## Fundamentals of Contemporary Mass Spectrometry

Chhabil Dass, Editor Wiley–Interscience Series on Mass Spectrometry D. M. Desiderio and N. M. Nibbering, Series Editors 111 River Street Hoboken, NJ 07030-5774, USA ISBN 978-0-471-68229-5 Copyright © 2007; Hardcover, \$110.00 US, 585 pp

Reviewed by Paul Vouros Northeastern University Department of Chemistry 360 Huntington Avenue Boston, MA 02115, USA p.vouros@neu.edu

Mass spectrometry has undergone dramatic growth over the past several years and, remarkably, it is still in a very dynamic growth curve. Writing a mass spectrometry text book that includes the term "contemporary" in its title is a daring undertaking. Yet, this is what the author has accomplished in this publication by producing a text that covers almost all of the most pertinent areas of modern mass spectrometry. The book should satisfy educational needs for the novice who not only wants to be introduced to the principles of mass spectrometry but also still wants to familiarize himself/herself with currently evolving techniques and applications.

The book is divided into three principal parts: Part I (pp 1–194) deals with instrumentation; Part II (pp 195–286) discusses fundamentals of organic mass spectrometry; and Part III (pp 287–585) is dedicated to biological mass spectrometry. The organization is logical and well streamlined.

Following some general background, the Instrumentation section begins with a discussion of ionization methods ranging from the classical (EI, CI) to the most recent methods such as desorption electrospray ionization (DESI). Consistent with the historical development and the generally easiest way to visualize the principles of ion separation, the discussion of mass analyzers begins with magnetic systems and concludes with the newly introduced Orbitrap as well as ion mobility separations. The coverage is succinct and clear and sets the stage very nicely for the next chapter, which deals with tandem MS techniques and hybrid instruments. Part I concludes with the chapter on hyphenated methodsthat is, the interfacing of gas and liquid chromatography as well as capillary electrophoresis with mass spectrometry. In all cases the author has made sure to include a short discussion on some of the basic and most important principles of these separation methods as they pertain to their operation with MS.

Part II consists of two chapters dedicated to Organic and Inorganic Mass Spectrometry. Predictably—and

unavoidably—the chapter on Organic MS is largely a microcosm of the Fred McLafferty classic: *Interpretation of Mass Spectra of Organic Compounds*. In fact, most of the examples are drawn from editions of that book. The examples have been carefully selected to illustrate the principles of ion formation and fragmentation, such as the  $\alpha$ -cleavage, retro-Diels Alder mechanism, and, of course, the McLafferty rearrangement. Conceivably, this chapter may have benefited from a few more examples of application of EIMS to structure characterization, but this in no way diminishes its presence in the book.

As everyone knows, the applications of mass spectrometry to the biological sciences are numerous and expanding continuously. In Part III, the author had the daunting task of producing a comprehensive, yet concise representative coverage of the field. This has been accomplished in a way that should satisfy almost every type of user of MS. Moreover, for each class of biomolecules discussed in Part III, the author has included a short summary of other classical methods used for their analysis to place the MS methodologies in a broader perspective. The chapter on peptides and proteins has a nice coverage of the principles for amino acid sequencing of peptides, such as nomenclature for fragmentation in terms of a,b,c/x,v,z ions, immonium ions, and so forth. The CID spectra of two different peptides, in one case the collision induced fragmentation of a singly protonated peptide and in the second that of a doubly protonated parent ion, are discussed in more detail to take the reader through the steps of peptide sequencing. However, I find it a little out of synch that qualitative and quantitative proteomics precedes the aforementioned discussion of the basic principles of peptide sequencing.

Two more chapters are committed to the mass spectrometry of proteins to address topics such as identification of disulfide bonds, post-translational modifications, glyco- and phospho-proteins, and the use of mass spectrometry to evaluate higher-order states and conformational states by H/D exchange and ion mobility methods. A comparison of some ion activation techniques, such as post source decay, electron-transfer (or capture) and collision-induced dissociation, are presented here in conjunction with some of these topics. The mass spectrometry of two other key classes of biomolecules oligosaccharides, lipids, and nucleic acids-follows pretty much the same pattern as that used for the peptides and proteins. There is a clear discussion of the nomenclature for ion fragmentation of biopolymers by MS/MS and this is followed in each case with specific applications.

Even though short in pages, a chapter titled "Miscellaneous Topics" should be very useful to anyone interested in learning about mass spectrometry and its broader value in bioanalytical chemistry. Applications

of mass spectrometry to the study of enzyme kinetics or other types of reaction monitoring processes receive appropriate attention. Some of the "miscellaneous topics" are established areas such as forensic applications and combinatorial chemistry. On the other hand, the reader also has an opportunity to become acquainted with the potential utility of MS techniques to emerging areas of research such as metabolomics, disease biomarkers, and imaging of biological tissues.

A useful feature of the book is the inclusion of an overview section in each chapter that summarizes its most important points. These overview sections provide a nice perspective of the contents of each chapter and are useful whether they are read before or after one has already studied the material. The reader (or student) has an opportunity to review the material and test his/her understanding by tackling the exercises that

have been included at the end of each chapter and are, for the most part, well thought out. In addition, and most importantly, the author has provided an excellent if not exhaustive list of past and current literature citations at the end of each chapter. It is also refreshing to see the inclusion of some historical background in several of the sections, which makes the reader appreciate the current developments. Finally, in terms of its physical appearance, the book is very well designed with easy-to-read print and clear figures.

In summary, the book accomplishes the author's objectives. It provides a thorough coverage of the field of mass spectrometry both in terms of recent technological developments and of its most important applications to the biological sciences. Depending on the instructional circumstances, it can be used as either a full text or a reference text for a graduate course.