

Techniques of Combined
Gas Chromatography/
Mass Spectrometry:
Applications in Organic Analysis

WILLIAM MCFADDEN

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Preface

It is now sixteen years since the first attempt to couple gas chromatography with mass spectrometry.¹ Both of these techniques were proven, powerful analytical tools and their merger was inevitable. Many technical and financial obstacles had to be overcome, but developments of the past decade have successfully reduced these problems. Today, GCMS analysis is applied in every branch of organic chemistry.^{2, 3}

To understand GCMS, the chemist must be knowledgeable in gas chromatography, mass spectrometry, vacuum technology, and computer science. In addition, he must have a feeling for interface problems and the necessary operational modifications. Many excellent textbooks are available for each of the individual disciplines. Unfortunately, these texts give scant consideration to the interface between the combined instruments, and necessary operational modifications are seldom discussed. Vacuum technology, for example, is very important in GCMS, but it is glossed over in almost every standard mass spectrometry text.

The purpose of this book is to provide the organic chemist with a single volume that gives the necessary background for understanding GCMS. Each of the important technologies is considered. Special emphasis is given to the GCMS interface and to the problems and restraints demanded in the combined system.

The text material has been carefully selected from the many questions that have been posed during the ten years in which I have lectured on GCMS. It has always been obvious that a beginner in GCMS is familiar with the problems of gas chromatography but not with those of mass spectrometry. Consequently, the discussion of mass spectrometric instrumentation (Chapter 2) is considerably more extensive than that of gas chromatographic instrumentation. At times, the reader may even feel that Chapter 2 is not directed toward GCMS per se. Nevertheless, every section illustrates some important facet of GCMS. For example, comparison of the two popular double-focusing mass spectrometers (Mattauch-Herzog and Nier-Johnson) is given because of the significant difference that the double-focus mode plays in recording high-resolution mass spectra. The other sections are similarly chosen because of a direct relationship to the overall theme of GCMS.

PREFACE

My experience in computerization of the GCMS system has been as a user rather than as a developer. However, Chapter 7 is not written with the purpose of teaching computer technology, but rather with illustrating the importance of automatic data treatment in GCMS, and evaluating various output options in current use. Throughout the chapter, the reader is continually reminded of the cost of this tool relative to the anticipated use and is urged to evaluate fully both the advantages and disadvantages of automation.

Interpretation of mass spectral data is outside the scope of the present volume and except for a discussion on computer interpretation of GCMS data, the subject has been avoided. There are many excellent textbooks on mass spectral interpretation⁴⁻¹¹ which the reader will find more entertaining than a hurried chapter in a book primarily devoted to GCMS techniques.

The final chapter presents a selection of GCMS applications from several fields of organic chemistry and biochemistry. Originally, I had intended to write this section by the conventional method of reviewing significant papers from the literature. However, such an approach can lead to a sterile review that omits the more exciting, personal facets of a research program. To avoid such flatness, I invited several GCMS users to write a two³ or three-page review of their favorite application. The response was extremely gratifying. Most of the applications have thus been described by the original workers and reflect their interests and enthusiasms. For my part, editorial changes have been minimal, although comments were added to some examples to emphasize specific points. The selfless cooperation of these coauthors has provided an unexpected personal reward, and I will always be indebted for this display of true scientific devotion.

The author also acknowledges the help and encouragement given by his many professional friends and coworkers. Special thanks are due to Dr. A. L. Burlingame for urging me to write this volume and for his support during my stay at the Space Sciences Laboratory. I wish to thank members of the Space Sciences Mass Spectrometry Group who have provided me with data, information, and stimulating discussion.

It is impossible to mention everyone who has worked with me over the past decade and contributed to my appreciation of GCMS, but it is necessary to thank my early coworkers, Drs. Roy Teranishi and Ron Buttery, for contributing indispensable gas chromatographic expertise. Mr. Dale Black, who worked with me from 1961 to 1967 in the mass spectrometry laboratory at Western Regional Laboratories (USDA, Albany, California), deserves special mention for his tireless efforts that assured the success of each new project.

PREFACE

There is an endless list of friends who have given encouragement, have read and criticized parts of the book, have made innumerable suggestions, and have supplied data and information. I thank each of them most sincerely.

Berkeley, California

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1

Introduction

Before the advent of combined gas chromatography/mass spectrometry (GCMS),^{1, 12-14} it was impractical to consider a complete qualitative analysis on a complex organic mixture of 20 components or more. Even the separation and identification of two or three major components could require more than a year's work using classical analytical methods. The minimum quantity of sample needed for each component was usually several milligrams. In contrast, today an organic chemist may submit a mixture containing 100 components (to the 0.1% level) to a GCMS laboratory and expect, within a day or two, some degree of qualitative identification for nearly every peak. Furthermore, this analysis will be performed on less than a milligram of the total mixture. The chromatogram shown in Figure 1.1 provides a typical example. Each numbered peak, including even such miniscule components (less than 0.1%) as peaks 45, 50, 70, 75, etc., was identified.¹⁵

Gas-liquid partition chromatography was first introduced in 1952.¹⁶ The analytical applications of this powerful separation method were recognized immediately, and within three or four years, gas chromatography was used in many laboratories for both qualitative and quantitative organic analysis. Excellent results were easily obtained. The initial success was so exciting that many chemists jested that the other methods of instrumental analysis were obsolete. Quite the contrary. Like any other good research tool, gas chromatography opened up many new analytical problems as it solved old ones.

In its simplest form, qualitative analysis by gas chromatography is performed using the retention time of the unknown as a means of identification. This direct approach may be the best for easy straight-forward analyses, but