

Department of Biomedical Engineering



In vitro metabolic profiling of the synthetic cannabinoid receptor agonist CUMYL-THPINACA using high resolution mass spectrometry

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Background

- Synthetic cannabinoid receptor agonists (SC) remain popular drugs of abuse.¹
- Currently, SC-adulterated CBD-hemp is sold as drug-hemp.
- Effects comparable to THC, but generally far more potent.
- Severe health risks for consumers due to high potency, reflected in several (lethal) overdose cases.²
- Forensic and clinical analyses: Knowledge on the in vivo



- metabolism of SC are a prerequisite for detection of an ingestion as metabolites are the main targets in urine screenings.³
- Information on the metabolizing isoenzymes: helps predicting metabolic drug-drug interactions.⁴⁻⁵



A) Examples of MS² spectra of CUMYL-THPINACA and one major metabolite (M18)

Material & Methods

In vitro metabolism:

- Pooled human liver microsomes (pHLM)
- Recombinant Cytochrome P450 liver enzymes (rCYP: CYP3A4, CYP2C9, CYP2E1, CYP3A5, CYP2C8, CYP2B6, CYP2A6, CYP1A2, CYP2D6, CYP2C19, CYP3A5, CYP2B6)

Sample preparation (Figure 1):

- 1. Incubation with enzymatic model system for 0.5; 1; 1.5; and 2 h.
- 2. Solid phase extraction (SPE, Strata Phenyl cartridge) of incubation solution
- Extract analysis with ThermoFisher[™] LC-HRMS (LC: Ultimate 3000, MS: Q Exactive Orbitrap, equipped with Hypersil Gold[™] analytical column) investigating diagnostic product ions using Compound Discoverer[™] software.

Results & Discussion

Discovery: 28 Metabolites of CUMYL-THPINACA

- CUMYL-THPINACA was extensively hydroxylated, resulting in various mono-, di-, and tri-hydroxylated metabolites (Figure 2

B) Extracted ion chromatogram of a pHLM sample (2 h incubation)

Transformation	Formula	[M+H]+	Mass change	Number of metabolites	Label	Retention time
monohydroxylation	C23H27N3O3	394.2118	+ O (16.9949 amu)	2	M21a-b, M22	1.99, 2.15
dihydroxylation	C23H27N3O4	410.2074	+ 2 x O (31.9898 amu)	8	M1, M9a-e, M16, M18	0.89, 1.23-1.54, 1.62, 1.69
dihydroxylation + dehydration	C23H25N3O3	392.1969	+ 2 x O - H2O (13.9792 amu)	5	M11a-b, M14, M19, M23	1.39-1.43, 1.54, 1.81, 2.39
trihydroxylation	C23H27N3O5	426.2023	+ 3 x O (47.9847 amu)	7	M2a-b, M4, M6, M8, M10, M12, M13	0.9-1.0, 1.08, 1.19, 1.23, 1.27, 1.42
trihydroxylation + dehydration	C23H27N3O5	408.1918	+ 3 x O - H2O (29.9741 amu)	6	M3, M5, M7, M15, M17, M20	1.08, 1.16, 1.20, 1.62, 1.88
CUMYL-THPINACA (parent)	C23H27N3O2	378.2176	_	_	_	3.07
Table 1: Summary of all detected metabolites						

Conclusion & Outlook

CUMYL-THPINACA is extensively metabolized, as observed for other SCs. Therefore, metabolites need to be considered when screening *urine samples*.
To rule out in-source dehydration, further investigation, and potentially sample derivatization, should be conducted.
No drug-drug interactions are expected - as several CYP isoforms contribute to the metabolism of CUMYL-THPINACA.
In vitro models are not able to fully mimic the *in vitro* situation: *in vivo* analysis of authentic urine samples is required to elucidate the most relevant metabolites.
Further investigations will include analysis of authentic urine samples (where available), activity studies of metabolites, and occurrence of in-source dehydration.

and Table 1)

- Additional metabolites were formed by oxidation and subsequent dehydration at the oxacyclohexane moiety.
- Due to in-source dehydration being observed for M21* and M22*, further investigation is required of corresponding di- and trihydroxylated + dehydrated metabolites that are co-eluting with the respective di- and tri-hydroxylated metabolites.
- CUMYL-THPINACA was metabolized by various CYP-isoforms, mainly: CYP3A4, CYP3A5, CYP2C8, CYP2D6, and 2C19.
 Relevant metabolic drug-drug interactions are, therefore, not expected.

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