

## FAST MULTIDIMENSIONAL GC/MS AND COMPREHENSIVE TWO-DIMENSIONAL GC/MS FOR RAPID SCREENING OF COMPLEX SAMPLES

Marriott, Philip

Australian Centre for Research on Separation Science, RMIT University, School of Applied Sciences, GPO Box 2476V, Melbourne 3001, Victoria, Australia

Fast separation methods are now becoming *de rigueur* in the modern analytical laboratory. Whilst in Olympic terms, faster becomes linked with 'higher, longer', we'd like to think that in separation science faster is linked with shorter and smaller. Thus we aim for fast elution peaks (viz. peaks with rapidly changing mass flux in the detector), with lower detectable amounts, and shorter analysis times. This then drives the requirements for the mass spectral transducer to provide adequate scan speed or data acquisition rate to follow the rapid chromatography signal, and provide unbiased mass sampling. Our routine chromatography peaks are of the order of 100 ms wide at basewidth ( $4\sigma$  of the chromatographic band), demanding that a mass spectrum be acquired about every 10 ms. The way we achieve rapid GC separation is to cryomodulate at the end of the primary GC column., passing the zone compressed band into a short second separation column. This then forms the basis for the two-dimensional GC separation techniques that we have pioneered, which will be described in this presentation.

In respect of total analysis time, however, for some methods, we cannot simply time-compress the total analytical process. Rather, we often try to expand the peak capacity within the available time of the regular analysis. This will then provide significant increase in component separation, which normally can only be realised in very long analysis times. Thus the new high capacity analysis is effectively a fast method, when one considers capacity-per-unit-time.

Our high resolution GC methods are based upon two basic technologies: (1) comprehensive two-dimensional gas chromatography (GC $\times$ GC); and (2) rapid sequential targeted multidimensional GC (MDGC). Whilst there is an argument that, for some applications, the need for mass spectrometry decreases as component separation increases, the informing ability of MS should still be considered a critical component of routine sample characterisation and identification.

In this presentation, a selection of the latest studies from our laboratory which demonstrate the technologies described above will be outlined. Thus amino acid analysis, pesticide and pollutant analysis, and some essential oil and petrochemical oil analyses will be used to highlight the principles and general applications of GC $\times$ GC and MDGC, with consideration of the hyphenated MS systems GC $\times$ GC-TOFMS, and MDGC-TOFMS for the identification step.