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# **CHARACTERIZATION OF BACTERIAL LIPID PROFILES BY USING RAPID SAMPLE PREPARATION AND FAST COMPREHENSIVE TWO-DIMENSIONAL GAS CHROMATOGRAPHY IN COMBINATION WITH MASS SPECTROMETRY**

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Mass spectrometry coupled to a gas chromatography (GC) separation is a very powerful tool for the identification of unknown volatile compounds; however, the presence of co-eluting compounds can cause misidentification and quantitative errors. In order to minimize such a problem, the GC separation power can be enhanced by using comprehensive two-dimensional GC. In the latter method, two capillaries with distinct selectivity (positioned together in a single, or individually in two GC ovens) are connected in series, with a transfer device, defined as modulator. The occurrence of peak overlapping is greatly reduced, because this undesirable chromatographic feature would require equal elution times on both columns.

In any GC technique, separation efficiency is related to three parameters: I) column physical parameters and selectivity, II) oven temperature program, III) carrier gas linear velocity. In the present work, all the parameters aforementioned have been optimized by employing a dual-oven GC x GC system and using a split-flow device previously introduced by Tranchida et al. The availability of an oven for each dimension, enables the application of an independent temperature program for each column. Furthermore, the generation of optimum gas linear velocities in both dimensions can be attained by splitting gas flows at the outlet of the first dimension.

In the present investigation, the analytical 2D column will be connected to a rapid-scanning quadrupole MS, while a retention gap will split part of the flow to waste (atmospheric pressure). The optimized GC x GC-MS system will be applied to the analysis of bacterial acid methyl esters (BAMEs), since the bacterial fatty acid profile is an important fingerprint used in taxonomic classification. A very fast sample preparation process (~ 5 min) will be combined with a rapid GC x GC-MS analysis (~ 15-20 min); the latter will be achieved by using a 1D 0.1 mm ID capillary and a 2D 0.05 mm ID column. It will be shown that a specific microorganism can be recognized very rapidly on the basis of GC x GC-MS information.