EXPLORING “EXTRA-DIMENSIONS” TO CAPTURE METABOLITE FINGERPRINTS IN METABOLICALLY HEALTY AND UNHEALTHY OBESE PATIENTS BY GC×GC-TANDEM IONIZATION-TOFMS

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The study exploits the information potential of comprehensive two-dimensional gas chromatography combined with time of flight mass spectrometry (GC×GC-TOFMS) featuring hard and soft ionization in tandem to study changes in saliva and urine metabolic signatures in obese individuals. Samples are taken from two sub-populations of severely obese (BMI> 40 kg/m2) patients, named “metabolically healthy obese” (MHO) and “metabolically unhealthy obese” (MUHO) within a four-week diet plus exercise inpatient program. Saliva and urines samples (24 h) collected at study entry and end are submitted to standard derivatization by oximation-silylation and 2D fingerprints acquired at hard (70 eV) and soft (10-16 eV) ionization energies submitted to pattern recognition by template matching procedures.

Automated Untargeted and Targeted fingerprinting (UT fingerprinting) for 2D data elaboration is adopted for the most inclusive data mining of GC×GC patterns from tandem signals. The UT fingerprinting strategy performs a fully automated peak-region features fingerprinting and combines results from pre-targeted compounds and unknowns across the sample-set. A dedicated work-flow for tandem signals is presented and results are discussed in terms of: absolute sensitivity, S/N ratio, precision and consistency of patterns, complementary information provided by soft ionization fragmentation patterns. Cross-validation and fingerprint data transferability between tandem signals is also discussed in view of a comprehensive exploitation of the all available information.

Metabolites patterns showing statistically relevant differences between sample groups are delineated through different chemometrics while suggesting metabolic derangements to correlate with clinical outcomes. Visual features fingerprinting is also used to track individual variations during dietary intervention and exercise, and represent a valuable tool for personalized metabolomic phenotyping.