LAAN-A-MS-E029

SHIMADZU

Application News

Gas Chromatography Mass Spectrometry No.M263

Effectiveness of Fast Scanning Measurement Using GC×GC-MS

■ Introduction

A GC×GC-MS system (Fig. 1) incorporates 2 chromatographic columns with different separation characteristics, non-polar and polar columns, permitting acquisition of comprehensive 2-dimensional chromatograms by orthogonal separation according to boiling point and polarity. Excellent separation is obtained with an extremely narrow chromatographic peak width on the order of hundreds of milliseconds. Even compounds that are difficult to separate by conventional GC-MS can now be separated using GC×GC-MS. It is an extremely effective system for qualitative analysis, which requires the separation of target substances in complex matrices, common in natural substances, as well as impurity analysis. However, due to the requirement for MS capable of very fast scan speed, quadrupole MS systems have been considered to be unsuitable for GC×GC-MS. The GCMS-QP2010 Ultra resolves this problem with a scan speed as high as 20,000 *u*/sec.

■ Importance of Scan Speed

Components eluted from the first dimension column are concentrated for several seconds in a cryofocusing trap, and are then introduced into the second dimension column, consisting of a 1 to 3 m narrow-bore column, where they are further separated. Due to the extremely narrow bandwidth of peaks eluted from the second dimension column (on the order of hundreds of milliseconds) a very fast MS scan speed is required.
Fig. 2 shows total ion current chromatograms of fatty acid methyl esters acquired using scan speeds of 3,333, 10,000, and 20,000 *u*/sec, and the respective two dimensional GC chromatographic images. It is obvious that the peaks were not resolved at the slower scan speed due to insufficient data acquisition. However, when using a scan speed of 20,000 *u*/sec, it is clear that the peaks were reliably acquired with good separation.

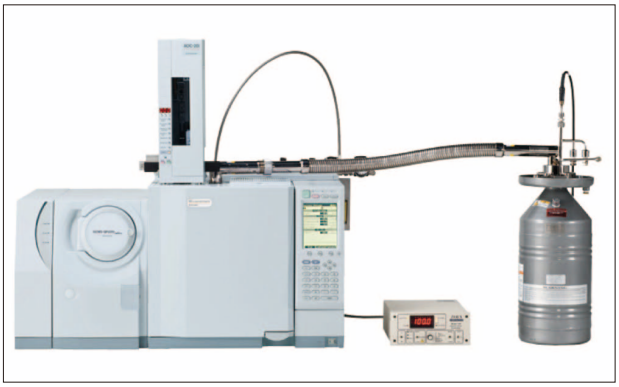

Fig. 1 GC×GC-MS System
(ZX1-GC×GC Modulator + GCMS-QP2010 Ultra)

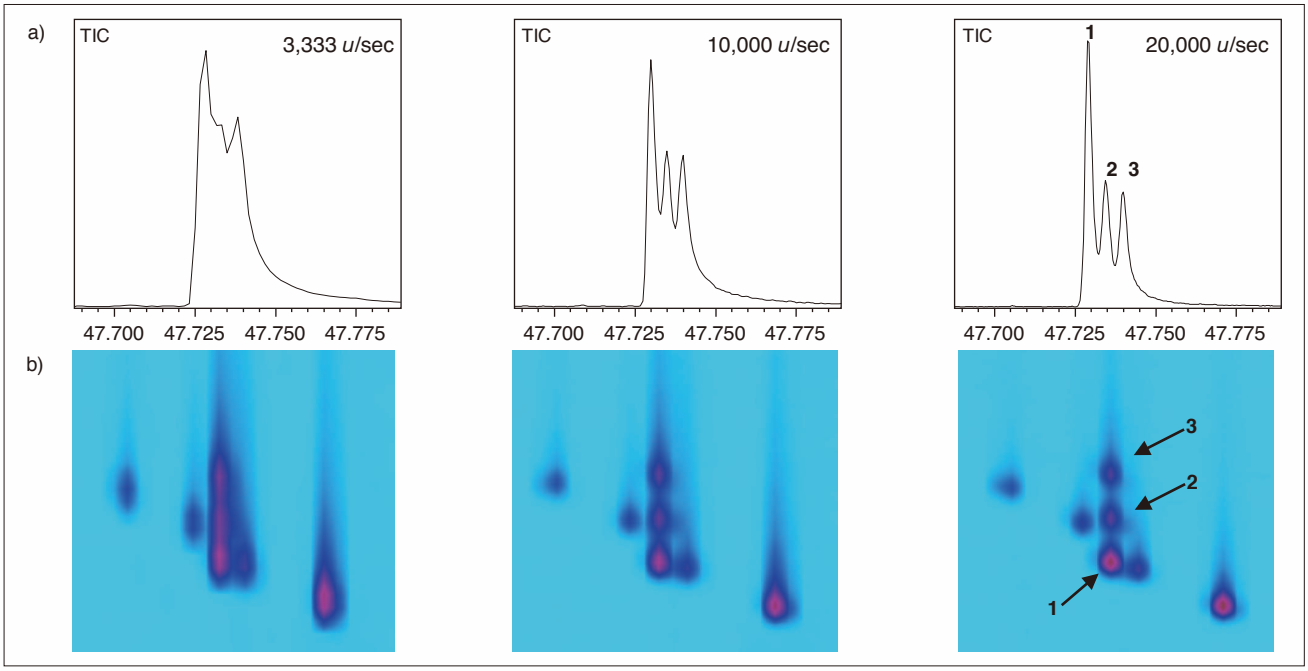

Fig. 2 Analytical Results for Fatty Acid Methyl Esters Using GC×GC-MS
a) Total Ion Current Chromatograms b) Two Dimensional GC Chromatographic Images
1:Methyl oleate (C18:1 ω9, *cis*), 2:Methyl linolelaidate (C18:2 ω6, *trans*), 3:Methyl linolenate (C18:3 ω6, *cis*)

■ Quality of Mass Spectrum

Fig. 3 shows the total ion current chromatogram of stearic acid methyl ester acquired at a scan speed of 20,000 *u*/sec, in addition to the NIST library search results based on the mass spectrum obtained for each data acquisition point. The GCMS-QP2010 Ultra is equipped with special high speed scan control technology (ASSP: Advanced Scanning Speed Protocol), which effectively controls sensitivity reduction in the high mass region. Therefore, any data acquisition point on the peak is sufficient to obtain high-similarity library search results.

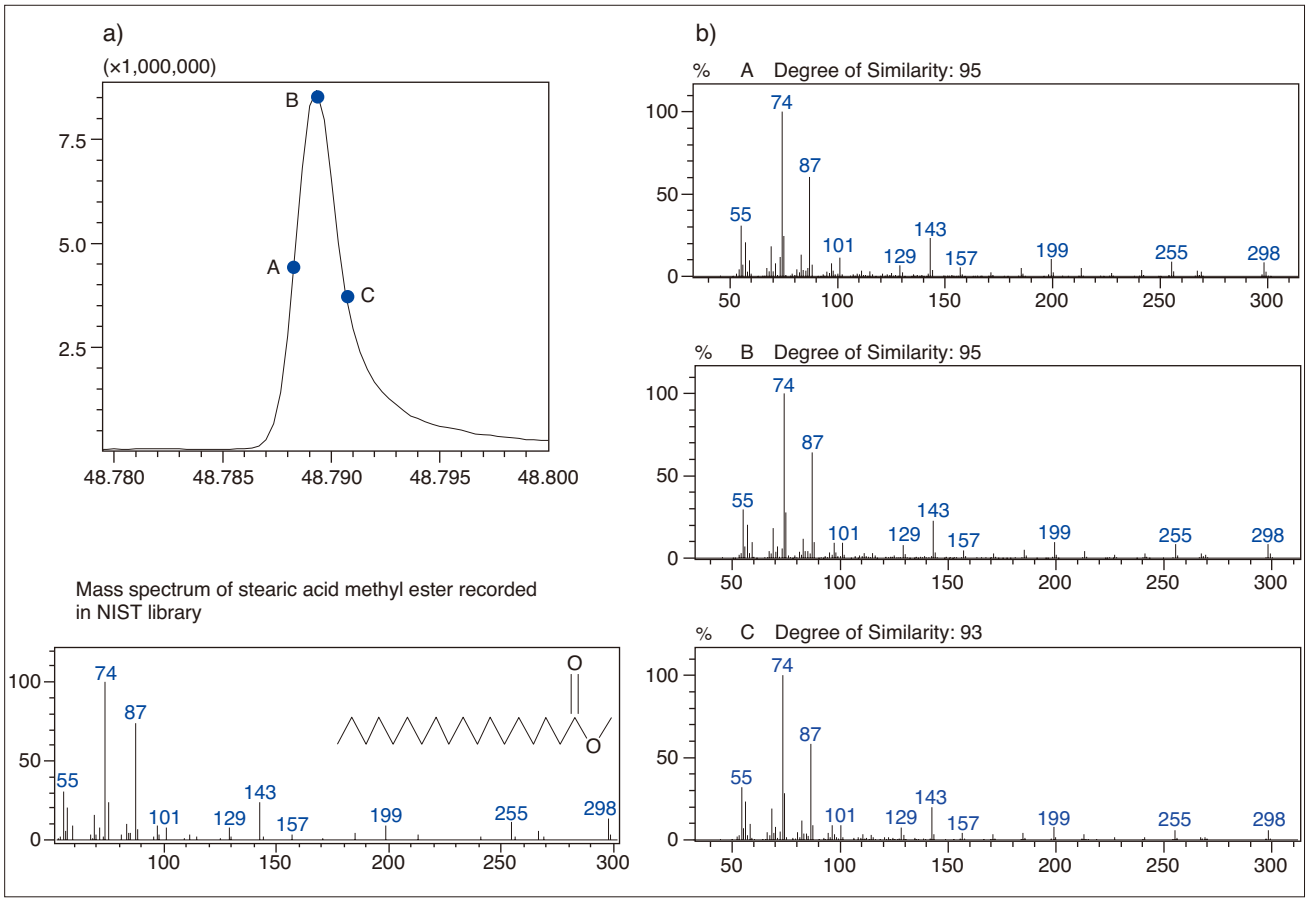

Fig. 3 Analytical Results for Stearic Acid Methyl Ester Using GC×GC-MS
a) Total Ion Current Chromatogram b) Mass Spectrum of Each Data Acquisition Point and Similarity Results Using NIST Library

■ Summary

Excellent peak resolution is obtained with GC×GC-MS; however, very fast MS scan speed is required. The GCMS-QP2010 Ultra, featuring a maximum scan speed of 20,000 *u*/sec, is the best quadrupole mass spectrometer for GC×GC-MS measurement.

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