Poster

[P26-10] P26-10: Assay of toxicants

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[P26-10-5] Quantitative analysis of THC and metabolites from multiple matrices using UPLC-MS/MS for forensic toxicology applications

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Background

Cannabis continues to be a highly abused recreational drug. The increasing number of states legalizing it for medical use, combined with the trend towards legalization for recreational purposes, means than analytical methods for the quantification of Δ-9-tetrahydrocannabinol (THC) and its metabolites continue to be necessary. In addition to urine and whole blood, there is a growing need for plasma- and oral fluid-specific analytical techniques. In addition to the unique analytical challenges posed by THC and its metabolites, the individual properties of these 4 matrices also need to be addressed during method development. This work details the optimization of methods for THC, 11-hydroxy Δ-9-THC (THC-OH) and 11-nor-9-Carboxy-Δ-9-THC (THC-COOH) in plasma, oral fluid (OF), whole blood, and urine. Further, the extraction and analysis these compounds from all 4 matrices using a novel reversed-phase sorbent, followed by direct analysis by UPLC-MS/MS is described. Matrix specific adjustments in SPE protocols and chromatographic methods were employed to optimize each analysis.

Methods

For all 4 matrices, Waters' Oasis PRiME HLB Elution plates were used and all samples were pretreated as appropriate for each matrix. The pretreated samples were directly loaded onto μElution plates without conditioning or equilibration. Elution solvents were optimized for each matrix. The final eluates were diluted with water for direct LC-MS/MS analysis without evaporation/reconstitution.

Results

Analysis was rapid and reproducible, with all analytes eluting within 3 minutes. Excellent recoveries and minimal matrix effects were obtained on all four biological samples. More than 90% of phospholipids were removed from the whole blood and plasma samples as compared to protein precipitation. Quality control values were accurate and precise for all analytes in all 4 matrices. All results were within 12% of expected values and %RSDs were under 10%. The excellent accuracy and precision demonstrate the consistency and robustness of the methods.

Conclusions

This application highlights the quantification of THC and its metabolites in multiple biological matrices. Matrix specific optimization strategies, resulting in consistent recoveries and minimal matrix effects, contributed to method consistency and robustness. The μElution format enabled the direct injection of extracts without evaporation or reconstitution, minimizing the risk of nonspecific binding. The method also eliminated phospholipids - that would normally co-elute with analytes of interest - resulting in decreased

matrix effects.
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