

METABOLOMICS: TOOL FOR CELLULAR PROCESS

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Introduction

Metabolomics is a multidisciplinary field of research that delves into the intricate chemical processes undergone bv metabolites, which are the end products of cellular metabolism. It encompasses the systematic study of a diverse range of metabolites present in cells, organs, and tissues, as well as their dynamic alterations in response to disease states, environmental factors, and other stimuli over time (Idle et al., 2007). Metabolome refers to the complete set of small-molecule. Metabolites to be found within a biological sample, such as a single organism. Metabolite is defined as any naturally occurring or endogenous organic molecule that can be detected within the body, typically characterized by a relatively low molecular weight of less than 1500 Daltons (Da). This diverse category encompasses a wide range of biomolecules, including peptides, oligonucleotides, simple sugars, nucleosides, organic acids, ketones, toxins, pharmaceutical drugs, food-derived metabolites and additives, lipids, amino acids, and various another low-molecularweight compound

OMICS of Biology:

Genomics (DNA) → Transcriptomics (RNA) → Proteomics (Proteins) → Metabolomics (Metabolites)

1. **Genomics (DNA)**: The study of the complete set of genetic instructions encoded in an organism's DNA, revealing potential genetic predispositions and possibilities.

- 2. **Transcriptomics (RNA)**: The analysis of the transcriptome, comprising all RNA transcripts, to understand gene expression and identify apparent cellular activities.
- 3. **Proteomics (Proteins)**: The systematic study of proteins, including their structure, function, and interactions, to uncover the molecular mechanisms driving biological processes.
- 4. **Metabolomics** (Metabolites): The comprehensive analysis of metabolites, the end products of cellular metabolism, to reveal the dynamic biochemical changes and precise events occurring within cells and organisms.

Why Metabolomics?

- As we transition from analysing DNA to investigating the metabolome, the complexity and variability of the data increase exponentially. This escalation in variability unlocks a treasure trove of information, given that DNA and RNA are comprised of merely 4 bases, proteins are constructed from 20 amino acids, and metabolites encompass a vast, diverse array of compounds.
- The metabolome is inextricably linked to an organism's genotype, physiology, and environmental interactions, rendering metabolomics an unparalleled tool for elucidating both genetic and phenotypic aspects (Shulaevet al., 2007).
- Metabolites represent the culmination of intricate cellular pathways, enabling researchers to pinpoint subtle changes or aberrations at the cellular level.

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 Crucially, not all genomic or transcriptomic anomalies necessarily manifest as observable phenomena. Moreover, these approaches often overlook the profound impact of environmental factors on subsequent stages of biological processes

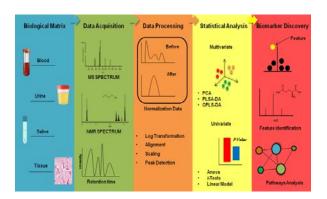
Metabolic Profiling:

A comprehensive, quantitative analysis of a specific subset of metabolites, including both known and unknown compounds, that are directly involved in or associated with a particular metabolic pathway (Roessner*et al.*, 2009) This approach provides detailed insights into the metabolic flux and regulation within the pathway.

Metabolic Fingerprinting:

A high-throughput, semi-quantitative method that rapidly assesses a select subset of metabolites, generating a unique metabolic "fingerprint" or signature (Putriet al., 2013). This approach involves minimal differentiation or quantitation of individual metabolites, instead focusing on recognizing patterns and correlations within the metabolic profile

Basic Workflow of Metabolomics



- 1. Sample collection, treatment, and processing
- 2. Separation techniques:
 - o GC-MS, GC
 - LC-MS
 - o HPLC, UPLC
 - Capillary Electrophoresis

- 3. Detection techniques:
 - o NMR, MS
- 4. Data analysis using multivariate analysis (e.g., PCA, pathway mapping, PLS, heat maps, orthogonal PLS)
- 5. Validation followed by clinical trials

Conclusion:

As metabolomics continues to evolve as a cutting-edge field, leveraging highthroughput technologies, significant strides have been made in sequencing numerous organisms and refining methods for analyzing cellular products derived from proteins. Currently, robust and relatively efficient technologies are in place for acquiring metabolome data, paving the way for future innovations. The development of more sophisticated and practical techniques for data analysis and interpretation is anticipated, facilitating a deeper understanding of the intricate relationships between molecular biology, the metabolome, and organismal health, and ultimately yielding practical applications in fields like personalized medicine, biomarker discovery, therapeutic development

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