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Application News

DPiMS™ QT Probe Electrospray Ionization Kit
LCMS™-9030 Quadrupole Time-of-Flight Liquid Chromatograph Mass Spectrometer

Qualitative Screening of Drugs in Whole Blood by DPiMS QT installed LCMS-9030

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User Benefits

- Screening of drugs in biological samples is possible with simple sample preparation.
- Separation using a column is not necessary, and a comprehensive qualitative analysis can be conducted in a measurement time of 3 min.
- *iDIA* which has narrower *m/z* window, and makes it possible to comprehensively acquire MS/MS spectra.

■ Introduction

A simpler and faster technique for identification of the relevant drugs in acquired samples has been required in analyses of drugs and poisons in forensic medicine and scientific criminal investigations.

This Application News introduces a new analysis technique combining the DPiMS QT which is a probe kit of electrospray ionization unit and an LCMS-9030 quadrupole time-of-flight mass spectrometer (Fig. 1) for screening of drugs in human whole blood. The DPiMS QT makes it possible to conduct direct analysis and minimize the time required from sample preparation to analysis. Use of the newly-developed *iDIA* measurement method makes it possible to comprehensively acquire MS/MS spectra for all ionized compounds.

Fig. 1 Appearance of DPiMS™ QT and LCMS™-9030

■ Analysis Technique

In the DPiMS QT, the attached probe repeatedly carries out sampling from the sample plate, and simultaneously ionizes the sample material adhering to the probe surface by applying a voltage to the probe tip. Then, the ionized samples are introduced directly into the mass spectrometer. In this study, a spiked human whole blood sample (500 ng/mL) was prepared by spiking human whole blood with 17 drug compounds. After diluting 10 µL of the spiked human whole blood sample with 90 µL of water, the solution was mixed with 100 µL of ethanol. The mixtures were then centrifuged, and 10 µL of the supernatant was dripped on the sample plate.

The *iDIA* method, which is realized by a combination of the DPiMS QT and LCMS-9030, was used in qualitative screening of the spiked human whole blood sample. *iDIA* is a technique for acquiring MS/MS spectra which are set to minimize the range of precursor ions to the limit. Here, MS/MS spectra were acquired comprehensively for a window width of 1 Da, and a search of the MS/MS spectra acquired by PESI-Q-TOFMS using the DPiMS QT was conducted using a spectrum library constructed in advance by LC-ESI-Q-TOFMS using standard substances of the various drugs. Table 1 shows the analysis conditions.

Table 1 Analysis Conditions

Mass spectrometer	
System	: DPiMS QT+LCMS-9030
Polarity	: Positive
DL temp	: 250 ˚C
Heat block temp	: 50 ˚C
Interface Voltage	: 3.5 kV
TOF-MS	: *m/z* 120-770
Precursors of MS/MS	: *m/z* 140-770 (Fixed window size 1 Da)
MS/MS	: 20-780 *m/z*
Collision energy ramp	: 10-50 V
Measurement Time (TOF-MS)	: 3 min
Measurement Time (MS/MS)	: Each group within 0.1 min (Total 30 groups)

■ Analysis of Spiked Human Whole Blood Sample

Table 2 shows the 17 drug compounds spiked in the human whole blood and the library scoring results for each drug. All of the spiked drugs received library scores of 84 to 100, demonstrating that extremely good identification results could be obtained with simple sample preparation and a high-speed analysis with a measurement time of 3 min.

Fig. 2 shows the MS/MS spectra when each drug was compared with the spectrum library. Because the MS/MS spectra are acquired with a window width of 1 Da, it is possible to reduce the effects of contaminant components and isotopic ions.

Table 2 Library Scores of Drugs (500 ng/mL) in Human Whole Blood

#	Compounds	Formula	$[M+H]^+$	Library Score
1	7-Aminonitrazepam	C15H13N3O	252.1132	97
2	Aconitine	C34H47NO11	646.3222	100
3	Blonanserin	C23H30FN3	368.2497	95
4	Carbamazepine	C15H12N2O	237.1023	84
5	Clotiazepam	C16H15ClN2OS	319.0667	95
6	Colchicine	C22H25NO6	400.1755	100
7	Dextromethorphan	C18H25NO	272.2009	100
8	Donepezil	C24H29NO3	380.2221	100
9	Dosulepin	C19H21NS	296.1468	87
10	Escitalopram	C20H21FN2O	325.1711	95
11	Lidocaine	C14H22N2O	235.1805	94
12	Methylphenidate	C14H19NO2	234.1489	97
13	Mosapramine	C28H35ClN4O	479.2572	98
14	Propericiazine	C21H23N3OS	366.1635	96
15	Temazepam	C16H13ClN2O2	301.0739	99
16	Trazodone	C19H22ClN5O	372.1586	96
17	Zolpidem	C19H21N3O	308.1758	96

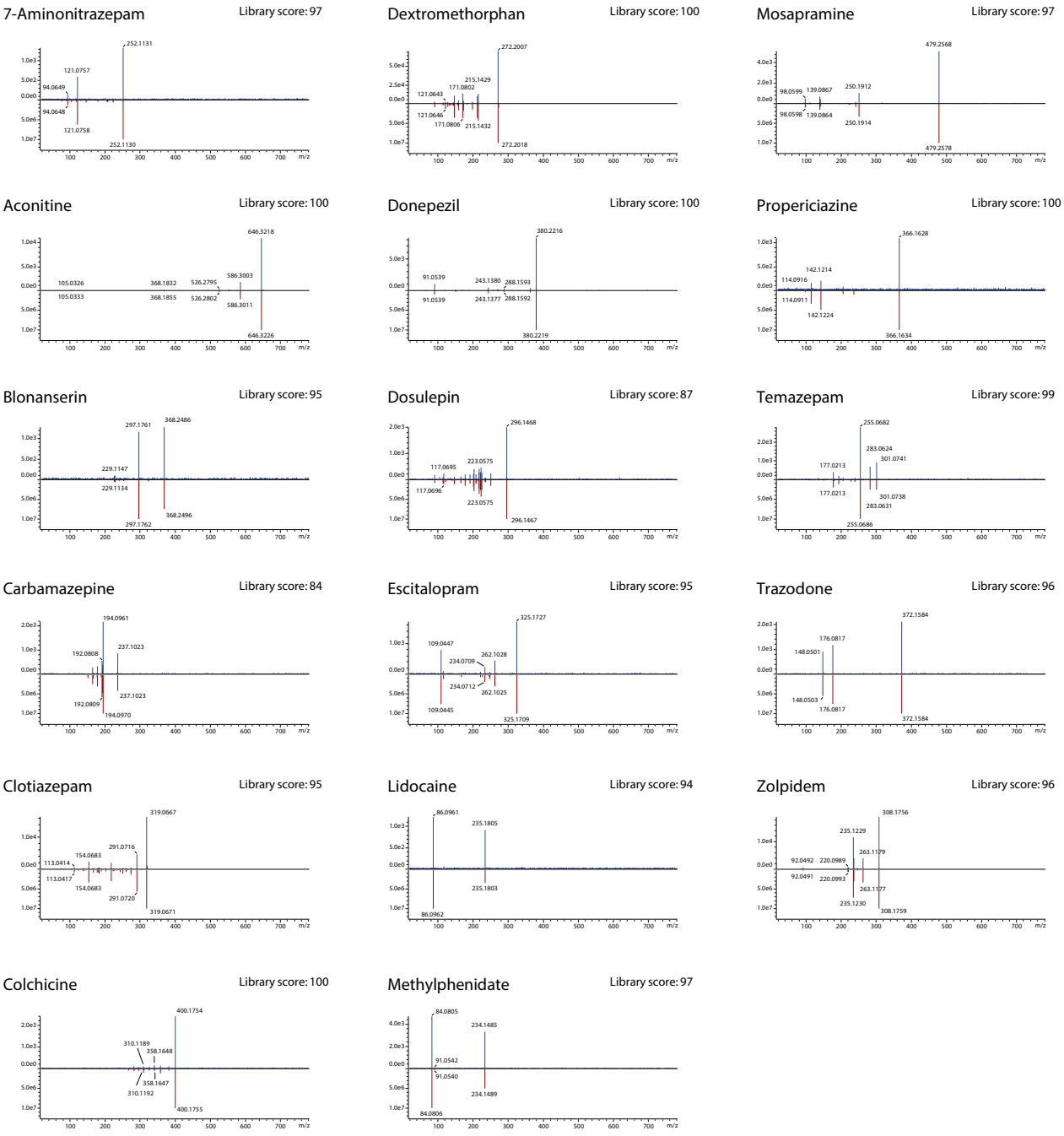

Fig. 2 (Top) MS/MS Spectra and Library Scores of Drugs (500 ng/mL) in Human Whole Blood Acquired Using *iDIA* and (Bottom) MS/MS Spectra of Standard Substances of Drugs Acquired by LC-ESI-Q-TOFMS

■ Conclusion

The *iDIA* measurement method for comprehensively acquiring the MS/MS spectra of all ionized components in a sample was developed by using the DPiMS QT and LCMS-9030. Extremely good results were obtained as a result of screening of 17 drug compounds spiked in human whole blood, as the library scores for all drugs were from 84 to 100.

The effects of contaminant components and isotopic ions contained in biological samples can be reduced by acquiring MS/MS spectra with the width of the precursor ion window set to 1 Da. Quick and comprehensive qualitative screening of drugs in biological samples is possible with simple sample preparation and a measurement time of 3 min.

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