

High mass resolution MALDI-TOF MS for profiling biomolecules in mixtures

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Abstract

Intact biomolecules carry its identity through its atomic constituents and mass, while fragmented biomolecules require reconstruction for their identity to be retrieved. Hence, for profiling biomolecules in mixtures, the goal would be the gentle ionization of biomolecules by mass spectrometry without inducing fragmentation. Doing so generates an ensemble of ionized intact biomolecules able to be profiled by high sensitivity time-of-flight detector for accurate determination of each biomolecule mass, and thus, identity. Specifically, in time-of-flight detection, high mass resolution determination would require high sensitivity in detecting small differences in time of arrival of biomolecule ions to the detector. While current time-of-flight mass spectrometry provides high mass resolution, greater mass resolution is needed for discriminating different biomolecules in a mixture, where mass differences between biomolecules could be at the sub-Dalton level. With the ability to reliably detect biomolecules with sub-Dalton mass resolution, mass spectrometry with time-of-flight detector such as matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) could find use in identifying the compendium of biomolecules present in a mixture without tedious and time-consuming separation. The larger question would subsequently be coupling sample preparation needs with the conditions conducive for MALDI-TOF MS analysis. Overall, high mass resolution mass spectrometry techniques for profiling biomolecules would find use as an enabling tool in many areas of analytical science and biological sciences such as proteomics and metabolomics.

Keywords: fragmentation, ionization, time-of-flight, high mass resolution, mass differences, sub-Dalton level, mass spectrometry, MALDI-TOF MS, biomolecules, mixture,

Subject areas: biotechnology, bioengineering, biochemistry, cell biology, biophysics,

Conflicts of interest

The author declares no conflicts of interest.

Author's contribution

The author thought about the difficulty of using chemical fragment libraries for identifying compounds in tandem MS/MS, and realized that since each biomolecule has a unique mass, accurate quantification of a biomolecule's mass through high mass resolution mass spectrometry would provide the biomolecule's identity. With current technology and the need for not inducing fragmentation in the biomolecule, high mass resolution mass spectrometry would necessarily be

implemented in matrix-assisted laser desorption/ionization time-of-flight (MALDI-TOF) mass spectrometry. He wrote the abstract preprint to share his ideas with the scientific community.

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