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Deciphering the complexity of lipids by hyphenated mass spectrometric methods

Lipids comprise a highly diverse group of biomolecules with various biological functions. However, the role of lipids is less investigated compared to other 'omics'-fields such as genomics or proteomics. In recent years, the importance of lipids for the understanding of numerous diseases and pathological conditions has been recognized, which is why lipidomics has gained in importance and thus, various analytical techniques and methods have been developed.

A relevant lipid category are phospholipids with a variety of different head groups in combination with fatty acid chains featuring different numbers of carbon atoms and double bonds. The already huge structural diversity is further increased by oxidation. High resolution mass spectrometry (HRMS) is capable of identifying lipid species in combination with fragmentation experiments (MS/MS) based on the accurate m/z and fragmentation pattern. For the differentiation of isomeric lipids or isobaric interferences, however, powerful additional separation techniques are required. Furthermore, oxidation of unsaturated lipids poses a special challenge, as they are usually present in low concentrations and further isomeric species, e.g. hydroperoxylated vs dihydroxylated products.

Hence, powerful multidimensional analysis techniques are required for the analysis of the diversity of phospholipids and their oxidation products. The presented hyphenated mass spectrometric approaches provide increased information content and peak capacity for in-depth phospholipid characterization.