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# Multi-dimensional Mass Spectrometry for Lipid Analysis

HAN Xian-lin
(*Washington University School of Medicine*, *St. Louis MO* 63110, *USA*)

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Multi-dimensional mass spectrometry (MD-MS) is a newly emerging technology in mass spectrometry, which is analogous to multi-dimensional nuclear magnetic resonance spectroscopy. Each series of ramped changes in one of the instrumental conditions (i. e., one variable) facilitate the generation of a dimension. These variables include: sample introduction (e. g., solvents, pH, reagents, and flow rates), ionization (e. g., temperature and voltage), fragment monitoring (e. g., neutral fragments in neutral loss scanning and fragment ions in precursor-ion scanning), and collision-induced dissociation (e. g., collision energy, collision gas pressure, and collision gas type), among others. Each of these variables constitutes a member of the MD-MS family. We recognized the power of MD-MS for analyses of individual lipid molecular species in lipidomics and have developed a technology based on MD-MS (i. e., shotgun lipidomics). By varying the pH of an infused solution, we have achieved optimal separation and maximal ionization of some specific lipid classes in the ion source (i. e., intrasource separation and selective ionization). By monitoring certain fragments (which represent building blocks of each lipid class or group) through either neutral loss or precursor-ion scanning, we have identified and quantified hundreds to thousands of individual lipid molecular species directly from a lipid extract of a biological sample. By applying various amounts of collision energy during collision-induced dissociation, we are able to study the differential fragmentation kinetics of each individual lipid molecular species in a lipid class of interest. Collectively, MD-MS greatly facilitates not only the identification and quantitation of individual lipid molecular species by shotgun lipidomics, but also the determination of lipid biophysical properties and interactions for lipidomics.