

Qualitative and Quantitative Mass Spectrometry in Salivary Metabolomics and Proteomics

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Streszczenie

The metabolomics and proteomics analysis of saliva, an excellent biofluid that is a rich source of biological compounds, allows for the safe and frequent screening of drugs, their metabolites, and molecular biomarkers of various diseases. One of the most frequently used analytical methods in saliva analysis is liquid chromatography coupled with mass spectrometry (LC-MS) and tandem mass spectrometry. The low ionisation efficiency of some compounds and a complex matrix makes their identification by MS difficult. Furthermore, quantitative analysis by LC-MS frequently cannot be performed without isotopically labelled standards, which usually have to be specially synthesised. This review presented reports on qualitative and quantitative approaches in salivary metabolomics and proteomics. The purpose of this manuscript was to present the challenges, advances, and future prospects of mass spectrometry, both in the analysis of salivary metabolites and proteins. The presented review should appeal to those interested in the recent advances and trends in qualitative and quantitative mass spectrometry in salivary metabolomics and proteomics, which may facilitate a diagnostic accuracy, the evaluation of treatment efficacy, the early diagnosis of disease, and a forensic investigation of some unapproved drugs for any medical or dietary administration.

Słowa kluczowe

saliva, metabolomics, proteomics, LC-MS, quantitative analysis, isobaric labelling reagents, ionisation enhancers, isotopically labelled standards

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