Mass Spec

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1 Basics of Mass Spectrometry

Mass spectrometry has been described as the smallest scale in the world, not because of the mass spectrometer's size but because of the size of what it weighs – molecules. Over the past decade, mass spectrometry has undergone tremendous technological improvements allowing for its application to proteins, peptides, carbohydrates, DNA, drugs, and many other biologically relevant molecules. Due to ionization sources such as electrospray ionization and matrix-assisted laser desorption/ ionization (MALDI), mass spectrometry has become an irreplaceable tool in the biological sciences. This chapter provides an overview of mass spectrometry, focusing on ionization sources and their significance in the development of mass spectrometry in biolecular analysis. A mass spectrometer determines the mass of a molecule by measuring the mass-to-charge ratio (m/z) of its ion. Inducing either the loss or gain of a charge from a neutral species generates ions. 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 can provide molecular mass and even structural information. An analogy can be drawn between a mass spectrometer and 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, such as an electron multiplier, for example.

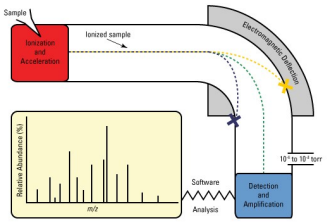

Figure 1: The example of Mass Spectrum

2 Physical principles (Mass selection)

I will explain only the middle part of the process, the Mass selection. Mass analyzers separate the ions according to their mass-to-charge ratio. The following two laws govern the dynamics of charged particles in electric and magnetic fields in vacuum:

$$E = Q(E + v * B)$$

(Lorentz force law)

$$F = ma$$

(Newton's second law of motion in non-relativistic case, i.e. valid only at ion velocity much lower than the speed of light).

Here F is the force applied to the ion, m is the mass of the ion, a is the acceleration, Q is the ion charge, E is the electric field, and v B is the vector cross product of the ion velocity and the magnetic field Equating the above expressions for the force applied to the ion yields:

This differential equation is the classic equation of motion for charged particles. Together with the particle's initial conditions, it completely determines the particle's motion in space and time in terms of m/Q. Thus mass spectrometers could be thought of as "mass-to-charge spectrometers". When presenting data, it is common to use the (officially) dimensionless m/z, where z is the number of elementary charges (e) on the ion (z=Q/e). This quantity, although it is informally called the mass-to-charge ratio, more accurately speaking represents the ratio of the mass number and the charge number, z. There are many types of mass analyzers, using either static or dynamic fields, and magnetic or electric fields, but all operate according to the above differential equation. Each analyzer type has its strengths and weaknesses. Many mass spectrometers use two or more mass analyzers for tandem mass spectrometry (MS/MS). In addition to the more common mass analyzers listed below, there are others designed for special situations. There are several important analyser characteristics. The mass resolving power is the measure of the ability to distinguish two peaks of slightly different m/z. The mass accuracy is the ratio of the m/z measurement error to the true m/z. Mass accuracy is usually measured in ppm or milli mass units. The mass range is the range of m/z amenable to analysis by a given analyzer. The linear dynamic range is the range over which ion signal is linear with analyte concentration. Speed refers to the time frame of the experiment and ultimately is used to determine the number of spectra per unit time that can be generated.

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References

[1] McLuckey S.A. Busch K.L., Glish G.L. *Mass Spectrometry/Mass Spectrometry: Techniques and Applications of Tandem.* John Wiley Sons, 1989.