

## EXPLORING THE SCENT OF SILENE BY TD-GC×GC-MS

Damien Eggermont<sup>1</sup>, Steven Mascrez<sup>1</sup>, Natasha Spadafora<sup>2-3</sup>, Fabienne Van Rossum<sup>4</sup>, Giorgia Purcaro<sup>1</sup>

(1) Gembloux Agro-Bio Tech, University of Liège, Passage des Déportés, 2, Gembloux, B-5030, Belgium.

(2) Department of Biology, Ecology and Earth Sciences, University of Calabria, Via Ponte P. Bucci 6b, 87036, Arcavacata di Rende Cosenza, Italy

(3) Markes International Ltd, 1000B Central Park, Western Avenue, CF31 3RT, Bridgend, United Kingdom

(4) Meise Botanic Garden, Nieuwelaan 38, B-1860, Meise, Belgium

*Silene* is one of the largest genera of the world's flora, including about 700 species. Amongst them, the nocturnal moth-pollinated *Silene nutans* appeared to be a species complex comprising at least seven genetically differentiated lineages. Flower scent is known to be involved in the attraction of specific pollinators. We characterized the scent of four reproductively isolated genetic lineages of *S. nutans* from different regions of Western Europe. The volatiles were trapped in controlled chamber conditions using thermal desorption tubes placed at flower proximity among flowering plants. Thermal desorption (TD) enables rapid and robust in-situ sampling of VOCs onto sorbent tubes, which can be capped and safely transported back to the laboratory for analysis. High sensitivity is achieved through pre-concentration of VOCs on a focusing trap prior to GC analysis. Here, we used comprehensive two-dimensional gas chromatography coupled with mass spectrometry (GC×GC-MS) to provide enhanced separation of these complex samples. The pre-concentration effect of TD, combined with improved separation and highly-sensitive detection by GC×GC-MS provided a comprehensive chemical fingerprint in a single analytical run. The differences among lineages and regions were investigated at a first stage using a novel data mining and chemometrics software, which enabled automatic alignment of chromatograms and extraction of useful information in a simple and straightforward way using powerful multivariate statistical analysis, with the attempt to identify characteristic markers.