Cannabinoid Metabolites as Inhibitors of Major Hepatic CYP450 Enzymes, with Implications for Cannabis-Drug Interactions

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ABSTRACT

The legalization of cannabis in many parts of the United States and other countries has led to a need for a more comprehensive understanding of cannabis constituents and their potential for drug-drug interactions. Although (-)-trans-Δ9-tetrahydrocannabinol (THC), cannabidiol (CBD), and cannabinol (CBN) are the most abundant cannabinoids present in cannabis, THC metabolites are found in plasma at higher concentrations and for a longer duration than that of the parent cannabinoids. To understand the potential for drug-drug interactions, the inhibition potential of major cannabinoids and their metabolites on major hepatic cytochrome P450 (P450) enzymes was examined. In vitro assays with P450-overexpressing cell microsomes demonstrated that the major THC metabolites 11-hydroxy-Δ9-tetrahydrocannabinol and 11-nor-9-carboxy-Δ9-THC-glucuronide competitively inhibited several major P450 enzymes, including CYP2B6, CYP2C9, and CYP2D6 (apparent \( K_{i} \) values = 0.086 ± 0.066 μM and 0.90 ± 0.54 μM, 0.057 ± 0.044 μM and 2.1 ± 0.81 μM, 0.15 ± 0.067 μM and 2.3 ± 0.54 μM, respectively). 11-Nor-9-carboxy-Δ9-tetrahydrocannabinol exhibited no inhibitory activity against any CYP450 tested. THC competitively inhibited CYP1A2, CYP2B6, CYP2C9, and CYP2D6; CBD competitively inhibited CYP3A4, CYP2B6, CYP2C9, CYP2D6, and CYP2E1; and CBN competitively inhibited CYP2B6, CYP2C9, and CYP2E1. THC and CBD showed mixed-type inhibition for CYP2C19 and CYP1A2, respectively. These data suggest that cannabinoids and major THC metabolites are able to inhibit the activities of multiple P450 enzymes, and basic static modeling of these data suggest the possibility of pharmacokinetic interactions between these cannabinoids and xenobiotics extensively metabolized by CYP2B6, CYP2C9, and CYP2D6.

SIGNIFICANCE STATEMENT

Major cannabinoids and their metabolites found in the plasma of cannabis users inhibit several P450 enzymes, including CYP2B6, CYP2C9, and CYP2D6. This study is the first to show the inhibition potential of the most abundant plasma cannabinoid metabolite, THC-COO-Gluc, and suggests that circulating metabolites of cannabinoids play an essential role in CYP450 enzyme inhibition as well as drug-drug interactions.

INTRODUCTION

Cannabis and cannabis-derived substances are the most widely consumed psychopharmaceuticals in the world (Atakan, 2012). The legal and ethical implications of their use continue to be the subject of intense global debate because of potential medical applications of cannabis-derived products and the progressive legalization of its use as a recreational drug. Modern clinical applications include treatment of multiple disorders, sleep disorders, psychosis, glaucoma, and Tourette syndrome among others (Solimini et al., 2017). However, concurrent usage of cannabis products (both recreational and medicinal) with conventional medications, nonprescription remedies, and other psychoactive substances can often lead to substance-use disorders (National Institute on Drug Abuse report, July 2020), suggesting that more information is needed to fully understand the effects of cannabis as a psychopharmaceutical (Weinberger et al., 2016).

More than 500 phytochemicals have been detected in commercial strains of the Cannabis sativa plant, with (-)-trans-Δ9-tetrahydrocannabinol (THC), cannabidiol (CBD), and cannabinol (CBN) being the three main active constituents (Aizpurua-Olaizola et al., 2016). THC is the most well described psychoactive constituent and interacts with the cannabinoid receptor type 1 (CB1) receptor and the complex network of neurologic transmitters to induce psychopharmacological effects (Pertwee, 2008). Guidelines from the Food and Drug Administration (FDA) classify any cannabis-derived substance that contains more than 0.3% THC as a schedule I controlled substance, whereas products with less than 0.3% THC are classified as the agricultural product hemp. CBD does not bind to the CB1 receptor and does not produce the same

ABBREVIATIONS: AUC, area under the curve; AUCR\text{rap}, hepatic AUC ratio; AUCR\text{sys}, systemic AUC ratio; CB1, cannabinoid receptor type 1; CBD, cannabidiol; 7-OH-CBD, 7-hydroxy-cannabidiol; CBD-COOH, 7-carboxy-cannabidiol; CBN, cannabinol; FDA, Food and Drug Administration; \( f_{u} \), unbound fraction of cannabinoid in incubations with either HLMs or HEK293 microsomes; HLM, human liver microsome; IS, internal standard; \( K_{i} \), inhibitory constant; LC, liquid chromatography; MS, mass spectrometry; MS/MS, tandem MS; 11-OH-THC, 11-hydroxy-Δ9-tetrahydrocannabinol; P450, cytochrome P450; TDI, time-dependent inhibition; THC, (-)-trans-Δ9-tetrahydrocannabinol; THC-COO-Gluc, 11-nor-9-carboxy-Δ9-tetrahydrocannabinol glucuronide; THC-COOH, 11-nor-9-carboxy-Δ9-tetrahydrocannabinol; UGT, UDP-glucuronosyltransferase; UPLC, ultra-high-performance LC.
psychoactive responses. In fact, when CBD and THC are administered simultaneously, CBD appears to block some of the effects of THC by acting as an antagonist at the cannabinoid receptors (Pertwee, 2008). CBD administered without THC has been shown to reduce subjective anxiety in both animals and humans and is thought to produce a positive effect on conditions such as inflammation, diabetes, cancer, and neurodegenerative diseases (Maroon and Bost, 2018). CBN is only weakly psychoactive and appears to be formed primarily from the degradation of THC within the Cannabis plant itself (Russo and Marcu, 2017).

Upon consumption, the first step of metabolism of THC is hydroxylation mediated by CYP2C9, resulting in the active metabolite 11-hydroxy-\(\Delta^2\)-tetrahydrocannabinol (11-OH-THC; see Fig. 1). Although 11-OH-THC predominates as the first oxidation product, small amounts of 8\(\beta\)-hydroxy-THC (8\(\beta\)-OH-THC) and 8\(\alpha\)-hydroxy-THC (8\(\alpha\)-OH-THC) are also formed (Matsunaga et al., 1995). Much lower plasma 11-OH-THC concentrations (approximately 10% of THC concentrations) are found after cannabis smoking than after oral administration (Wall et al., 1983). Further hydroxylation by CYP2C9 leads to the inactive carboxylic acid derivative 11-nor-9-carboxy-\(\Delta^2\)-tetrahydrocannabinol (THC-COOH), which does not interact with the CB1 receptor. THC-COOH is a substrate for UDP-glucuronosyltransferase (UGT) enzymes that add a glucuronide moiety to form 11-nor-9-carboxy-\(\Delta^2\)-tetrahydrocannabinol-glucuronide (THC-COO-Gluc), the major end product of THC biotransformation in most species, including humans (Huestis, 2007). CBN is the nonenzymatic oxidation byproduct of THC and is most commonly found after prolonged storage, especially at higher temperatures.

CBD follows the same metabolic scheme as THC, with hydroxylation on the homologous 7 carbon via CYP2C19 and CYP3A4 to form 7-hydroxy-CBD (7-OH-CBD) and 7-carboxy-CBD (CBD-COOH), which is followed by glucuronidation to form 7-carboxy-CBD-glucuronide. However, 7-OH-CBD is only a minor biotransformation product in the plasma after cannabis inhalation, with unchanged CBD and, to a lesser extent, glucuronidated CBD as the main excretion products in urine (Harvey and Mechoulam, 1990; Huestis, 2007).

Cannabinoids are highly lipophilic, eventually concentrating in adipose tissue, liver, lung, and spleen, with slow release back into the bloodstream. This leads to varying plasma concentrations of active and inactive metabolites that persist in the bloodstream for a much wider timeframe than that of THC. Plasma concentrations of THC and its active metabolite 11-OH-THC change rapidly over time and vary widely depending on the mode of consumption and expertise of the user (occasional vs. frequent user, depth of inhalation, puff duration, and breath-hold) (Sharma et al., 2012). In contrast, the inactive metabolites THC-COOH and THC-COO-Gluc remain at relatively high levels regardless of the mode of consumption. Inhaled and ingested THC produces the same approximate level of THC-COOH. Once reaching maximal levels at approximately 80 minutes and 2 hours postinhalation, the level of THC-COOH and its glucuronide THC-COO-Gluc remain very stable in the bloodstream over many days, whereas THC is rapidly metabolized and cleared from the circulation (Huestis, 2007; Schwone et al., 2011; Sharma et al., 2012).

Although previous studies have shown that the cannabinoids THC, CBD, and CBN can inhibit several major hepatic P450s (Yamaori et al., 2010, 2011a,b; Jiang et al., 2013; Cox et al., 2019), no studies have focused on the inhibitory potential of the major abundant metabolites of THC. The present study is the first to perform a comprehensive analysis of the inhibition activities of major cannabinoids and THC metabolites against major human hepatic CYP450 enzymes.

Material and Methods

Chemicals and Reagents. The purchase of THC, 11-OH-THC, THC-COOH, THC-COO-Gluc, CBD, and CBN was approved by the Drug Enforcement Agency, and they were obtained from Cayman Chemicals (Ann Arbor, MI) or Sigma-Aldrich (St. Louis, MO). The internal standards (ISs) 7\(\alpha\)-THC and 7\(\beta\)-THC were purchased from Sigma-Aldrich. Pooled human liver microsomes (HLMs; \(n = 50\) subjects, mixed sex) were obtained from Sekisui Xenotech, LLC (Lenexa, Kansas). NADPH-regenerating system (1.3 mM NADP, 3.3 mM glucose 6-phosphate, and 0.4 U/ml glucose 6-phosphate dehydrogenase) was obtained from Corning (Bedford, MA). CYP450 probe substrates (phenacetin,

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**Fig. 1.** Major metabolic pathways and metabolic structures of cannabinoids. (A) Metabolic pathways for THC and CBD. (B) Structure of cannabinoids and major THC metabolites.
bupropion, (S)-bufuralol hydrochloride, amodiaquione, diclofenac, omeprazole, dextromethorphan, chloroxazone, and midazalom) and their corresponding metabolite standards (acetaminophen, hydroxybupropion, hydroxybupropion-D6, 4-hydroxydiclofenac, 4-hydroxydiclofenac-D6, 5-hydroxymepazone, dextrophan, dextrophan-D6, 6-hydroxychloroxazone, and 1-hydroxymidazolam) along with probe inhibitors (furafylline, clopidogrel, montelukast, sufentanyl, tranlycypromine, quinidine, chlomethazone, and ketocazone) were all purchased from Sigma-Aldrich. (–)Warfarin and efavirenz were purchased from Cayman Chemicals (Ann Arbor, MI). LC-MS grade methanol, acetonitrile, and formic acid as well as ultra–low-binding microcentrifuge tubes were obtained from Fisher Scientific (Waltham, MA). All other chemicals and reagents were of analytical grade or the highest grade that was commercially available. Dulbecco’s modified Eagle’s medium, Dulbecco’s phosphate-buffered saline, fetal bovine serum, and gentecin (G418) were purchased from Gibco (Grand Island, NY). Bicinchoninic acid protein assays were purchased from Pierce (Rockford, Illinois).

In Vitro CYP450 Activity Assays and Metabolite Detection. Human embryonic kidney (HEK) 293 cells individually overexpressing V5-tagged P450 isoforms 1A2, 3A4, 2B6, 2C8, 2C9, 2C19, 2D6, or 2E1 were developed and described previously (Peterson et al., 2017b). Microsomal membrane fractions of P450-overexpressing cell lines were prepared by differential centrifugation as previously described, with protein concentrations estimated using the bicinchoninic acid assay as per the manufacturer’s recommendations (Dellinger et al., 2006; Peterson et al., 2017a,b). An initial screen of the inhibition potential of individual cannabinoids and their metabolites against major P450s (1A2, 2B6, 2C8, 2C9, 2C19, 2D6, 2E1, and 3A4) were determined using microsomes and recombinant P450 enzymes and incubation conditions were optimized according to the following criteria: 1) metabolite formation was detected by LC-MS/MS methods. Determination of IC50 and Ki Values. For those cannabinoids/THC metabolites that exhibited a >50% decrease in relative P450 activity for any given probe substrate at ≤10 μM, IC50 determinations were performed in both microsomes from HEK293 CYP450-overexpressing cell lines (described above) and in HLMs using multiple concentrations (ranging between 0.5 and 100 μM) of cannabinoid/metabolite in incubations as described above, with all determinations performed for three independent experiments with three replicates per experiment.

To identify possible metabolism-dependent inhibition of the potential enzymes, IC50 shift studies (Parkinson et al., 2011) were performed using HEK-overexpressing cell lines. Reactions containing the test cannabinoid or THC metabolite (inhibitor) but no probe substrate were incubated with or without NADPH at 37°C for 30 minutes. After this 30-minute preincubation, probe substrate was added to the incubation mixture and incubated at 37°C for up to 30 minutes (Supplemental Table 1). Peak areas corresponding to the probe metabolite were determined, and the percentage of relative activity was calculated by comparing the peak area in incubations containing the inhibitors to incubations containing only the vehicle control, as described below. The differences between the IC50 values obtained with or without the NADPH preincubation period were compared, and the fold-IC50 shift was determined. The cannabinoid/THC metabolite with a fold-IC50 shift of ≥1.5 was considered a time-dependent inhibitor as recommended by the FDA guidelines.

IC50 data were used as a guide to generate appropriate probe substrate and test inhibitor concentrations for the determination of the Ki values for each isoform. The P450 enzyme-specific probe substrate concentrations used were 1–25 μM phencetin for CYP1A2, 12.5–100 μM bupropion for CYP2B6, 2.5–30 μM diclofenac for CYP2C9, 0.5–5 μM omeprazole for CYP2C19, 1–10 μM dextromethorphan for CYP2D6, 12.5–100 μM chloroxazone for CYP2E1, and 1–25 μM midazolam for CYP3A4A.

Data were exported and analyzed using an Excel spreadsheet (Microsoft®). The amount of metabolite formed at each concentration relative to the control (percent relative activity) of specific enzyme in the presence and absence of probe inhibitor or test compound was calculated as:

\[
\% \text{ Relative activity} = \left( \frac{\text{Peak area with inhibitor/Peak area without inhibitor}}{1} \right) \times 100
\]

Percent Inhibition = [(Peak area without inhibitor – peak area with inhibitor)/peak area without inhibitor] × 100

The IC50 values were calculated by plotting the percent inhibition of P450 enzyme activities versus the log concentration of the test inhibitors using GraphPad Prism 7.04 software (GraphPad Software Inc., San Diego, CA).

To calculate Ki values, inhibition data were fit to different models of enzyme inhibition (competitive, uncompetitive, or noncompetitive) by nonlinear least-squares regression analysis using the GraphPad Prism 7.04 software. Ki values were calculated with the use of nonlinear regression according to the equations:

\[
v = \left( \frac{V_{\text{max}} S}{K_{\text{m}} + S} \right) \left( 1 + \frac{1}{K_{I}} \right) + S
\]

where I is compound concentration, Ki is the inhibition constant, S is the substrate concentration, and Km is the substrate concentration at half of the Vmax of the reaction (Cornish-Bowden, 1974).

Bound versus Unbound Cannabinoid Determinations. Cannabinoid binding to proteins and tube walls in the incubation mixture (τmixture) was measured using the tube adsorption method as described previously (Ishihara et al., 2004; Patilca-Virana et al., 2019). Briefly, in separate incubations, 50 μl of 30 μM THC, 11-OH-THC, THC-COO-Glu-Glu, CBD, or CB1 was added to each of two 0.6-mL low-binding centrifuge tubes containing buffer without protein, two 0.6-mL low-binding centrifuge tubes containing buffer with HLMs (25 μg), or two 0.6-mL low-binding centrifuge tubes containing buffer with HEK293 microsomal protein (30 μg). This was performed for each cannabinoid separately. Mixtures were incubated for 30 minutes at 37°C with occasional shaking. For one tube of the three incubations (buffer alone, buffer + HLMs, and buffer + HEK293 microsomes), ice-cold acetonitrile (100 μl) containing D3-labeled cannabinoid IS was added (subgroup A). For the other tube of each condition, the entire 50-μl mixture was removed and added to a fresh tube that contained 100 μl ice-cold acetonitrile with D3-labeled cannabinoid IS (subgroup B). Samples were processed for UPLC-

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MS/MS as described above for the in vitro assay experiments. All analyses were performed in three independent experiments with four replicates per experiment. The separation and detection of individual cannabinoid was achieved using the same ACQUITY XEVO TQD (Waters Corporation, Milford, MA) chromatographic system described above using a Waters BEH C18 column 1.7 mm, 2.1 × 50 mm, at 40 °C. UPLC-MS/MS was performed with a gradient elution using mobile phase A (0.1% formic acid in water) and mobile phase B (0.1% formic acid in acetonitrile) at a flow rate of 0.4 mL/min under the following conditions: 5% B for 1.0 minute, increasing to 95% B from 1.0 to 4.0 minutes, 95% B held for 2 minutes, which was followed by a return to initial conditions for 1.5 minutes for a total time of 7.5 minutes. Detection of cannabinoids was performed in multiple reaction monitoring (ES) mode using the following mass transitions: m/z 315.1 → 193.2 for THC, m/z 331.3 → 313.1 for 11-OH-THC, m/z 315.2 → 181.1 for CBD, m/z 311.2 → 223.0 for CBG, and m/z 521.2 → 345.0 for THC-COO-Gluc. Cone voltages (V) of 40, 40, 50, and 30, respectively, and collision energies of 25, 18, 20, and 27, respectively, were used for THC, 11-OH-THC, CBD, CBG, and THC-COO-Gluc. Because of the nonavailability of deuterated CBD or CBG at the time of this study and because of the similar molecular weights and UPLC retention times between these cannabinoids, THC-D3 was used as the IS for the quantification of THC, CBD, and CBG; 11-OH-THC-D3 was used to quantify 11-OH-THC; and THC-COO-Gluc-D3 was used to quantify THC-COO-Gluc. The internal standards were detected using the same cone voltages and collision energies as their respective standards, with the following mass transitions: m/z 318.1 → 196.2 for THC-D3, m/z 334.3 → 316.1 for 11-OH-THC-D3, and m/z 523.2 → 348.0 for THC-COO-Gluc-D3.

The unbound fraction of cannabinoid in incubations with either HLMs or HEK293 microsomes (fu, inc) was calculated using the following equation:

$$ f_{u, \text{inc}} = \frac{C_B}{C_B - C_{BA}} \left( \frac{C_P - C_{PB}}{C_P} \right) $$

where CBA is the total (adsorbed and unadsorbed) test compound in buffer only, and CB is unadsorbed test compound in buffer. So, CBA - CB is the test compound adsorbed to the tube wall, and CB/CA = CB - CB is the ratio of unbound test compound relative to the test compound adsorbed to the wall. CA is the total (adsorbed and unadsorbed) test compound in the incubation mixture, and Cφ is unbound test compound in presence of protein substrate (incubation mixture). CPφ = CP is the test compound adsorbed to the tube wall when mixed with microsomes. Calculations of f_{u,\text{inc}} were performed in three independent experiments with four replicates per group. IC_{50,u} and K_{u} values were calculated using the following equations:

$$ IC_{50,u} = f_{u,\text{inc}} \times IC_{50} $$

$$ K_u = f_{u,\text{inc}} \times K_i $$

**Prediction of Potential In Vivo Drug-Drug Interactions by Static Modeling.** To predict the risk of a clinical drug-drug interaction, basic static models of reversible inhibition were used following FDA recommended guidelines. The predicted hepatic and systemic area under the curve ratios (AUCR_{hep} and AUCR_{sys}, respectively) were calculated to determine the overall effect of cannabinoids and their metabolites on a given probe substrate. The basic static model is described by the following equations:

$$ AUCR_{hep} = 1 + \frac{I_{hep-u}}{K_u} $$

where $I_{hep-u} = \frac{F_u \times C_{max} + C_{max} + C_P \times Dose}{Q_{hep}/R_B} $ \hspace{1cm} (2)

$$ AUCR_{sys} = 1 + \frac{I_{sys}}{K_u} $$

where $I_{sys} = C_{max} \times $ \hspace{1cm} (3)

AUCR_{hep} is calculated using eq. 1, in which $I_{hep-u}$ is the unbound maximum hepatic inlet concentration, and $K_u$ is calculated for each inhibitor as described above. The $I_{hep-u}$ is calculated using eq. 2, in which $F_u$ is the unbound concentration of drug in plasma and was set at 0.03 based on the plasma protein binding of THC (Garrett and Hunt, 1974), which was suggested to be accurate for 11-OH-THC, CBD, and CBG as well as THC-COO-Gluc in previous studies (Skopp et al., 2002). C_{max} is the maximum concentration of total drug in plasma (parameters described below), $F_u$ is the fraction of dose absorbed from the gut lumen [set to 1 as recommended by the FDA (Food and Drug Administration, 2020)], $K_b$ is the rate of intestinal absorption time [set to 0.02; (Cox et al., 2019)], $R_b$ is the ratio of drug concentration in blood (C_b) to drug concentration in plasma [set to 0.4 as recommended by Schwilke et al. (2009)], and Q_{hep} is the hepatic blood flow = 1500 mL/min (Food and Drug Administration, 2020). For THC, the C_{max} was set to 65 nM for a 40-mg oral dose of THC and 254 nM for a 54-mg inhaled dose of THC (Schwecke et al., 2011; Cox et al., 2019). For 11-OH-THC, the C_{max} was set to 69.7 nM for a 20-mg oral dose of THC and 50 nM for a 46-mg inhaled dose of THC (Ménétrey et al., 2005; Hunault et al., 2008). For THC-COO-Gluc, the C_{max} was set to 405 nM for an oral dose of 50 mg of THC and to 385 nM for a 54-mg inhaled dose of THC (Spindler et al., 2020). For CBD, the C_{max} was set to 703 nM for an oral dose of 800 mg of CBD and to 103 nM for a 20-mg inhaled dose of CBD (Manini et al., 2015; Cox et al., 2019).

The AUCR_{sys} is calculated using eq. 3, in which $I_{sys}$ is equal to C_{max,u}, which is the maximum concentration of total unbound drug in plasma (C_{max}/K_u).

An AUCR_{sys} ≥ 1.25 or an AUCR_{sys} ≥ 1.02 indicates a strong presystemic hepatic or systemic drug interaction potential.

**Results**

Prescreening of THC, 11-OH-THC, THC-COOH, THC-COO-Gluc, CBD, and CBG as potential CYP450 inhibitors showed that 10 µM THC decreased the relative activity of several P450 isoforms to approximately 50%, including CYP1A2 (35%), CYP2B6 (50%), CYP2C9 (48%), CYP2D6 (48%), and CYP2C19 (51%), as compared with reactions without added cannabinoid (Fig. 2A). Similar levels of inhibition were observed for 11-OH-THC against CYP2B6, CYP2C9, and CYP2D6, with 10 µM 11-OH-THC resulting in relative activity levels between 27% and 48% for the three enzymes (Fig. 2B). Although no significant inhibition was observed using up to 10 µM THC-COOH against any of the P450 enzymes tested (Fig. 2C), 10 µM THC-COO-Gluc resulted in 25%–49% relative activity for CYP2B6, CYP2C9, and CYP2D6 (Fig. 2D). In addition, decreases in the relative activity to less than 50% was observed for 10 µM CBD against several P450 enzymes (CYP1A2, CYP2B6, CYP2C9, CYP2C19, CYP2D6, CYP2E1, and CYP3A4) and for 1 µM CBD against CYP1A2 (45%), CYP2B6 (50%), CYP2E1 (49%), and CYP3A4 (47%; Fig. 2E). Similar decreases in relative activity were observed for CBN against CYP2B6, CYP2C9, and CYP2E1, with 75%, 55%, and 80% decreases in activity observed for 10 µM CBN against all three enzymes and a 77% decrease observed for 1 µM CBN against CYP2E1 (Fig. 2F). Initial screening results were validated in assays using commercially prepared pooled HLMs (unpublished data).

Using microsomes from both specific recombinant CYP450 (cCYP)-overexpressing HEK-293 cell lines and HLMs, the inhibitory effects of THC, 11-OH-THC, THC-COOH, THC-COO-Gluc, CBD, and CBG were extended to establish IC_{50} values for each cannabinoid against the P450 enzymes shown to be inhibited in the cCYP screening assays (described above). The unbound fraction (f_{u,inc}) of THC, 11-OH-THC, THC-COO-Gluc, CBD, and CBG in incubation mixtures (f_{inc}) was calculated as 0.051 ± 0.033 and 0.043 ± 0.012, 0.094 ± 0.014 and 0.078 ± 0.042, 0.43 ± 0.071 and 0.45 ± 0.061, 0.098 ± 0.023 and 0.062 ± 0.011, and 0.052 ± 0.081 and 0.030 ± 0.052 in mixtures containing HLMs or microsomes from HEK293 cells, respectively. The range in f_{u,inc} was from 0.030 (CBN) to 0.45 (THC-COO-Gluc) for HEK293 microsomes and 0.051 (THC) to 0.43 (THC-COO-Gluc) for HLMs. The values for HLMs were similar to those obtained for HEK293 microsomes for all cannabinoids tested. Interestingly, THC-COO-Gluc exhibited a f_{inc} that was approximately 10-fold higher than the other cannabinoids, indicating less adsorption to the components of the incubation mixture.

CBD exhibited strong inhibition against every CYP450 tested, with a range in IC_{50,u} values of 0.037–0.22 µM, with the strongest inhibition...
exhibited slightly stronger inhibition against rCYP2D6 (IC50,u values of
\(0.35 \pm 0.054\) M and 3.5 ± 2.0 \(\mu\)M, respectively). CBN exhibited strong inhibition against rCYP2B6 (IC50,u values of 0.63 ± 0.26 \(\mu\)M), rCYP2C9 (IC50,u = 0.42 ± 0.13 \(\mu\)M), and rCYP2E1 (IC50,u = 0.28 ± 0.030 \(\mu\)M) microsomes. Similar IC50 values were obtained for HLMs using specific probe substrates for all cannabinoids tested in rCYP2E1 microsomes (IC50,u = 0.037 ± 0.0081 \(\mu\)M; Table 1). Additionally, THC exhibited strong inhibition against rCYP1A2, rCYP2B6, rCYP2C9, and rCYP2D6 microsomes (IC50,u values of 0.12 \(\mu\)M ± 0.052 \(\mu\)M, 0.43 ± 0.28 \(\mu\)M, 0.19 \(\mu\)M ± 0.13 \(\mu\)M, 0.15 ± 0.030 \(\mu\)M, and 0.47 \(\mu\)M ± 0.077 \(\mu\)M, respectively). The THC metabolites 11-OH-THC and THC-COO-Gluc both exhibited slightly stronger inhibition against rCYP2D6 (IC50,u values of 0.34 ± 0.12 \(\mu\)M and 3.5 ± 0.72 \(\mu\)M, respectively) and rCYP2B6 (IC50,u values of 0.55 ± 0.26 \(\mu\)M and 2.5 ± 0.72 \(\mu\)M, respectively) than THC, while exhibiting similar or less effective inhibition against rCYP2C9 microsomes (IC50,u values of 0.30 ± 0.086 \(\mu\)M and 6.8 ± 2.0 \(\mu\)M, respectively). CBN exhibited strong inhibition against rCYP2B6 (IC50,u = 0.63 ± 0.26 \(\mu\)M), rCYP2C9 (IC50,u = 0.42 ± 0.13 \(\mu\)M), and rCYP2E1 (IC50,u = 0.28 ± 0.030 \(\mu\)M) microsomes. Similar IC50 values were obtained for HLMs using specific probe substrates for all cannabinoids tested (Table 1).

To confirm the high level of inhibitory activity observed with cannabinoids against CYP2B6, CYP2C9, and CYP2D6, IC50 determinations were also performed for three additional probe substrates. Strong inhibition of activity against efavirenz, bufuralol, and S-warfarin in microsomes from rCYP2B6, rCYP2D6, and rCYP2C9 cell lines, respectively, was observed with THC, 11-OH-THC, THC-COO-Gluc, CBD, and CBN (Supplemental Table 2). Consistent with that observed for CBN with dextromethorphan as a probe substrate for CYP2D6, no inhibition was observed with this cannabinoid for bufuralol. These data suggest that the inhibition observed with these cannabinoids against these three enzymes is seen across multiple substrates.

IC50-shift assays were performed for microsomes from each CYP450-overexpressing cell line with the goal of evaluating the time-dependent inhibition (TDI) potencies of cannabinoid metabolites (Table 2). Using a value of 1.5 as the cutoff, none of the cannabinoids tested demonstrated TDI, with the possible exception of CBD for CYP2D6 with an exhibited shift of 1.5.

Additional experiments to determine \(K_{inhibitor}\) values were performed to further understand the strength and type of inhibition interactions occurring between the cannabinoids and the P450 enzymes. As shown in Lineweaver-Burk plots, the CYP2B6-catalyzed 4-hydroxylation of bupropion in microsomes from the rCYP2B6-overexpressing cell line was shown to be inhibited in a competitive manner by the THC metabolites 11-OH-THC and THC-COO-Gluc (Fig. 3) and the cannabinoids THC, CBD, and CBN (Supplemental Fig. 2), with \(K_{inhibitor}\) values similar for all inhibitors ranging from 0.068 ± 0.015 \(\mu\)M for CBD to 0.90 ± 0.054 \(\mu\)M for THC-COO-Gluc (Table 3). Slightly higher \(K_{inhibitor}\) values were observed for inhibition in HLMs, ranging from 0.22 ± 0.052 \(\mu\)M for CBD to 1.1 ± 0.47 \(\mu\)M for THC-COO-Gluc (Table 3).

\(K_{inhibitor}\) values for the inhibition of rCYP2C9 were determined by monitoring the hydroxylation of the CYP2C9 probe substrate dextromethorphan. Lineweaver-Burk plots for the inhibition of rCYP2C9 (Fig. 3; Supplemental Fig. 2) indicated a competitive type of inhibition for all cannabinoids tested in rCYP2C9-overexpressing cell microsomes, with \(K_{inhibitor}\) values ranging from 0.057 ± 0.044 \(\mu\)M for 11-OH-THC to 2.1 ± 0.081 \(\mu\)M for THC-COO-Gluc (Table 3). The inhibition of dextrophen hydroxylation in HLMs was similar, ranging from 0.17 ± 0.046 \(\mu\)M for THC to 3.4 ± 0.28 \(\mu\)M for THC-COO-Gluc. Slightly higher \(K_{inhibitor}\) values were observed for inhibition in HLMs, with THC and THC-COO-Gluc exhibiting mixed-type inhibition, whereas 11-OH-THC, CBD, and CBN exhibited competitive inhibition (Table 3).

For CYP2D6, \(K_{inhibitor}\) values were determined by examining the \(O\)-demethylation of dextromethorphan to dextrophan. Lineweaver-Burk plots for the inhibition of CYP2D6 (Fig. 3; Supplemental Fig. 2) suggested a competitive type of inhibition for all inhibitors for both rCYP2D6 microsomes and HLMs. The \(K_{inhibitor}\) values for THC, TH
TABLE 1

<table>
<thead>
<tr>
<th>THC</th>
<th>11-OH-THC</th>
<th>THC-COO-Gluc</th>
<th>CBD</th>
<th>CBN</th>
<th>Phenacetin rCYP1A2</th>
<th>Midazolam rCYP3A4</th>
<th>Bupropion rCYP2B6</th>
<th>Omeprazole rCYP2C19</th>
<th>Dextromethorphan rCYP2D6</th>
<th>Chlorzoxazone rCYP2E1</th>
<th>HLM</th>
</tr>
</thead>
<tbody>
<tr>
<td>IC₅₀,u</td>
<td>2.7 ± 1.2</td>
<td>5.2 ± 2.1</td>
<td>10.6 ± 6.4</td>
<td>4.5 ± 3.0</td>
<td>7.2 ± 2.6</td>
<td>4.2 ± 1.4</td>
<td>11.8 ± 5.3</td>
<td>15.3 ± 3.3</td>
<td>-0.21 ± 0.056</td>
<td>0.43 ± 0.31</td>
<td>NA</td>
</tr>
<tr>
<td>IC₅₀,u</td>
<td>0.12 ± 0.022</td>
<td>0.27 ± 0.11</td>
<td>0.43 ± 0.28</td>
<td>0.97 ± 0.12</td>
<td>0.37 ± 0.13</td>
<td>0.45 ± 0.24</td>
<td>0.34 ± 0.12</td>
<td>0.47 ± 0.27</td>
<td>0.34 ± 0.077</td>
<td>0.75 ± 0.34</td>
<td>NA</td>
</tr>
</tbody>
</table>

Values are the mean ± S.D. in nM for four independent experiments with three replicates per group.

Prior to the present analysis, a comprehensive inhibition study of hepatic P450 enzymes by all major THC metabolites (11-OH-THC, THC-COOH, and THC-COO-Gluc) had not been previously

THC-COO-Gluc, and CBD against rCYP2D6 were 0.11 ± 0.015 μM, 0.15 ± 0.067 μM, 2.3 ± 0.54 μM, and 0.074 ± 0.048 μM, respectively; similar Kᵢ,u values were observed for dextromethorphan-O-demethylation activity for the four cannabinoids in HLMs (Table 3).

In addition to CYP2B6, CYP2C9, and CYP2D6, THC also inhibited CYP1A2-catalyzed phenacetin O-deethylation in rCYP1A2 microsomes, with a Kᵢ,u value of 0.090 ± 0.027 μM; a similar level of inhibition (Kᵢ,u = 0.12 ± 0.074 μM) was also observed for CBD. Inhibition by THC was determined to be competitive, whereas inhibition by CBD was mixed (Table 3). Highly similar Kᵢ,u values were observed for the two cannabinoids in HLMs (Table 3).

Among the cannabinoid compounds tested, only CBD inhibited CYP3A4-catalyzed midazolam 1'-hydroxylation. This inhibition was competitive, with Kᵢ,u values of 0.093 ± 0.037 μM and 0.22 ± 0.044 μM in rCYP3A4 microsomes and HLMs, respectively. CYP2C19-catalyzed omeprazole 5'-hydroxylation activity was inhibited by THC with a mixed-type inhibition mechanism for rCYP2C19 microsomes (Kᵢ,u = 0.056 ± 0.018 μM) and HLMs (Kᵢ,u = 0.21 ± 0.082 μM) and by CBD with a competitive mechanism in rCYP2C19 microsomes and a mixed-type in HLMs (Kᵢ,u = 0.050 ± 0.0057 μM and 0.092 ± 0.0062 μM, respectively). CYP2E1-catalyzed chlorzoxazone 6-hydroxylation activity was competitively inhibited by CBD and CBN, with Kᵢ,u values for rCYP2E1 of 0.021 ± 0.0061 μM and 0.063 ± 0.029 μM, respectively; the Kᵢ,u values for the inhibition of chlorzoxazone 6-hydroxylation activity in HLMs were again similar to those observed for rCYP microsomes, with Kᵢ,u values of 0.058 ± 0.023 μM and 0.17 ± 0.047 μM for CBD and CBN, respectively (Table 3).

A basic mechanistic static model populated with Kᵢ,u data from the present study predicts AUCRₘₚ and AUCRₘₚ, with a strong potential for pharmacokinetic interactions between CBD (both oral and inhaled) and CYP1A2, CYP3A4, CYP2B6, CYP2C9, CYP2C19, CYP2D6, and CYP2E1 (Table 4). For oral dosing of THC, the potential for pharmacokinetic interactions was observed for CYP1A2, CYP2C9, CYP2C19, and CYP2D6, whereas for inhaled THC there is a potential for pharmacokinetic interactions with CYP1A2, CYP2B6, CYP2C9, CYP2C19, and CYP2D6. 11-OH-THC showed potential for pharmacokinetic interactions with CYP2B6, CYP2C9, and CYP2D6 for both oral and inhaled dosing of THC.


### TABLE 2

<table>
<thead>
<tr>
<th>Cannabinoid</th>
<th>CYP3A4</th>
<th>CYP2B6</th>
<th>CYP2C9</th>
<th>CYP2C19</th>
<th>CYP2D6</th>
<th>CYP2E1</th>
</tr>
</thead>
<tbody>
<tr>
<td>THC</td>
<td>NA</td>
<td>19 ± 5.1</td>
<td>3.4 ± 2.3</td>
<td>3.2 ± 2.5</td>
<td>13 ± 0.67</td>
<td>NA</td>
</tr>
<tr>
<td>11-OH-THC</td>
<td>1.2 ± 0.31</td>
<td>1.1 ± 0.07</td>
<td>5 ± 1.6</td>
<td>1.2 ± 0.08</td>
<td>1.3 ± 0.13</td>
<td>NA</td>
</tr>
<tr>
<td>THC-COOH</td>
<td>1.1 ± 0.07</td>
<td>1.1 ± 0.07</td>
<td>5 ± 1.6</td>
<td>1.2 ± 0.08</td>
<td>1.3 ± 0.13</td>
<td>NA</td>
</tr>
<tr>
<td>THC-COO-Gluc</td>
<td>1.1 ± 0.07</td>
<td>1.1 ± 0.07</td>
<td>5 ± 1.6</td>
<td>1.2 ± 0.08</td>
<td>1.3 ± 0.13</td>
<td>NA</td>
</tr>
<tr>
<td>CBD</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
</tr>
<tr>
<td>CBN</td>
<td>1.4 ± 0.18</td>
<td>1.4 ± 0.18</td>
<td>1.4 ± 0.18</td>
<td>1.4 ± 0.18</td>
<td>1.4 ± 0.18</td>
<td>NA</td>
</tr>
</tbody>
</table>

a($/C_0$), IC$_{50}$ ± S.D. of three experiments with 30-min preincubation of test cannabinoid with enzyme without NADPH.

bShift ($\Delta$IC$_{50}$) minus NADPH.

cShift ($\Delta$IC$_{50}$) plus NADPH.
cannabis interact, co-users tend to report that cannabis increases the ketamine high and can, in some instances, exacerbate effects like drowsiness and dizziness (Garcia-Romeu et al., 2016).

The CYP2C9 hydroxylation of diclofenac was also strongly inhibited by the cannabinoid metabolites 11-THC-OH and THC-COO-Gluc in a reversible manner, with a competitive type in the rCYP and mixed in HLMs. Previous studies have also found potent inhibition of CYP2C9 by THC, CBD, and 11-OH-THC (Bansal et al., 2020). CYP2C9 is one of the most abundant P450 enzymes in the liver (about 20% of the hepatic total P450 content) (Ghodke-Puranik and Lamba, 2017). It metabolizes several important drugs, including anticancer agents, nonsteroidal anti-inflammatory agents, selective cyclooxygenase-2 inhibitors, antibiotics, antiepileptics, antihypertensives, anticoagulants, and antihyperlipidemics (Ghodke-Puranik and Lamba, 2017). Drug-drug interactions have been shown to arise when a CYP2C9 inhibitor is added to a therapeutic regimen, including low therapeutic index drugs like (S)-warfarin, tolbutamide, or phenytoin. In these cases, patients can risk life-threatening bleeding episodes, hypoglycemia, and neurotoxicity as a result of the diminished CYP2C9 enzyme activity. These in vitro predictions are largely consistent with many clinical CBD- or THC-drug interactions reported to date. In clinical studies, an increased anticoagulant effect of warfarin was previously observed in smokers of cannabis, potentially due to inhibition of CYP2C9-mediated warfarin metabolism by cannabinoids and THC metabolites (Yamreuedwong et al., 2009). In addition, a case report showed that phenytoin caused severe adverse effects when coadministered with cannabis (Jessen, 2004).

THC, 11-OH-THC, THC-COO-Gluc, and CBD also strongly inhibited the dextromethorphan-O-demethylase activity of CYP2D6 in a reversible and competitive manner. Although CYP2D6 comprises a relatively small percentage (2%-6%) of the total CYP450 protein in the liver, it is involved in the metabolism of 25% of the most commonly prescribed drugs (e.g., antidepressants, antipsychotics, opioids, and β blockers) (Shannon, 2007). Although there are no reports on in vivo drug interactions between cannabinoids and CYP2D6 substrates, the results from the present study can potentially explain the in vivo mechanism for increased adverse effects or potency of CYP2D6-metabolized agents. For example, dextromethorphan is a widely used antitusiv agent metabolized by CYP2D6 into an active metabolite, dextrophen. Using dextromethorphan together with cannabis has been shown to increase side effects, such as dizziness, drowsiness, confusion, and difficulty concentrating (Ziaee et al., 2005). In addition, the widely used anticancer drug and CYP2D6 substrate tamoxifen showed decreased tamoxifen metabolism in vivo, and the level of CYP2D6-mediated active metabolite endoxifen decreased in plasma in subjects also taking cannabinoids (Parihar et al., 2020). For CYP1A2 and CYP2C19, a mixed-type inhibition was observed for CBD and THC, respectively, in both rCYPs and HLMs, suggesting that, in contrast to the competitive type inhibition observed for most of the cannabinoid- and THC metabolites analyzed in this study, THC and CBD are not interacting with CYP1A2 and CYP2C19 in a similar fashion. In addition, CYP2C9 and CYP2C19 showed different types of inhibition when analyzing their corresponding rCYP microsomes versus HLMs; with THC, THC-COO-Gluc, and CBD all exhibiting competitive inhibition in the rCYP and mixed inhibition in HLMs, possibly due to a confounding effect of the presence of multiple P450s within HLMs.

Although cannabis can be consumed through oral dosing, smoking cannabis is still the most common way of consumption. These differences become important when analyzing metabolite levels, as the major THC metabolites will differ in plasma concentration based on the route of administration. After smoking a cannabis cigarette containing 10 mg THC, the plasma AUCs of THC, 11-OH-THC, and THC-COO-Gluc are 110 µg·h/l (0.35 µM), 19 µg/l (0.06 µM), and 840 µg/l (1.6 µM), respectively. In contrast, after oral dosing of a consumable containing 10 mg of THC, the AUCs of THC and 11-OH-THC are even higher at 360 µg/l (1.14 µM) and 14,600 µg/l (28 µM), respectively (Nadulski et al., 2005). THC-COO-Gluc levels were 139 µg/l (0.35 M) and 14,600 µg/l (28 M), respectively (Newmeyer et al., 2016). The
## TABLE 3
Summary of $K_i$ values and inhibition type for major cannabinoids and THC metabolites against hepatic CYP450 enzymes

<table>
<thead>
<tr>
<th>Microsomal Protein</th>
<th>THC 11-OH-THC</th>
<th>THC-COO-Gluc</th>
<th>CBD</th>
<th>CBN</th>
</tr>
</thead>
<tbody>
<tr>
<td>rCYP1A2</td>
<td>$2.1 \pm 0.62$</td>
<td>$0.090 \pm 0.027$</td>
<td>$1.7 \pm 1.2$</td>
<td>$0.12 \pm 0.074$</td>
</tr>
<tr>
<td>HLM</td>
<td>$2.0 \pm 1.1$</td>
<td>$0.10 \pm 0.056$</td>
<td>$1.5 \pm 0.59$</td>
<td>$0.093 \pm 0.037$</td>
</tr>
<tr>
<td>rCYP3A4</td>
<td>NA</td>
<td>NA</td>
<td>$2.2 \pm 0.45$</td>
<td>NA</td>
</tr>
<tr>
<td>HLM</td>
<td>$5.7 \pm 1.0$</td>
<td>$0.25 \pm 0.043$</td>
<td>$3.0 \pm 1.2$</td>
<td>$0.40 \pm 0.050$</td>
</tr>
<tr>
<td>rCYP2B6</td>
<td>$7.5 \pm 0.56$</td>
<td>$0.38 \pm 0.029$</td>
<td>$2.6 \pm 1.1$</td>
<td>$0.50 \pm 0.052$</td>
</tr>
<tr>
<td>HLM</td>
<td>$1.7 \pm 0.53$</td>
<td>$0.073 \pm 0.023$</td>
<td>$4.7 \pm 1.8$</td>
<td>$0.80 \pm 0.052$</td>
</tr>
<tr>
<td>rCYP2C9</td>
<td>$3.4 \pm 0.91$</td>
<td>$0.17 \pm 0.046$</td>
<td>$7.8 \pm 0.65$</td>
<td>$0.90 \pm 0.052$</td>
</tr>
<tr>
<td>HLM</td>
<td>$1.3 \pm 0.42$</td>
<td>$0.056 \pm 0.018$</td>
<td>NA</td>
<td>NA</td>
</tr>
<tr>
<td>rCYP2C19</td>
<td>$4.1 \pm 1.6$</td>
<td>$0.21 \pm 0.082$</td>
<td>$0.94 \pm 0.063$</td>
<td>$0.15 \pm 0.064$</td>
</tr>
<tr>
<td>HLM</td>
<td>$2.5 \pm 0.35$</td>
<td>$0.11 \pm 0.015$</td>
<td>$1.4 \pm 1.1$</td>
<td>$0.32 \pm 0.014$</td>
</tr>
<tr>
<td>rCYP2D6</td>
<td>$5.4 \pm 0.58$</td>
<td>$0.28 \pm 0.030$</td>
<td>$3.4 \pm 1.7$</td>
<td>$0.34 \pm 0.098$</td>
</tr>
<tr>
<td>HLM</td>
<td>NA</td>
<td>NA</td>
<td>$0.59 \pm 0.20$</td>
<td>$0.33 \pm 0.091$</td>
</tr>
</tbody>
</table>

Values are expressed as $\mu$M; shown are the mean $\pm$ S.D. for three independent experiments performed for the inhibition of each CYP450 enzyme by each cannabinoid.

T, type of inhibition. C, competitive inhibition; M, mixed inhibition.

The probe substrate used were phenacetin, midazolam, bupropion, diclofenac, omeprazole, dextromethorphan, and chlorzoxazone for CYP1A2, CYP3A4, CYP2B6, CYP2C9, CYP2C19, CYP2D6, and CYP2E1, respectively.

NA, not analyzed.

## TABLE 4
Prediction of P450-mediated clinical drug interaction potential after oral or inhaled dose of THC or CBD

<table>
<thead>
<tr>
<th>Enzyme</th>
<th>THC 11-OH-THC</th>
<th>THC-COO-Gluc</th>
<th>CBD</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Oral AUCR$_{exp}$</td>
<td>AUCR$_{sys}$</td>
<td>Oral AUCR$_{exp}$</td>
</tr>
<tr>
<td>CYP1A2</td>
<td>1.25</td>
<td>1.02</td>
<td>1.08</td>
</tr>
<tr>
<td>CYP3A4</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
</tr>
<tr>
<td>CYP2B6</td>
<td>1.09</td>
<td>1.01</td>
<td>1.03</td>
</tr>
<tr>
<td>CYP2C9</td>
<td>1.31</td>
<td>1.03</td>
<td>1.10</td>
</tr>
<tr>
<td>CYP2C19</td>
<td>1.40</td>
<td>1.03</td>
<td>1.13</td>
</tr>
<tr>
<td>CYP2D6</td>
<td>1.20</td>
<td>1.02</td>
<td>1.07</td>
</tr>
<tr>
<td>CYP2E1</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
</tr>
</tbody>
</table>

The AUCR$_{exp}$ and AUCR$_{sys}$ were calculated for THC, 11-OH-THC and THC-COO-Gluc based on oral or inhaled dosing of THC; the AUCR$_{exp}$ and AUCR$_{sys}$ were calculated for CBD based on oral or inhaled dosing of CBD as described in Materials and Methods.

NA, not analyzed.
Cannabinoid Metabolites as CYP450 Inhibitors


Bansal S, Mahanwar N, Pame MF, and Unadkat JD (2020) Predicting the potential for cannabinoids to precipitate pharmacokinetic drug interactions via reversible inhibition or inactivation of major cytochromes P450. Drug Metab Dispos 48:1008–1017.


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