Mass Spectrometry Strategies for Lipids and Low Molecular Carbohydrates Analysis

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LC-ESI-MS and GC-MS were the most important techniques currently devoted to structural analysis, being employed to several sciences, such as chemistry, biology, medicine and forensics. Many classes of low molecular biomolecules, such as glycosides, oligosaccharides and several lipids have been identified by mass spectrometer. Using different ionization sources we have been improving the determination and composition of the biomolecules and their molecular mass. The use of different adducts (Li^+, Na^+ and K^+) on ESI-MS resulted different fragmentation behavior of oligosaccharides. Li^+ ions produced more fragments with lower energy and different fragment ratios, giving rise to distinct patterns for glycosidic and linkage configuration. ESI-MS ionization was standardized for phospholipids and glycolipid analysis. A comprehensive lipid profile was carried out from archaea *Haloarcula marismortui* and many phospholipids and a glycolipid were identified by negative and positive ESI-MS analysis, indicating the presence of archaeol, a structure with two branched alcohols with 20 carbons (geranylgeraniol), bond to glycerol via eter linkages. Using GC-MS and adapting the reduction/acetylation strategies, we had performed the derivatization of all monosaccharide class, as well as amino acids and OH-fatty acids as from different glycoconjugates. Uronic acids gave characteristic ions at m/z 143, 156 and 173, and amino acids derivatives gave molecular ions $[M]^+$ and daughter ions of $[M-59]^+$ and $[M-43]^+$ on EI-MS, which provide their rapid identification. Lipid analysis by GC-MS showed sphingosine, cholesterol and 1-*O*-alkylglycerolipids ethers with characteristic ions at m/z 43, 59, 117, 159 and $[M-59]^+$; $C_{16:0}$ (342 m/z), $C_{16:1}$ (340 m/z), $C_{17:0}$ (354 m/z), $C_{17:1}$ (352 m/z), $C_{18:0}$ (368 m/z) and $C_{18:1}$ (366 m/z) were detected in biological tissues as acetate derivatives.

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