Mass Spectrometry

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1 Introduction

Mass spectrometry is an analytical tool used for measuring a sample's molecular mass. Mass spectrometry has undergone immense technological advancements allowing for its application to proteins, peptides, carbohydrates, DNA, drugs, and many other biologically relevant molecules. Due to ionization sources such as electrospray ionization (ESI) and matrix-assisted laser desorption/ionization (MALDI), mass spectrometry has become a unique asset in the biological sciences.

A mass spectrometer determines the mass of a molecule by measuring the mass-to-charge ratio (m/z) of its ion. Ions are generated by inducing either the loss or gain of a charge from a neutral species. Once formed, ions are electrostatically directed into a mass analyzer where they are separated according to m/z and finally detected. The result of molecular ionization, ion separation, and ion detection is a spectrum that gives molecular mass and even structural information. A mass spectrometer bears resemblance to a prism, as shown in Figure 1.1. In the prism, light is separated into its component wavelengths which are then detected with an optical receptor, such as visualization. Similarly, in a mass spectrometer the generated ions are separated in the mass analyzer, digitized and detected by an ion detector.

2 How does a mass spectrometer work?

To measure the characteristics of individual molecules, a mass spectrometer is used to convert them to ions so that they can be free to roam about and be manipulated by external electric and magnetic fields. The three fundamental parts of a mass spectrometer are the ionization source, the mass analyzer, and the detector. A small sample is ionized to cations by loss of an electron. The ions are sorted and separated according to their mass and charge. The separated ions are then measured, and the results displayed on a chart. Due to their volatile and ephemeral nature, the ions' formation and manipulation must be conducted in a vacuum. Atmospheric pressure is around 760 torr (mm of mercury), and the pressure under which ions may be handled is from 10-5 to 10-8 torr (less than a billionth of an atmosphere).

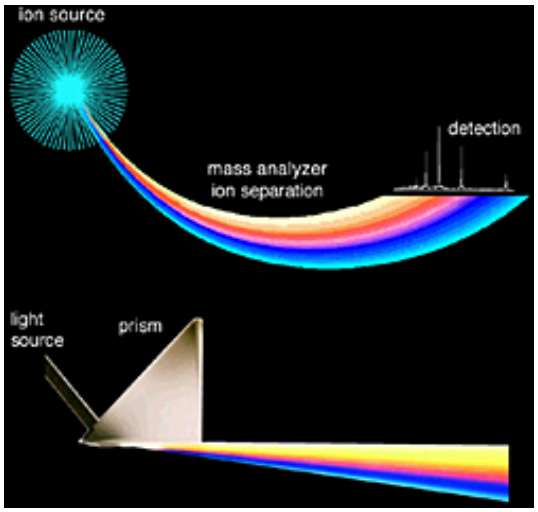

Figure 1: Figure 1.1. The mass analysis process the dispersion of light by a prism

3 Analysis and Separation of Sample Ions

The mass analyzer's primary purpose is to separate/resolve the ions formed in the mass spectrometer's ionization source according to their mass-to-charge (m/z) ratios. There are a number of mass analyzers currently available. The most well-known ones are quadrupoles, time-of-flight (TOF) analyzers, magnetic sectors, and both Fourier transform and quadrupole ion traps. These mass analyzers have different features, including the m/z range that can be covered, the mass accuracy, and the achievable resolution. The compatibility of different analyzers with different ionization methods varies. For example, all of the analyzers listed above can be used in conjunction with electrospray ionization, whereas MALDI is not usually coupled to a quadrupole analyzer.

4 Detection and recording of sample ions

The detector monitors and amplifies the ion current. Afterwards, the signal is transmitted to the data system where it is recorded in the form of mass spectra. The m/z values of the ions are plotted against their respective intensities to show the number of components in the sample, the molecular mass of each component, and the relative abundance of the various components in the sample. The type of detector is supplied to accommodate the type of analyzer; the most common ones are the photomultiplier, the electron multiplier and the micro-channel plate detectors.

5 Electrospray ionization

Electrospray Ionization (ESI) is one of the Atmospheric Pressure Ionization (API) techniques and is suitable for the analysis of polar molecules ranging from less than 100 Da to more than 1,000,000 Da in molecular mass. The m/z values can be expressed as follows: m/z = (MW + nH+)/n where m/z = the mass-to-charge ratio marked on the abscissa of the spectrum; MW = the molecular mass of the sample n = the integer number of charges on the ions H = the mass of a proton = 1.008 Da.

6 Matrix Assisted Laser Desorption Ionization

Matrix Assisted Laser Desorption Ionization (MALDI) deals well with thermolabile, non-volatile organic compounds especially those of high molecular mass. It is also used to analyze proteins, peptides, glycoproteins, oligosaccharides, and oligonucleotides. The mass accuracy depends on the type and performance of the mass spectrometer's analyzer, but most modern instruments should be capable of measuring masses to within 0.01% of the molecular mass of the sample, at least up to ca. 40,000 Da.

MALDI is also a "soft" ionization method. It generates singly charged molecular-related ions regardless of the molecular mass, which is why the spectra are relatively easy to interpret. Fragmentation of the sample ions does not usually occur. In positive ionization mode the protonated molecular ions (M+H+) are usually the dominant species, although they can be accompanied by salt adducts, a trace of the doubly charged molecular ion at approximately half the m/z value, and/or a trace of a dimeric species at approximately twice the m/z value. Positive ionization is used in general for protein and peptide analyses. In negative ionization mode the deprotonated molecular ions (M-H-) are usually the most abundant species, accompanied by some salt adducts and possibly traces of dimeric or doubly charged materials. Negative ionization can be used for the analysis of oligonucleotides and oligosaccharides.

If the sample has functional groups that readily accept a proton (H+) then positive ion detection is used. If the sample has functional groups that readily lose a proton then negative ion detection is used .

7 Reference list

Ashcroft, Alison. "An Introduction to Mass Spectrometry." Astbury. Web. 26 Oct. 2015.

http://www.astbury.leeds.ac.uk/facil/MStut/mstutorial.htm