

# Multimodal Approaches for Untargeted Screening for Medical Applications of the Human Volatilome

Pierre-Hugues Stefanuto;<sup>1</sup> Delphine Zanella;<sup>1</sup> Florence Schleich;<sup>2</sup> Joeri Vercammen;<sup>3</sup> Thibaut Dejong;<sup>1</sup> Monique Henket;<sup>2</sup> Renaud Louis;<sup>2</sup> Jean-François Focant;<sup>1</sup>

<sup>1</sup> Organic and Biological Analytical Chemistry Group, MolSys, University of Liège, Belgium

<sup>2</sup> Respiratory Medicine, GIGA I3, CHU Sart-Tilman, University of Liège, Belgium

<sup>3</sup> ISX and Interscience, Breda, The Netherlands

## Abstract

The ballistic rise of analytical technologies has opened a large playground for all type of untargeted “omics” screening. In that trend, there is a rising interest for the characterization of the human volatilome. Indeed, the characterization and the understanding of the volatile organic compounds (VOCs) production in different *ex vivo* matrices could open the route for improved diagnosis approach and new treatment. In the field of volatilomics, separation science based on multidimensional methods such as comprehensive two-dimensional gas chromatography (GC×GC) appeared as one of the methods of choice for the characterization complex VOC mixtures. At the price of high cost equipment and limited adaptability to routine medical usage, GC×GC offers the possibility to almost completely characterize a sample. For large scale screening, direct introduction instruments such as selected ion flow tube mass spectrometry (SIFT-MS) offered the capacity to perform both targeted and untargeted analyses within a few minutes. SIFT-MS can generate compositional patterns from direct sample introduction at the same time than other routine medical actions. These two orthogonal approaches for pathology screening should ideally conduct to identical sample classifications but have never been directly compared over an identical set of patients.

In order to evaluate their complementarity, breath from 50 well-characterized asthmatic patients were analyzed by both approaches. Breath samples were collected using Tedlar<sup>®</sup> bags. For GC×GC-HRTOFMS analyses, the bags were transferred onto thermal desorption tubes prior to injection. For SIFT-MS, the bags were directly emptied into the instrument. Next, data were analyzed using identical processing workflow. We observed that both approaches offered similar classification capacities. GC×GC-HRTOFMS allowed identifying the putative markers for comparison with previous studies and metabolic interpretation, while SIFT-MS offered a faster screening capacity.