Short Communication

Bedaquiline Metabolism: Enzymes and Novel Metabolites

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ABSTRACT

Bedaquiline is a recently approved drug for the treatment of multidrug-resistant tuberculosis. Adverse cardiac and hepatic drug reactions to bedaquiline have been noted in clinical practice. The current study investigated bedaquiline metabolism in human hepatocytes using a metabolomic approach. Bedaquiline N-demethylation via CYP3A4 was confirmed as the major pathway in bedaquiline metabolism. In addition to CYP3A4, we found that both CYP2C8 and CYP2C19 contributed to bedaquiline N-demethylation. The $K_m$ values of CYP2C8, CYP2C19, and CYP3A4 in bedaquiline N-demethylation were 13.1, 21.3, and 8.5 μM, respectively. We also identified a novel metabolic pathway of bedaquiline that produced an aldehyde intermediate. In summary, this study extended our knowledge of bedaquiline metabolism, which can be applied to predict and prevent drug-drug interactions and adverse drug reactions associated with bedaquiline.

Illustration of BDQ metabolism will provide valuable information to predict and prevent drug-drug interactions and adverse drug reactions associated with BDQ. CYP3A4 is involved in BDQ metabolism, leading to the formation of a dominant but less active N-desmethyl metabolite (Janssen Pharmaceutical Companies, 2012). BDQ and its metabolites, including N-desmethyl BDQ, N-didemethyl BDQ, and two hydroxyl metabolites, are mainly excreted via feces (Cuyckens et al., 2008; Meermann et al., 2012). However, limited information is available for bioactivation pathways of BDQ that may be related to BDQ toxicity. In addition, it is unknown whether CYP3A4 is the only cytochrome P450 (P450) that contributes to BDQ metabolism. The current study was designed to explore novel metabolic pathways of BDQ metabolism using a metabolomic approach. The involvement of P450s in BDQ N-demethylation, the dominant pathway in BDQ metabolism, was also investigated using recombinant P450s. We identified a novel pathway in BDQ metabolism that produces an aldehyde intermediate. We also found that CYP2C8 and CYP2C19, together with CYP3A4, are involved in BDQ N-demethylation.

Materials and Methods

Chemicals. BDQ was purchased from Adooq Bioscience (Irvine, CA). Hepatocyte maintenance medium, dexamethasone, and insulin were obtained from Lonza (Walkersville, MD). Penicillin G/streptomycin and amphotericin B were obtained from Gibco Laboratories (Grand Island, NY). Type I (rat-tail) collagen was purchased from BD Biosciences (Bedford, MA). The recombinant human P450s and human liver microsomes were purchased from Xenotech, LLC (Lenexa, KS). Formic acid, β-nicotinamide-adenine dinucleotide 2'-phosphate reduced tetrasodium salt hydrate, dimethylsulfoxide, ethyl acetate, and methoxylamine (MeONH$_2$) were obtained from Sigma-Aldrich (St. Louis, MO).

BDQ Metabolism in Human Hepatocytes. Fresh isolated human hepatocytes were plated at a cell density of 0.5 × 10$^5$ cells/well in 12-well plates previously coated with 0.2 mg/ml type I collagen. The isolated hepatocytes (>80% viability) were maintained in human maintenance medium supplemented with 100 nM dexamethasone, 100 nM insulin, 100 U/ml...
penicillin G, 100 μg/ml streptomycin, and 10% bovine calf serum and kept at 37°C in a humidified incubator with 95% air/5% CO₂. The hepatocytes were allowed to attach to the plate for 4 hours and the medium was then replaced with serum-free human maintenance medium. For the metabolism study, human hepatocytes were incubated with 30 μM BDQ for 18 hours. The medium was collected and hepatocytes were lysed by adding 200 μl acetonitrile/H₂O (1:1, v/v). Both medium and hepatocyte lysates were extracted by adding a 4-fold volume of ethyl acetate. The mixture was then vortexed for 1 minute and centrifuged at 15,000 g for 10 minutes. The organic phase was transferred to a glass tube and dried under a gentle stream of nitrogen. The residue was reconstituted by 100 μl acetonitrile/H₂O (1:1, v/v). Five microliters of the solution was injected onto a system combining ultra-performance liquid chromatography coupled to time-of-flight mass spectrometry (UPLC-QTOFMS) for metabolite analysis.

**BDQ Metabolism in Recombinant P450s and Human Liver Microsomes.** Incubations were carried out in 1 x phosphate-buffered saline (pH 7.4), containing cDNA-expressed P450 isoforms and 30 μM BDQ with or without 5 mM of the aldehyde trapping reagent MeONH₂ in a final volume of 190 μl. The reactions were initiated by adding 10 μl of 20 mM β-nicotinamide-adenine dinucleotide 2⁻-phosphate reduced tetrasodium salt hydrate and continued for 20 minutes with gentle shaking. The kinetics of N-desmethyl BDQ formation by cDNA-expressed P450s were determined by incubating BDQ at different concentrations up to 100 μM. Incubations were also carried out in human liver microsomes and in the presence of MeONH₂ (5 mM) to trap aldehyde metabolites of BDQ.

**UPLC-QTOFMS Analysis.** Chromatographic separation of BDQ metabolites was performed on an Acquity UPLC BEH C18 column (2.1 × 100 mm, 1.7 μm; Waters, Milford, MA). The flow rate of the mobile phase was 0.40 ml/min and the column temperature was maintained at 50°C. QTOFMS was operated in positive mode with electrospray ionization. The source and desolvation temperatures were set at 120°C and 350°C, respectively. Nitrogen was applied as the cone gas (10 l/h) and desolvation gas (700 l/h). Argon was applied as the collision gas. The capillary and cone voltages were set at 3.5 kV and 35 V. QTOFMS was calibrated with sodium formate and monitored by the intermittent injection of lock mass leucine enkephalin in real time. Screening and identification of BDQ metabolites were performed by using MarkerLynx software (Waters) based on accurate mass measurement (mass errors less than 10 ppm). Product ion scans with collision energy ramping from 15 to 45 V were used for structural elucidations of BDQ and its metabolites.

**Data Analysis.** Mass spectra were acquired by MassLynx 4.1 (Waters) in centroid format from m/z 50 to 1000. Centroid and integrated mass chromatographic data were processed by MarkerLynx software to generate a multivariate data matrix. These data were imported to EZinfo software (Umetrics, San Jose, CA) for orthogonal partial least-squares discriminant analysis on Pareto-scaled data. The corresponding data matrices were then exported into SIMCA-P+ (version 13; Umetrics) for multivariate data analysis.

![Fig. 1. BDQ N-dealkylation and formation of an aldehyde and a carboxylic acid metabolite.](image-url)

(A–C) Identification of a carboxylic acid metabolite of BDQ (M6) in human hepatocytes. (A) Extracted ion chromatograph of M6. (B and C) MS/MS spectrum of M6 at m/z 542 and 544. (D–F) Trapping of the aldehyde (M5) intermediate in BDQ metabolism in human liver microsomes. MeONH₂ was used as a trapping agent. (D) Extracted ion chromatograph of M5-oxime. (E) and (F) MS/MS spectrum of M5-oxime at m/z 555 and 557. (G) Proposed mechanism for the formation of aldehyde (M5) and carboxylic metabolite (M6) in BDQ metabolism.
Results and Discussion

Profiling of BDQ Metabolites in Human Hepatocytes. Metabolomics has proved to be a powerful tool for profiling drug metabolism and bioactivation pathways (Ma et al., 2008; Li et al., 2011). In the current study, an UPLC-QTOFMS–based metabolomic approach was used to profile BDQ metabolism. The results of chemometric analysis on the ions produced by the UPLC-QTOFMS assay of control and BDQ-treated human hepatocytes are shown in Supplemental Fig. 1. The orthogonal partial least-squares discriminant analysis revealed two clearly separated clusters corresponding to the control and BDQ-treated groups (Supplemental Fig. 1A). The corresponding S-plot displays ions contributing to the group separation (Supplemental Fig. 1B). The top-ranking ions were identified as BDQ metabolites (Fig. 1 and Supplemental Figs. 3 and 4) based on mass defect shifts and bromide isotopic patterns. Overall, eight metabolites were identified in human hepatocytes, including six previously reported metabolites (M1, M2, M3, M4, M7 and M8) and two novel metabolites (M5 and M6). All BDQ metabolites identified in human hepatocytes were also found in the feces of mice treated with BDQ (data not shown). The BDQ metabolites are summarized in Supplemental Table 1.

Identification of Novel BDQ Metabolites. M6 was found as a novel BDQ metabolite during metabolomic analysis (Supplemental Fig. 1). The retention time of M6 was 8.90 minutes with protonated ions [M + H]+ at a mass-to-charge ratio (m/z) of 542 and 544 in a nearly 1:1 ratio because of the 79Br/81Br isotopic pattern (Fig. 1). The MS/MS spectrum of M6 showed major fragment ions at m/z 327/329, 310/312, 236/238, and 91 (Fig. 1, B and C). Compared with the MS/MS spectrum of BDQ (Supplemental Fig. 2), the absence of ions at m/z 58, 229 suggest that the dimethylamino moiety has been removed. M6 was proposed as a carboxylic acid metabolite (Fig. 1A). In theory, M6 is an oxidized product of an aldehyde, which can be generated in N-dealkylation of BDQ. The aldehyde intermediate M5 was confirmed in the incubations with human liver microsomes. MeONH2 was used as a trapping agent that produced M5-oxime as a stable adduct (Fig. 1D). M5-oxime was eluted at 9.52 minutes with protonated ions [M + H]+ at m/z 555 and 557. Compared with fragment ions of M6 (Fig. 1, B and C), these same ions were observed in MS/MS analysis of M5-oxime, including m/z 327/329, 310/312, 236/238, and 91 (Fig. 1, E and F). These results suggest that BDQ N-dealkylation occurred and produced an aldehyde (M5) (Fig. 1G). Further studies demonstrated that M5 formation is primarily mediated by CYP3A4 (Supplemental Fig. 5). In general, production of an aldehyde is considered as an unwanted pathway in drug metabolism because aldehydes are more reactive and they may lead to toxicity (Uchida, 2000; O’Brien et al., 2005). Thus, this study provides a clue to investigate adverse drug reactions associated with BDQ in relation to BDQ N-dealkylation.

Role of P450s in BDQ N-Demethylation. When BDQ is metabolized, N-demethylation is the major metabolic pathway and N-desmethyl BDQ (M1) is the main circulating metabolite (FDA, 2012a). Compared with BDQ, M1 has a 3- to 6-fold lower antimycobacterial activity. However, M1 is more cytotoxic and is a stronger inducer of phospholipidosis than BDQ (Mesens et al., 2007). The formation of M1 is mediated primarily by CYP3A4 (Janssen Pharmaceutical Companies, 2012). We found that CYP2C8 and CYP2C19 are also involved in BDQ N-demethylation (Fig. 2A). The Km values of CYP2C8, CYP2C19, and CYP3A4 in M1 formation were 13.1, 21.3, and 8.5 μM, respectively (Fig. 2B). These results indicate that CYP3A4 is not the only enzyme in BDQ N-demethylation. Thus, when patients receive BDQ together with drugs that are CYP3A4 inhibitors, BDQ N-demethylation may not be completely blocked, because CYP2C8 and CYP2C19 also contribute to BDQ N-demethylation. However, when patients receive BDQ together with drugs that are CYP3A4 inducers, such as ligands of the pregnane X receptor, BDQ N-demethylation may be extremely accelerated because activation of the pregnane X receptor induces the expression of CYP2C8, CYP2C19, and CYP3A4 (Gerbal-Chaloin et al., 2001; Luo et al., 2002).

In summary, BDQ metabolism was investigated in human hepatocytes by using a metabolomics approach. BDQ N-dealkylation was identified as a novel metabolic pathway of BDQ that produces an aldehyde intermediate. CYP2C8 and CYP2C19, together with CYP3A4, were involved in BDQ N-demethylation. These results can be applied to predict and prevent drug–drug interactions and adverse drug reactions associated with BDQ.

Authorship Contributions

Participated in research design: K. Liu, Li, Ma.
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References


FDA (2012a) Briefing Package: NDA 204-384: Sirturo, Division of Anti-Infective Products, Office of Antimicrobial Products, US Food and Drug Administration Center for Drug Evaluation, Silver Spring, MD.

FDA (Press release, December 31, 2012b) FDA Approves First Drug to Treat Multidrug-Resistant Tuberculosis. US Food and Drug Administration Center for Drug Evaluation, Silver Spring, MD.

FDA (2012b) Briefing Package: NDA 204-384: Sirturo, Division of Anti-Infective Products, Office of Antimicrobial Products, US Food and Drug Administration Center for Drug Evaluation, Silver Spring, MD.

FDA (Press release, December 31, 2012b) FDA Approves First Drug to Treat Multidrug-Resistant Tuberculosis. US Food and Drug Administration Center for Drug Evaluation, Silver Spring, MD.


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