1. Introduction

Due to the legalization of marijuana both recreationally and medicinally, use of the drug has increased drastically. It’s reported in 2018, more than 11.8 million young adults reported marijuana use in the past year. With this rapid expansion of marijuana use, testing has become even more critical. The prevalence of marijuana use and the passage of legislation regulating its use has mandated the development of analytical procedures for detecting Δ9-tetrahydrocannabinol (THC), the major psychoactive component of marijuana, and its metabolic products in biological matrices. Along with THC, several other cannabinoids have become of interest such as: CBDV, CBC, CBD, Δ8 THC, and CBG.

With CBD products on the rise, it is important to be able to detect all cannabinoids on GC-MS is extremely advantageous due to the fact terpenes, residual solvents and some pesticides can also be analyzed via GC-MS.

2. Experimental Methods

A cannabinoid mix from Cayman Chemical was procured for GC-MS analysis. The mix contained 11 cannabinoids; however only 9 are resolvable without derivatization. CBDV, THCV, CBC, CBD, Δ8 THC, and CBG. The standards were prepped at concentration levels of 0.5, 1.0, 5.0, 10.0, 50.0, 100.0 ppm. These standards were run via GC-MS proving to be linear from lowest to highest concentration.

To prepped to determine CBD content. The four samples were validify this method with a real world scenario, CBD lotion was

3. Analytical Conditions

System Configuration

GC-MS: GCMS-QP2020NX (Shimadzu)
Autosampler: AOC-20 i/s
GC Parameters

Column: RTX-35
Injector: 275 °C
Oven Temp.: 230 °C @1/min, 260 °C @15/min, 320 °C @ 25/min (1.7 min)
Carrier Gas Control: Helium, Constant Linear Velocity, 46.0 cm/sec
Injection Mode: Split 1:10
Total Program time: 6.07 min
MS Parameters

Interface Temp.: 250 °C
Ion Source Temp.: 200 °C
Ionization Mode: EI
Acquisition Mode: SIM

Table 1. SIM m/z

<table>
<thead>
<tr>
<th>m/z</th>
<th>SIM masses</th>
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<tbody>
<tr>
<td>314</td>
<td>232, 231, 218</td>
</tr>
<tr>
<td>455</td>
<td>314, 299, 296</td>
</tr>
<tr>
<td>456</td>
<td>314, 299, 296</td>
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<tr>
<td>457</td>
<td>314, 299, 296</td>
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</table>

Table 1 refers to the SIM masses used during the run for identifying specific cannabinoids at specific retention time ranges

4. Results

The cannabinoids standards were run from low to high and were qualitatively processed using the Wiley Mass Spectra of Designer Drugs 2019 providing high accuracy and exact match. The chromatograms below represent the high, middle and low concentrations (Figures 3, 4 and 5 respectively). Each peak is labeled with the respective cannabinoid.

The calibration curves shown in figure 6 and 7 represent Δ9 THC and CBD. The linearity for the calibration curves are 0.9996 and 0.9991 respectively.

5. Conclusion

The GC-MS method has proven to be extremely efficient and accurate in separating 9 major cannabinoids while also detecting them at low levels. Due to the fact this is run with pure standards, the next step in developing this method is to match matrices and continue with an LOQ and LOQ study to validate the method.

The GC-MS method has also proven to be a useful technique for customers currently using GC-Ms for other cannabis applications like terpenes and residual solvents.

6. References

1) Substance Abuse Center for Behavioral Health Statistics and Quality. Results from the 2018 National Survey on Drug Use and Health: Detailed Tables, SAMHSA. https://www.samhsa.gov/data/index.aspx?DID=55

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