KNLe.06

ADDING EXTRA-DIMENSIONS TO PRIMARY METABOLOME PROFILING BY GCXGC -TANDEM IONIZATION TOFMS: INSIGHTS ON HAZELNUT (CORYLUS AVELLANA L.) AROMA POTENTIAL

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This study addresses the primary metabolome of high-quality hazelnuts (*Corylus avellana* L.) from different geographical regions and submitted to different post-processing practices. The characteristic distribution (fingerprint) of primary metabolites, such as mono/di/trisaccharides, amino acids, low-molecular weight acids and amines, if accurately and consistently captured, could become a reliable predictor of hazelnut nutritional and hedonic quality. Most of primary metabolites are known to be precursors of (key)-aroma compounds and potent odorants (lysine and proline/1-pyrroline; lysine and arginine/2-acetylpyrroline; leucine/3-methylbutanal; alanine/pyrazines).

The information potential of comprehensive two-dimensional gas chromatography combined with time of flight mass spectrometry (GC×GC-TOFMS) with hard and soft tandem-ionization in is here applied to accurately delineate samples fingerprints. Samples are submitted to selective extraction/purification and standard derivatization (oximation-silylation) to obtain informative GC×GC patterns on apolar × semi-polar column combination. 2D tandem signals acquired at hard (70 eV) and soft (10-16 eV) electron ionization energies are explored with pattern recognition by template matching procedures and complementary information provided by tandem ionization on compounds fragmentation is evaluated.

Metabolites patterns showing statistically relevant differences between samples are revealed through different chemometrics while suggesting a different aroma potential and consequently hedonic quality.

The correlation between precursors and volatiles formed through Maillard Reaction and Streker degradation (known pathways) during roasting is discussed, thereby validating the approach as a valuable strategy for hazelnut quality assessment.