

Application

News

SSI-LCMS-046



# Quantitative Analysis of Cannabinoids using the LCMS-8040 Triple Quad MS



# LCMS-8040

# Summary

Evaluation and quantitation of a variety of cannabinoids on an LCMS-8040 triple quadrupole mass spectrometer.

#### Method

Cannabichromene (CBC), cannabigerol (CBG) and  $\triangle 9$ -THC Acid A (THCA) standards were purchased from Restek (Bellefonte, PA). Cannabinol (CBN),  $\triangle$ 8-THC (d8-THC),  $\triangle$ 9-THC (d9-THC), △9-THC-D3 (d9-THC-D3) and Cannabidiol (CBD) were purchased from Cerilliant (Round Rock, TX). A stock concentration of 1 µg/mL for each standard was used for MRM optimization. The standards were combined into one solution and then serially diluted with 70/30 (%) methanol/water using 2-fold dilutions yielding concentrations ranging from 8192 ng/mL to 1 ng/mL. The IS (d9-THC-D3) was added to all levels. The standards (Figure 1) were transferred to autosampler vials and injected into a Nexera-LCMS-8040 system for analysis.

A Thermo Hypersil Gold (1.9  $\mu$ m x 2.1 mm x 100 mm) was used with a binary gradient of 5 mM ammonium acetate in water and acetonitrile. The gradient conditions are shown in **Figure 2**. The flow rate was 0.5 mL/min with a run time of 6.8 min. The column temperature was 45° C and the injection volume was 5  $\mu$ L.

# LCMS-8040 Analysis

Dual ion electrospray ionization (DUIS) in both positive and negative modes was used for ionization of the analytes on the LCMS-80400. Multiple reaction monitoring (MRM) in positive and negative modes was used for analysis. At least one reference ion was monitored for each analyte. Details of the MS parameters are shown in **Table 1**.

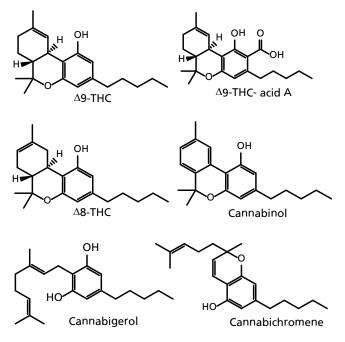


Figure 1. Chemical structures for cannabinoids.

# **Results and Discussion**

Peaks were smoothed using the standard method set to 2 counts and 2 sec for width. The auto integration setting was used with a setting of 1 max peak and 6 sec width. d8-THC was integrated by turning off peak integration from 4.9-5.3 minutes. Linearity was achieved from 1-8192 ng/mL for CBG, 2-4096 ng/mL for CBN, 4-4096 ng/mL for d9-THC, 8-8192 ng/mL

for d8-THC, 64-4096 ng/mL for THCA, 4-8192 ng/mL for CBD and CBC. The calibration curve was weighted using 1/C and not forced through zero. No standards were excluded over the included range and  $r^2$  values ranged from 0.998-0.999. A representative chromatogram and calibration curve for each analyte are shown in **Figures 4-11**.

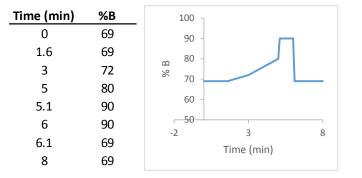


Figure 2. Gradient conditions.

MS Interface ParametersInterfaceDUISNebulizing gas flow2 L/minDrying gas flow15 L/minDL Temperature300 °CHeat Block Temperature500 °CPolarity(+) CBD, CBG, CBN, d8-THC, d9-THC, CBC<br/>(-) THCA

 Table 1. MS Interface parameters.

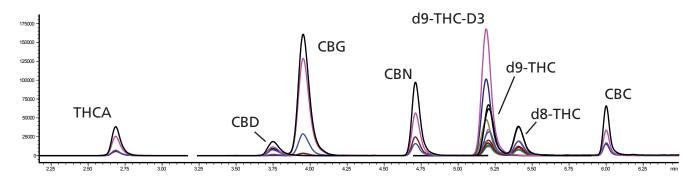


Figure 3. Representative chromatogram cannabinoids at 64 ng/mL.

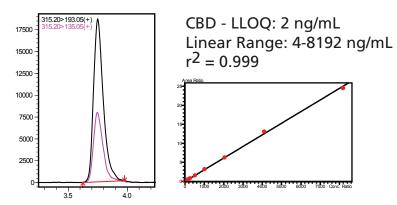


Figure 4. Chromatogram and calibration curve for cannabidiol (CBD).

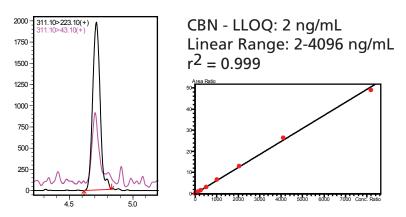


Figure 5. Chromatogram and calibration curve for cannabinol (CBN).

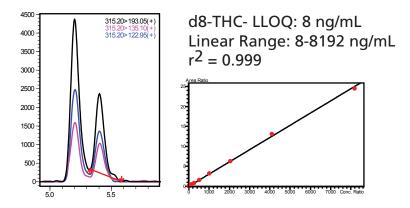


Figure 6. Chromatogram and calibration curve for d8-THC.

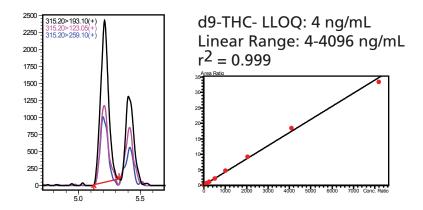


Figure 7. Chromatogram and calibration curve for d9-THC.

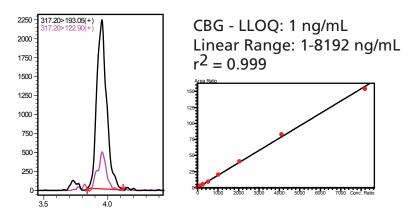


Figure 8. Chromatogram and calibration curve for cannabigerol (CBG).

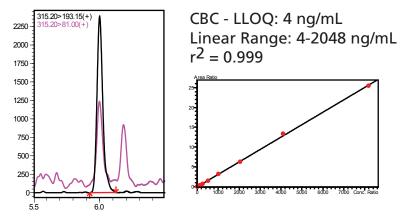


Figure 9. Chromatogram and calibration curve for cannabichromene (CBC).

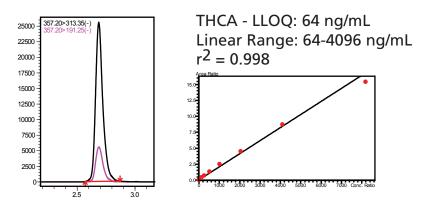
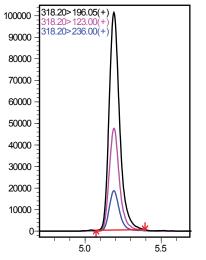


Figure 10. Chromatogram and calibration curve for d9-THC Acid A (THCA).



d9-THC-D3 - Internal Standard

Figure 11. Chromatogram for d9-THC-D3 internal standard.

# Conclusion

A method for rapid quantitation of various cannabinoids utilizing a Nexera X2 UHPLC coupled to an LCMS-8040 triple quadrupole mass spectrometer was developed. An 8 minute method was optmized, with the main limiting factor being the separation of d8-THC and d9-THC due to their structure being nearly identical. It is important to note that these results were achieved using standards without matrix, but the ability of the Nexera X2 system and LCMS-8040 mass spectrometer to enable simultaneous, accurate measurement of many of the cannabinoids on interest is highlighted by this method.



ULTRA FAST MASS SPECTROMETRY



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