH = 10–12) at 50°C for 24 hours, most of NBP was converted to M4. When the basic solution containing M4 was acidified below pH 3 with 0.1 M HCl, NBP became the predominant component observed, whereas M4 dwindled dramatically. Considering that the lactone moiety was susceptible to pH, M4 was proposed as the lactone-hydrolysis product of NBP.

Fig. 2. Metabolic profiles in pooled human plasma 1 hour after the oral administration of 200-mg NBP soft capsules, as detected by Q-TOF MS in positive (A) and negative (B) modes, and UPLC-UV chromatograms of pooled plasma (C) and human blank plasma (D). AU, arbitrary unit.
Metabolite M5. M5-1 and M5-2 were eluted at 5.8 and 7.8 minutes, respectively, with [M – H]⁻ ion at m/z 219.067 in ESI (–). In ESI (+), M5-2 showed [M + H]⁺/[M + Na]⁺ ions at m/z 221.093/243.074, whereas M5-1 gave only [M + Na]⁺ ion at m/z 243.060. The elemental composition of M5-1 and M5-2 was C₁₂H₁₂O₄, indicating dioxygenation with dehydrogenation compared with NBP. M5-1 was found in plasma and urine. It yielded several fragment ions at m/z 201.052 (–H₂O), 175.078 (–CO₂), 157.068 (–CO₂–H₂O), 147.046,
was also isolated from microbial transformation; however, the amount suggesting that an oxygen atom was attached to the aromatic ring. M5-1 m/z of 131.055, 119.051, and 103.058 in ESI (M7-2 Sulfation of M3-2
M11-2 Dihydroxylation +
M11-1 Dihydroxylation +
M9-5 Glucuronidation
M9-3 Glucuronidation
M9-2 Glucuronidation
M6-2 Hydroxylation of
M5-2 Hydroxylation of M5-2
M5-2 NBP-11-0-acid
M6-1 Hydroxylation of M5-2
M6-2 Hydroxylation of M5-2
M7-1 Sulfation of M3-1
M7-2 Sulfation of M3-2
M8 N-acetylcysteine conjugation
M9-1 Glucuronidation of M3-2
M9-2 Glucuronidation of M3-2
M9-3 Glucuronidation of M3-3
M9-4 Glucuronidation of M3-3
M9-5 Glucuronidation of M3-4
M9-6 Glucuronidation of M3-1
M10 Glucuronidation of M5-2
M11-1 Dihydroxylation + glucuronidation
M11-2 Dihydroxylation + glucuronidation

131.055, 119.051, and 103.058 in ESI (−). Elemental composition of m/z 119.051 and 103.058 were C₇HₓO and C₆Hₓ, respectively, suggesting that an oxygen atom was attached to the aromatic ring. M5-1 was also isolated from microbial transformation; however, the amount of M5-1 was insufficient for NMR analysis. Incubation of M2 in HLMs resulted in the trace formation of M5-1, implicating M5-1 being a hydroxylated product of M2. M5-2 was the most abundant metabolite in both human plasma and urine based on the UPLC-UV peak areas (Figs. 2C and 3C). Similar to the fragmentation profile of M1 in ESI (−), M5-2 also exhibited characteristic fragment ions at m/z 175.078 (−CO₂) and 131.089 (−2CO₂), underpinning the existence of two CO₂ moieties in M5-2. The reference standard of M5-2 was isolated and purified from microbial incubation. The ⁴⁰NMR and ¹³C NMR data of M5-2 are listed in Table 2. The H and C signals of CH₂-10
shifted downfield from 1.42 (δH) and 22.4 (δC) in NBP to 2.37 (δH) and 37.4 (δC) in M5-2, respectively, suggesting the presence of an electron-withdrawing group in C-11. Notably, the C-11 signal increased dramatically from 13.9 to 179.8, strongly indicating that M5-2 is a carboxylic acid. The disappearance of the H signal in CH3-11 further enhanced this assumption. Therefore, M5-2 was assigned as NBP-11-oic acid. The oxidation of 11-hydroxy-NBP by Jones reagent yielding M5-2 further supported the structure elucidation. A tentative fragmentation pattern of M5-2 is shown in Fig. 1.

Metabolite M6. M6-1 and M6-2 were found in human plasma and urine. With the chemical formula of C12H12O5, they displayed [M + H]⁺/[M + Na]⁺ ions at m/z 237.080/259.057 in ESI (+) and [M − H]⁻ ion at m/z 235.063 in ESI (−). Incubation of M5-2 in NADPH-fortified freshly prepared rat liver homogenate yielded a trace amount of M6-2; no M6-1 was detected, indicating M6-2 might be a hydroxylated product of M5-2. However, we could not exclude the possibility of M6-2 being from dioxygenated metabolites. In ESI (−), M6-2 yielded fragment ions at m/z 191.075 and 173.063, which were 15.997 Da larger than those of M5-2, suggesting that the hydroxyl group was attached on the alkyl side chain or C-3 of M5-2. M6-1 exhibited similar MS fragmentation pattern as that of M6-2, and was proposed as a regional isomer of M6-2.

Metabolite M7. Minor metabolites M7-1 (observed in urine) and M7-2 (found in plasma and urine) were eluted at 9.5 and 12.7 minutes, respectively. In ESI (−), M7-1 and M7-2 exhibited [M − H]⁻ ion at m/z 285.044 with elemental composition of C12H14O6S. They both formed fragment ion at m/z 205.091 by loss of 79.953 Da (SO3), illustrating M7-1 and M7-2 being sulfates of hydroxylated NBP.
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Incubation of M3-1 and M3-2 with human liver cytosol supplemented with 3'-phosphoadenosine-5'-phosphosulfate resulted in the trace formation of M7-1 and M7-2, respectively. Tentatively, M7-1 and M7-2 were proposed as the sulfate conjugates of M3-1 and M3-2, respectively.

**Metabolite M8.** M8, eluted at 14.5 minutes, was detected only in human urine and exhibited [M + H]⁺/[M + Na⁺] ions at m/z 352.123/374.099 in ESI (+) and [M − H⁻]⁻ ion at m/z 350.099 in ESI (−). The chemical composition of C₁₇H₂₁NO₅S suggested that M8 was an N-acetylcysteine (C₆H₇NO₅S) conjugate of NBP (C₁₇H₁₉O₂). In ESI (−) mode, M8 produced a fragment ion at m/z 221.065, corresponding to neutral loss of 129.040 Da (C₅H₇O₃S), which further supported the presence of an N-acetylcysteine moiety in M8 (Scholz et al., 2005). The reference substance of M8 was isolated from human urine and subjected to NMR analysis. The NMR data of M8 are listed in Table 2. Comparison of the chemical shifts between NBP and M8 revealed that the n-butyl side chain and the aromatic ring signals were unchanged, whereas the C-3 signal of NBP (δC 81.4) and M3-1 (δC 107.5), therefore M8 was confirmed as 3-N-acetylcysteine-NBP. Structurally, the side chain in both M3-1 and M8 remain unmodified, and incubation of M3-1 in freshly prepared rat liver homogenate supplemented with NADPH and N-acetylcysteine yielded a minor amount of M8, but similar incubation of NBP did not generate detectable M8. The formation of M8 might be related to the sulfate conjugate of M3-1, which contains a good leaving group. More efforts are currently underway to better understand the formation mechanism of this uncommon metabolite.

**Metabolite M9.** M9-1−M9-5 were detected in human plasma and urine, whereas M9-6 was only found in human urine. In ESI (+), M9-1−M9-6 displayed a major fragment ion at m/z 205.086 via neutral loss of 176.032 Da (C₆H₈O₆), indicating M9-1 of M9-6 was only found in human urine. In ESI (+), M10 generated almost the same fragment ions as M8, which was between those of NBP (δC 81.4) and M3-1 (δC 107.5), therefore M8 was confirmed as 3-N-acetylcysteine-NBP. Structurally, the side chain in both M3-1 and M8 remain unmodified, and incubation of M3-1 in freshly prepared rat liver homogenate supplemented with NADPH and N-acetylcysteine yielded a minor amount of M8, but similar incubation of NBP did not generate detectable M8. The formation of M8 might be related to the sulfate conjugate of M3-1, which contains a good leaving group. More efforts are currently underway to better understand the formation mechanism of this uncommon metabolite.

**Metabolite M10.** M10 was eluted at 8.0 minutes and detected only in urine. In ESI (+), M10 generated almost the same fragment ions as that of M5-2 with similar abundance. Among these ions, m/z 221.082 was 176.039 Da less than the precursor ion, implicating M10 being a glucuronide conjugate. The incubation of M10 fraction isolated from human urine in 0.05 M HCl at 60°C for 48 hours resulted in the formation of M5-2. Therefore, M10 was assigned as the glucuronide conjugate of M5-2.
Pharmacokinetics and Renal Elimination of NBP

After an oral administration of 200 mg NBP soft capsules to four healthy Chinese male volunteers, the concentrations of the parent drug NBP and its four major metabolites (i.e., M2, M3-1, M3-2, and M5-2) in human plasma were simultaneously quantified by a fully validated LC-MS/MS method using corresponding deuterated internal standards. The mean plasma concentration versus time profiles for NBP, M2, M3-1, M3-2, and M5-2 are shown in Fig. 5, and their main pharmacokinetic parameters are presented in Table 3. The peak plasma concentrations (C_{max}) of NBP, M2, M3-1, M3-2, and M5-2 were achieved at approximately 0.75 to 1.50 hours postdose, with mean values of 514, 516, 1370, 1681, and 1568 ng/ml, respectively. The average AUC0-∞ values of NBP, M2, M3-1, M3-2, and M5-2 were 864, 1370, 2478, 8902, and 3529 ng·h/ml, respectively. Therefore, the plasma exposures of M2, M3-1, M3-2, and M5-2 were approximately 1.6-, 2.9-, 10.3-, and 4.1-fold higher than that of NBP. The terminal elimination half-times (t_{1/2}) of NBP, M2, M3-1, M3-2, and M5-2 averaged 5.3, 2.3, 9.1, 3.9, and 3.3 hours, respectively.

Renal Elimination of NBP

The concentrations of M3-1 and M5-2 in human urine were determined using the UPLC-UV method. Other urinary metabolites were semi-quantified using M3-1 or M5-2 as the pseudoreference standard. Various metabolites, especially glucuronide conjugates, were recovered in human urine, and the total urinary excretion accounted for 81.6% of the administered dosage. The major metabolic elimination pathways of NBP were ω-carboxylation (and its glucuronide conjugation) and glucuronide conjugation of NBP monoxides, accounting for 23.4% and 21.3% of the dose, respectively.

Oxidation of NBP in HLMs

Incubation of NBP was performed in HLMs as an initial procedure toward identifying drug metabolizing enzymes. Seven oxidized metabolites were detected in NADPH-supplemented HLMs, as illustrated in Fig. 6, B and C. The major products were confirmed to be M3-1 and M3-2. M5-2 and M2 were found as minor metabolites, and M3-3 and M3-4 were also observed at trace amounts. MS analysis revealed another moderate metabolite, coeluted with M3-2 under the employed chromatographic condition. It was confirmed as 11-hydroxy-NBP by comparing it to a synthesized reference standard using a different gradient elution program (Supplemental Fig. 1). The yield of 11-hydroxy-NBP was approximately 20% that of M3-2 in terms of chromatographic area. The C and H signals of the aromatic proportion and CH3-8 to CH3-10 in 11-hydroxy-NBP were almost the same as those of NBP, whereas C and H signals of CH3-11 significantly shifted downfield, as listed in Table 2. Furthermore, four CH2 moieties were observed in the distortionless enhancement by polarization transfer spectrum.

General P450 inhibitors SKF525A or ABT were preincubated with HLMs to evaluate the role of P450s in the oxidative metabolite formation of NBP. Compared with the control samples without inhibitors, coinubcation of SKF525A strongly inhibited NBP metabolism with obviously decreased formation of M2, M3-1, M3-2, M5-2, and 11-hydroxy-NBP (Fig. 7). The preincubation of ABT with HLMs also inhibited NBP metabolism to a much larger extent than SKF525A (Fig. 7). This evidence suggests the involvement of P450s in the oxidative metabolism of NBP.

P450 Isoforms Responsible for NBP Hydroxylation

Further incubation of NBP with NADPH-supplemented individual recombinant human P450 enzymes was conducted to investigate which P450 enzyme(s) catalyzed NBP hydroxylation. NBP was catalyzed by an array of human P450 enzymes to form M3-1 to M3-4 and 11-hydroxy-NBP, as summarized in Table 4. Neither M2 nor M5-2 was detected in the tested isoenzyme incubation. After normalization with regard to the native hepatic abundance, CYP3A4 was the most active enzyme for M3-1 formation, followed by CYP2E1 and CYP3A5. CYP2E1 was the primary enzyme responsible for M3-2 generation, followed by CYP2B6 and 2C19. For M3-3 generation, CYP2E1 was the most efficient enzyme, followed by CYP3A4. Isoforms CYP2A6 and 2E1 contributed to M3-4 production. CYP1A2, 2B6, and 2E1 were the principal enzymes involved in the formation of 11-hydroxy-NBP. Specific chemical inhibition tests were performed to better evaluate the relative contribution of each isofrom to NBP hydroxylation. The results illustrate that neither of the P450 specific inhibitors displayed strong inhibition on the generation of M3-1 to M3-4 and 11-hydroxy-NBP (unpublished data), probably because NBP metabolism can be compensated by other isoenzymes via the same or alternative hydroxylation pathways when one particular P450 isoform is inhibited.

Insight into the Formation of M5-2

M5-2 is the principal metabolite in both human plasma and urine. However, M5-2 was only detected as a minor metabolite in NBP incubation with HLMs, which was not commensurate with the scenario in vivo. Carboxylic acid metabolites were generally formed via further oxidation of ω-hydroxylated intermediates by ADH and ALDH. Synthesized 11-hydroxy-NBP was incubated in ADH- and ALDH-rich human liver cytosol to evaluate whether ADH and ALDH participated in M5-2 generation. Our results indicate that approximately 95% of 11-hydroxy-NBP was converted to M5-2 in the presence of NAD. In the absence of NAD, metabolism of 11-hydroxy-NBP was negligible. Selective inhibitors of both enzymes were estimated to further confirm the functions of ADH and ALDH in catalyzing 11-hydroxy-NBP. Figure 8 shows that the presence of 4-MP (5 µM), a potent ADH inhibitor, moderately inhibited M5-2
formation by 36% and 4-MP at 50 μM showed vigorous inhibition on the M5-2 yield. The presence of 4-MP at 250 μM or above almost completely inhibited M5-2 formation. The presence of disulfiram, an ALDH-specific inhibitor, in human liver cytosol reduced M5-2 formation by 40% (Fig. 8). These results clearly support the involvement of ADH and ALDH in the generation of M5-2 from 11-hydroxy-NBP.

Despite the robust activity of ADH and ALDH in mediating M5-2 formation, approximately 30% conversion of 11-hydroxy-NBP to M5-2 was observed in NADPH-supplemented HLMs using 11-hydroxy-NBP as the substrate. Thus, P450 or flavin-containing monooxygenases (FMOs) can also catalyze M5-2 formation. Preheating HLMs at 50°C for 1 minute to inactivate FMOs displayed negligible effects on M5-2 formation, excluding the participation of FMOs. Further inhibition experiment was executed to evaluate the role of P450 in M5-2 formation. The presence of ABT in HLMs inhibited M5-2 formation by approximately 89%. Thus, P450 also contributed to the generation of M5-2. However, subsequent incubation of 11-hydroxy-NBP with NADPH-fortified recombinant P450 isoforms (CYP1A2, 1B1, 2A6, 2B6, 2C8, 2C9, 2C19, 2D6, 2E1, 3A4, 3A5, and 4A11) only yielded trace amounts of M5-2. The presence of 17-ODYA in HLMs decreased M5-2 formation by 59%, suggesting that the CYP4A or CYP4F subfamilies might be partially responsible for the biotransformation of 11-hydroxy-NBP to M5-2 in HLMs.

Although ALDH was proven to participate in the formation of M5-2 from 11-hydroxy-NBP in human liver cytosol, 11-aldehyde-NBP was not detected directly in the incubation mixture because of its obvious instability. Methoxylamine was used as the trapping agent to certify

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<td>$t_{1/2}$ (hours)</td>
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AUC, area under the curve; S.D., standard deviation.

Fig. 6. In vitro metabolism of NBP in HLMs. (A) UPLC-UV chromatogram of a control incubation performed without NADPH; (B) UPLC-UV chromatogram of an incubation performed with NADPH; (C) UPLC-Q/TOF MS chromatogram of an incubation performed with NADPH.
the presence of 11-aldehyde-NBP. The potential oxime derivative was detected in both NAD-supplemented human liver cytosol and NADPH-fortified HLMs (Supplemental Fig. 2), demonstrating that 11-hydroxy-NBP was first oxidized to 11-aldehyde-NBP followed by subsequent oxidation to M5-2.

Investigation on Metabolic Pathway to M2

Similar to the formation mechanism of M5-2, the ketone metabolite M2 can also be generated in either NAD-supplemented human liver cytosol or NADPH-fortified HLMs using M3-2 as the substrate. The metabolism of M3-2 in human liver cytosol demonstrated that approximately 4% of M3-2 was converted to M2. The presence of higher 4-MP concentration in human liver cytosol also showed enhanced inhibition on M2 generation (Supplemental Fig. 3), indicating that ADH is a potential contributor to M2 formation.

In a separate test, approximately 11% of M3-2 transformation to M2 was observed when M3-2 was incubated in HLMs. The addition of ABT in HLMs suppressed M2 formation by up to 61% (Supplemental Fig. 3), indicating that ADH is a potential contributor to M2 formation.

Elucidation on the Generation of M1

Structurally, M1 is two carbon units shorter than other oxidative metabolites, reminding the possible participation of β-oxidation. To test this assumption, aside from metabolites M2 and M3-1 to M3-4, two carboxylic acids, namely M5-2 and M1, were observed at lower levels. In the chemical inhibition experiments, preincubation with 4-PA, a β-oxidation inhibitor, potently suppressed M1 formation, which was approximately 75% lower than in control samples without 4-PA (Supplemental Fig. 4). M5-2 production increased by nearly 35% in samples supplemented with 4-PA than that in the control samples. These results indicate the possibility of β-oxidation in M1 formation.

Direct incubation of M5-2 in rat liver homogenate showed that a small fraction of M5-2 was converted to M1. In a separate test, the presence of 4-PA in rat liver homogenate incubated with M5-2 exhibited a 54% decrease in the M1 yield (Supplemental Fig. 4). Freshly prepared rat liver homogenate incubated with M5-2 in the presence of a mitochondrial β-oxidation enhancer, L-carnitine, did not increase M1 formation. Possibly the β-oxidation does not occur within the mitochondria.

Discussion

In the present study, the pharmacokinetics, metabolism, and excretion of NBP were investigated in healthy Chinese male volunteers after a single oral administration of 200 mg NBP. NBP was almost completely absorbed; unchanged NBP was not detected in either human urine and feces. Renal excretion was the major route of elimination, with roughly 81.6% of the original dose recovered from urine samples. NBP underwent extensive metabolism in humans after oral administration and generated a total of 23 metabolites in human plasma and urine. Metabolites M2, M3-1, M3-2, and M5-2 constituted the principal circulating metabolites, wherein the AUC0–∞ values were approximately 1.6-, 2.9-, 10.3-, and 4.1-fold higher than that of NBP.

Initial in vitro studies with HLMs suggested that NBP primarily went through hydroxylation on the n-butyl side chain and C-3, resulting in the formation of M3-1, M3-2, and 11-hydroxy-NBP; only a minor amount of M5-2 was produced. However, this scenario was rather different from that in vivo. In humans, M5-2 represented the second largest circulating metabolite in terms of AUC0–∞ values; and M5-2, together with its glucuronide conjugate, was the major elimination pathway. Furthermore, the potential precursor of M5-2, 11-hydroxy-NBP, which appeared as a moderate metabolite in HLMs, was not observed in humans after drug administration, indicative of further metabolism to generate secondary metabolites. To better understand the inconsistency between in vitro and in vivo metabolic profiles, the secondary oxidation rates were compared between M3-2 (forming M2) and 11-hydroxy-NBP. The preliminary kinetic analysis revealed that the formation velocities of M2 in NADPH-supplemented

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**Table 4**

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n.d. Not detected.

a The chromatographic peak area of the metabolites detected in individual recombinant CYP450 isoenzyme was normalized with respect to the nominal specific content of the corresponding CYP in native HLMs. Each CYP450 isoenzyme is expressed as the percentage of the total normalized peak area.
HLMs and NAD-fortified human liver cytosol were 45.0 and 16.2 pmol/min/mg protein and those of M5-2 were 91.7 and 390 pmol/min/mg protein, respectively. These formation velocities were observed when M3-2 and 11-hydroxy-NBP were set at 50 μM. On the basis of these data, the secondary metabolic rate ratio of 11-hydroxy-NBP to M3-2 was roughly 2.0 in HLMs, which surged up to 24.1 in human liver cytosol. Similar formation rate ratios of M5-2 to M2 were also observed in HLMs and human liver cytosol when M3-2 and 11-hydroxy-NBP were set at 5 μM. The significantly faster secondary oxidation rate of 11-hydroxy-NBP delivers plausible explanation for its complete disappearance in humans after drug administration. Thus, although 11-hydroxy-NBP is not detected in human plasma and urine after the oral administration of NBP, there is no reason to believe that the mechanism underlying M5-2 formation in vivo differs from the corresponding mechanism in vitro. It seems highly likely that once 11-hydroxy-NBP is formed, it subsequently undergoes further oxidation to generate M5-2 due to the robust activity of human ADH, ALDH, and CYP450s in the liver. Being different from M3-2 and 11-hydroxy-NBP, M3-1 possessed good metabolic stability in HLMs, which partially contributes to the longer half-time of M3-1 in plasma than those of NBP and other major metabolites.

Several drugs with alkyl side chains, such as CI-976, sameridine, and amidarone, can be metabolized to corresponding carboxylic acids (Sinz et al., 1997; Sohlenius-Sternbeck et al., 2000; Deng et al., 2011). The formation of these metabolites generally involves initial ω-hydroxylation of the alkyl side chain by CYP450s (Chmela et al., 2001; Walsh et al., 2002; Zollinger et al., 2011) and subsequent oxidation of the ω-hydroxylated metabolites to carboxylic acids by cytosolic ADH and ALDH (Mori et al., 1989; Aasmoe et al., 1998; Walsh et al., 2002; Miura and Ohkubo, 2007; Dalvie et al., 2008). Microsomal CYP450s also were occasionally reported to catalyze this metabolic pathway (Mori et al., 1989; Ling et al., 1995; Martin et al., 2005; Dalvie et al., 2008). In the present study, initial ω-hydroxylation was mediated mainly by CYP1A2, 2B6, and 2E1. In NAD-supplemented human liver cytosol, ω-hydroxy-NBP (11-hydroxy-NBP) was oxidized to 11-aldehyde-NBP by ADH, which underwent sequential catabolism to M5-2 in HLMs. Trapping tests with methoxylamine proved the presence of the 11-aldehyde-NBP intermediate in the incubation mixture of methoxylamine in human liver cytosol. Similar formation rate ratios of M5-2 to M2 were also observed in NADPH-supplemented HLMs displayed approximately 30% of transformation to M5-2. The addition of ABT in HLMs significantly decreased M5-2 formation, pointing to the contribution of P450 to the conversion besides ADH and ALDH. Sequential incubations of 11-hydroxy-NBP in a panel of commercially available human recombinant P450 isoforms only yielded trace amounts of M5-2 and the presence of 17-ODYA suppressed M5-2 formation by 59%, illustrating that the metabolic pathway of 11-hydroxy-NBP in a panel of commercially available human recombinant P450 isoforms contributes to the longer half-time of M3-1 in plasma than those of NBP and other major metabolites.

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Authorship Contributions

Participated in research design: Diao, Chen, Xie, Deng, Zhang, Zhong, Li.
Conducted experiments: Diao, Deng, Li.
Contributed new reagents or analytic tools: Diao, Li, Chen.
Performed data analysis: Diao, Chen, Deng, Xie.
Contributed to the writing of the manuscript: Diao, Chen, Deng, Xie, Zhong.

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Drug metabolism and disposition

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Metabolism and Pharmacokinetics of 3-n-Butylphthalide (NBP) in Humans: The Role of Cytochrome P450s and Alcohol Dehydrogenase in Biotransformation

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Figure Legends

**Fig. S1.** Extracted ion chromatograms of m/z 229.083 (sodium adducted ion of hydroxylated NBP) from the incubation of NBP in NADPH-supplemented HLMs (A) and in the mixed solution of M3-2 and 11-hydroxy-NBP (B).

**Fig. S2.** Extracted ion chromatograms of m/z 221.093 (M5-2) and of m/z 234.112 (protonated ion of the potential oxime derivative) from the incubation of
11-hydroxy-NBP in human liver cytosol (A) and HLMs (B), respectively, in the presence of methoxylamine. Mass spectrum (C) and the proposed fragmentation pattern (D) of the oxime derivative.

**Fig. S3.** Effect of 4-methylpyrazole (4-MP; 5 mM, 50 mM and 250 mM) on M2 formation from the incubation of M3-2 in NAD-fortified human liver cytosol (A); and the effect of 1-aminobenzotriazole (ABT, 1 mM) on M2 production from the incubation of M3-2 in HLMs. Data are reported as the mean of two separate determinations.

**Fig. S4.** Effect of 4-pentenoic acid (4-PA, 1 mM) on the formation of M5-2 and M1 from the incubation of NBP in freshly prepared rat liver homogenate (A); and the effect of 4-PA (1 mM) and L-carnitine (1 mM) on M1 production from the incubation of M5-2 in freshly prepared rat liver homogenate (B). Data are reported as the mean of two separate determinations.
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