Profiling small molecules for insights into biological systems throughGC-MS based metabolomics.

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Description

Gas Chromatography-Mass Spectrometry (GC-MS) is a powerful analytical technique widely employed in metabolomics, enabling the comprehensive analysis of small molecules in biological samples. Metabolomics aims to understand the global metabolic profile of a biological system, offering insights into its functional state [1]. Gas Chromatography-Mass Spectrometry (GC-MS) has emerged as a vital tool for metabolomic studies, enabling the simultaneous detection and quantification of a broad range of small molecules. GC-MS combines two complementary analytical techniques: Gas Chromatography and Mass Spectrometry [2]. In GC, metabolites are separated based on their volatility and affinity for a chromatographic column. The eluted compounds then enter the mass spectrometer, where they are ionized and fragmented, generating mass spectra. GC-MS is indispensable in drug discovery. It's used for identifying and quantifying drug compounds, studying their pharmacokinetics, exploring metabolomics for biomarker discovery, ensuring product quality and safety through impurity analysis, and accelerating drug development by providing essential analytical insights [3]. GC-MS enhances the efficiency and precision of drug research, helping researchers select promising candidates, understand their behaviour in biological systems, and ensure product quality, ultimately leading to safer and more effective medications [4].

Effective sample preparation is crucial in metabolomics. Biological samples, such as blood, urine, or tissue extracts, require extraction and derivatization to improve volatility and stability. Sample preparation steps must be optimized to ensure the accurate representation of the metabolome [5].

GC-MS generates complex data sets consisting of mass spectra and retention times. Data preprocessing involves peak detection, alignment, and normalization. Identification of metabolites is achieved by comparing mass spectra with reference libraries. Quantification is typically performed using internal or external standards. Advanced statistical and bioinformatics tools are employed to analyze the resulting data, identifying biomarkers and metabolic pathways associated with specific biological states or conditions [6].

With its capacity to analyse a broad variety of metabolite classes, high sensitivity, and repeatability, GC-MS in metabolomics has a number of benefits. It does have drawbacks, though, such the requirement for derivatization for certain metabolites and the potential inapplicability for strongly polar or non-volatile substances. Complementary methods, such as Liquid Chromatography-Mass Spectrometry (LC-MS), are frequently employed in conjunction with Gas Chromatography-Mass Spectrometry (GC-MS) in metabolomics investigations to offer a more thorough picture of the metabolome [7-10].

In conclusion, GC-MS is crucial to metabolomics because it makes it possible to thoroughly profile metabolites in biological materials. It has transformed our understanding of metabolism and offers insightful information in a number of areas, including as biomarker identification, illness diagnostics, medication development, and environmental studies . Despite its strengths, GC-MS in metabolomics faces challenges such as limited coverage of non-volatile and polar metabolites. Future developments should focus on enhancing the analytical capabilities of GC-MS, expanding its metabolite coverage, and improving the integration of data from multiple analytical platforms. Gas Chromatography-Mass Spectrometry (GC-MS) is a versatile and indispensable tool in metabolomics, enabling the comprehensive analysis of small molecules in biological systems. Its applications range from biomarker discovery to environmental and nutritional studies. Recent advancements and ongoing research hold promise for further expanding the utility of GC-MS in unraveling the complexities of metabolism and advancing our understanding of biological systems.

References

1. Kind T, Wohlgemuth G, Do Y L, Yun L, Mine P et al. (2009). FiehnLib: Mass spectral and retention index libraries for metabolomics based on quadrupole and time-of-flight gas chromatography/mass spectrometry. Anal Chem 81(24): 10038-10048.
2. Dunn, Warwick B, Paul B, Eva Z, Sue FM et al. (2011) Procedures for large- scale metabolic proiling of serum and plasma using gas chromatography and liquid chromatography coupled to mass spectrometry . Nature Protocols 6(7): 1060-1083.
3. Ralf T, Kevin C, Winnie U, Zhengjiang Z, Gary JP et al. (2012) An accelerated worklow for untargeted metabolomics using the METLIN database Nature Biotech 30 (9) 826-828.

4. Marielle D, Danilo G, Maxime S, Karim A, Eric G (2013) High-throughput and sensitive quantitation of plasma catecholamines by ultraperformance liquid chromatography-tandem mass spectrometry using a solid phase microwell extraction plate. Anal Chem 85(7):3539-3544.
5. Yu RL, Ji Won L, Jongki H, Bong C (2021) Simultaneous determination of polyamines and steroids in human serum from breast vancer patients using liquid chromatography–tandem mass spectrometry . Molecules 26(4): 1153.
6. Emilia M, Maria A, Marta T, Magí F, Roberta P et al. (2021) Ultra-High Performance Liquid Chromatography-High resolution mass spectrometry and high-sensitivity gas chromatography-mass spectrometry screening of classic drugs and new psychoactive substances and metabolites in urine of consumers applied microbiology and biotechnology . Int J Mol Sci 22(8): 4000.
7. Oliver Fiehn (2016) Metabolomics by gas chromatography-mass spectrometry: the combination of targeted and untargeted profiling . Curr Protoc Mol Biol 114:30.
8. Jia T, Alice C , Gwen D, Laís AA, Omer N et al. (2021) Assessing the oestrous cycle in a mouse model using portable and benchtop gas chromatography-mass spectrometry. R Soc Open Sci 8(9): 210172.
9. Dimitrios Tsikas (2023) GC–MS and GC–MS/MS measurement of malondialdehyde (MDA) in clinical studies: Pre-analytical and clinical considerations. J Mass Spectrom Adv Clin Lab 30: 10–24.
10. Andrea M, Juan C, Anja W, Claudia B (2023) A comparison between mobile and stationary gas chromatography–mass spectrometry devices for analysis of complex volatile profiles . Anal Bioanal Chem 415(1): 137–155.

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