EIEIO: Electron Impact Excitation of Ions from Organics (or Electron Induced Dissociation) for Near Complete Structural Characterization in Lipidomics

Tasaha Baba* and J. Larry Campbell
SCIEI, Sciex Life Science Division, Concord, ON, L4K 4V8 Canada

ABSTRACT

We describe a novel mass-spectrometry-based workflow for enhanced structural lipidomics that can yield a “nearly complete” informative data set with detection of all possible lipid structures, a lipid’s acyl chain composition, and its glycerol backbone composition. A library of diagnostic ions can be generated using liquid chromatography mass spectrometry–tandem mass spectrometry. Several new lipid classes, such as phosphatidylethanolamines (PEs) and phosphatidylglycerols (PGs), were identified in human serum. The proposed method provides the capability for characterizing the components of biological membranes, which is essential for the development of novel therapeutic agents. This method provides a tool for characterizing lipid species in biological samples, offering a comprehensive view of the lipidome.

INTRODUCTION

Lipids are critical components of many cellular assemblies and biological pathways, but accurate descriptions of their structure and function remain challenging. Several mass spectrometry methods report multiple assignments whenever a new structural feature is found, and these steps are generally quite time-consuming. Here, we describe a new MS-based method enabling rapid (EIEIO) mass spectral analysis for structural lipidomics. Mass spectrometry provides the ability to select the desired lipid composition from fragment ions unique in the sn 1 and 2 positions, and the positions of carbon-carbon double bonds in the fatty acid chains. Here, positive-ion MS spectra were generated using electron impact or electron impact ionization (EIEIO), a technique where the singly charged lipid ions are isolated by an electron beam, producing diagnostic product ions.

RESULTS

Head group identification (step 1): Ion time data analysis after obtaining an EIEIO spectrum (Fig. 2). EIEIO spectra were aligned at the C2 O6 ion (m/z 16) for glycerophospholipid (GPL) and glycerol backbone composition. This feature was allowed to be determined for all lipid classes. Additionally, an alignment of m/z 16 + 207 was obtained for all GPLs.

Acyl group and preparative identification (step 2): GPLs are given by the C1 O6 ion in the glycerol backbone, which is not allowed for fatty acids. CID (ref 2.3). We acknowledge a new MS-based method enabling rapid (EIEIO) mass spectral analysis for structural lipidomics. This diagnostic method was generated for any type of head group. Acyl chain designs at each position (Table 1).

EIEIO spectra were obtained for each of the acyl chains for each sample. The identification of the acyl chain was determined by the obtainable diagnostic ions in the EIEIO spectra. These ions were used to create the diagnostic ions for each lipid class. The diagnostic ion for each lipid class was obtained from the EIEIO spectra.

Determination of double bond location (step 5): EIEIO data were obtained at each sample to identify the diagnostic ions for each lipid class. These ions were used to create the diagnostic ions for each lipid class. The diagnostic ion for each lipid class was obtained from the EIEIO spectra.

The EIEIO spectra for each lipid class were obtained at each sample to identify the diagnostic ions for each lipid class. These ions were used to create the diagnostic ions for each lipid class. The diagnostic ion for each lipid class was obtained from the EIEIO spectra.

CONCLUSIONS

A new comprehensive method for phospholipid characterization has been developed using EIEIO based tandem mass spectrometry. A single experimental determines both class, acyl chains and positions on the glycerol backbone and carbon double bonds and locations of the diacylglycerol. This method is able to identify the position of the double bond, which is essential for the development of novel therapeutic agents. This method provides a tool for characterizing lipid species in biological samples, offering a comprehensive view of the lipidome.

REFERENCES


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