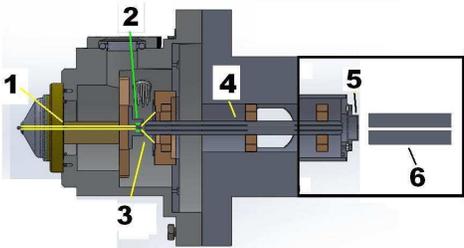


Introduction

Ambient ionization sources such as Direct Analysis in Real Time (DART) and Desorption Electrospray Ionization (DESI) were facilitated by the availability of high performance liquid chromatography/ mass spectrometry systems (LC/MS). Compared to gas chromatography MS (GC/MS) the number of these LC/MS systems in operation is relatively small.

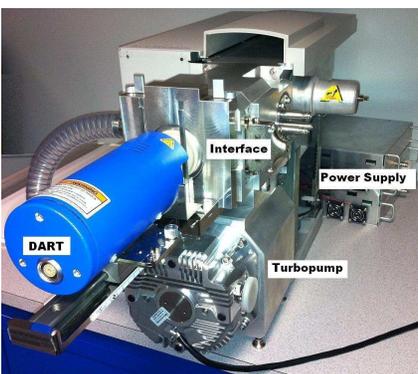
DART, an ambient pressure ionization source, generates intact [M+H]⁺ molecules by introducing the sample to a gas stream of metastable nitrogen molecules which can be heated to permit thermal desorption. In order to provide a more widely available platform for ambient ionization we have enabled an atmospheric pressure inlet for use with the Agilent 5973 series GC/MS along with DART. The instrument design includes a three stage vacuum system with capillary inlet and ion guide for optimum transfer of ions into the mass selective detector (MSD). The interface enables both DART and micro-electrospray ionization sources. Sensitivity of the device was measured using typical standards employed for DART. The modified GC/MSD system was utilized for the analysis of synthetic drugs available to the public.

Instrument



API-MSD Schematic

1. Heated capillary
2. Skimmer
3. Focus Lens
4. Ion guide
5. Exit Lens
6. Quadrupole



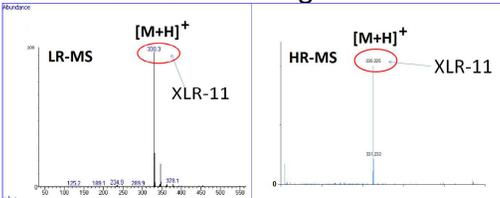
Picture of DART-MSD System

Synthetic Cannabinoids



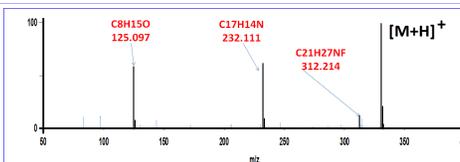
Two "incense" packets were purchased from a head shop in New Hampshire. XLR-11, a synthetic cannabinoid, was present on both samples. XLR-11 has yet to be added to the federal controlled substances act. DART-MS yielded a single intense peak at 330 m/z. All synthetic cannabinoid analyses were run with the DART gas at 250C.

Low Resolution-MS High Resolution-MS



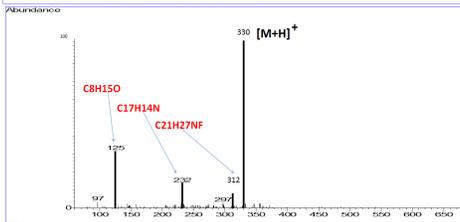
Accurate mass values from the high resolution JEOL DART AccuTOF mass spectrometer(MS) was searched against the NIST database of known synthetic cannabinoids leading to XLR-11 as a possible suspect. The LR-MS was ran with nitrogen as the gas source.

In-source fragmentation to confirm ID



Using accurate mass in-source fragmentation information from the NIST database it was confirmed that XLR-11 was present on the samples.

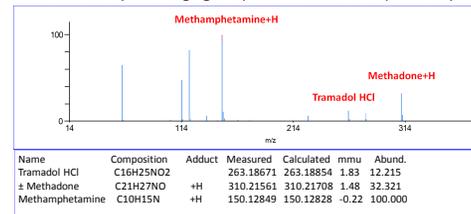
Calc. m/z	Abund %	mmu	DBE	Composition
125.096640	58.400	-0.26	2.5	C8H13O1
144.044939	12.200	0.34	7.5	C9H6O1N1
232.113767	57.400	2.87	7.5	C14H15O1N1F1
232.112624	57.400	1.72	11.5	C17H14N1
312.212752	12.900	-1.45	8.5	C21H27N1F1
314.192017	11.500	-4.18	8.5	C20H25O1N1F1
330.223317	100.000	1.21	7.5	C21H29O1N1F1



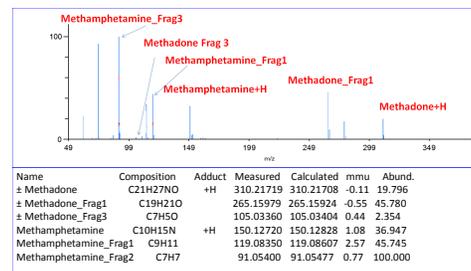
All of the major in-source fragment ions were detected using the modified DART-MSD.

Use of SPME LC Probes

Solid phase micro-extraction(SPME) LC probes, part # 57281-U, a 45µm C18-silica coated metal alloy 22 gauge wire, were used for rapid isolation and then DART analysis of drugs present in urine. The SPME LC probes were condition in DI with 10% methanol and then with methanol with 10% H₂O. The SPME coated portion of the probe is then submerged in the urine sample for 30 minutes. Finally, the probes are dipped into water to remove salts and non-bound material. The probe is then passed through the heated gas exiting the DART source. The MS spectra were collected using JEOL AccuTOF in under 10 seconds per analysis. The reusable probes were cleaned by submerging the probe in acetonitrile post-analysis.



Human urine has matrix effects that can make identifying compounds of interest difficult. Use of the SPME LC probes helped extract and concentrate the ions of interest rapidly. Total sampling time from start to finish is = 45 minutes.



The anticipated fragmentation pattern was obtained on a high resolution JEOL DART AccuTOF MS and was used as confirmation.

Conclusion

Synthetic cannabinoids were successfully fragmented and identified using a modified GC/MSD with DART. The results were confirmed using a high resolution JEOL DART AccuTOF MS with a matching fragmentation pattern. Total DART analysis time was under 5 minutes.

Use of SPME LC probe allowed for rapid analysis of drugs in human urine. The probe successfully helped reduce matrix effects and in-source fragmentation was used to confirm analysis results.

Acknowledgements

Many thanks to Dr. Chip Cody of JEOL, Peabody, MA; and Matt Curtis of University of the Pacific