BOOK OF ABSTRACTS

11th International Symposium on RECENT ADVANCES IN FOOD ANALYSIS

November 5-8, 2024 Prague, Czech Republic

Jana Pulkrabová, Monika Tomaniová, Stefan van Leeuwen, Michele Suman, Michel Nielen and Jana Hajšlová

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(MULTI)OMICS IN FOOD ANALYSIS

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FOOD METABOLOMICS SUPPORTS INDUSTRIAL QUALITY RESEARCH: UNREVEALING COMPOSITIONAL CHANGES IN GERMINATED PEANUTS BY MULTIDIMENSIONAL GAS CHROMATOGRAPHY PLATFORMS

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Peanuts (*Arachis hypogaea*) are among the most widely consumed legumes worldwide due to their nutritional value, taste, and affordability. The quality of peanuts is typically assessed based on their appearance, texture, flavor, and health benefits. Defining a quality standard for the peanut production chain is complex and requires understanding their chemical composition, stability, and sensory properties.

This study aims to investigate a germination defect known as splitting, where the two cotyledons of the peanut separate. Splitting is associated with early germination, leading to premature metabolic activation, which can negatively affect peanut quality by causing dull flavors or increasing the risk of over-roasting. To comprehensively map the chemical composition of peanuts and assess the impact of germination defects on roasted product quality, the study employs omics approaches.

Various peanut fractions were analyzed to understand the impact of germination defects. The study examined primary metabolites (*i.e.*, free amino acids, organic acids, and sugars) after defatting, extraction, derivatization, and subsequent comprehensive two-dimensional gas chromatographytime of flight mass spectrometry (GC×GC-TOF MS) profiling [1]. The lipid fraction was analyzed for the presence of esterified and free fatty acids by dedicated lipid extraction, transesterification of the esterified fatty acid fraction, Fisher esterification for the free fatty acid fraction, and GC-FID analysis [2]. Lastly, the volatile fraction was explored using headspace solid-phase microextraction (HS-SPME) followed by GC×GC-TOFMS analysis.

Results indicate that metabolic activation in split seeds leads to higher concentrations of monosaccharides such as mannitol and glucitol, while aroma precursors like valine, threonine, and sucrose are present in lower amounts compared to whole peanuts. Additionally, meaningful differences were also evident in the amount and distribution of lipids depending on the kernel state (whole *vs.* split). The volatilome confirmed further differentiation between kernel states, with compounds such as 2-pentyl furan and dihydro-3-methyl 2(3H)-furanone showing higher responses in split peanuts.

In summary, this study highlights the significant impact of germination defects on peanut quality, providing valuable insights for defining high-quality peanuts based on chemical and sensory characteristics.

[1] Cialiè Rosso, M., *et al.* Adding extra-dimensions to hazelnuts primary metabolome fingerprinting by comprehensive two-dimensional gas chromatography combined with time-of-flight mass spectrometry featuring tandem ionization: Insights on the aroma potential. *J. Chromatogr. A* 2020, *1614*, 1-11, doi:10.1016/j.chroma.2019.460739.

[2] Cialiè Rosso, M., *et al.* Shelf-Life Evolution of the Fatty Acid Fingerprint in High-Quality Hazelnuts (Corylus avellana L.) Harvested in Different Geographical Regions. *Foods* 2021, *10*, 685, doi:10.3390/foods10030685.

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