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Clayton S. Bloszies, Oliver Fiehn

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Using untargeted metabolomics for detecting exposome compounds

Clayton S. Bloszies[a] and Oliver Fiehn[a,b]

[a]NIH West Coast Metabolomics Center, University of California Davis, Davis, CA, 95616, United States

[b]Department of Biochemistry, King Abdulaziz University, Jeddah, Saudi-Arabia

Corresponding Author:
Oliver Fiehn, PhD
University of California, Davis
NIH West Coast Metabolomics Center
Genome and Biomedical Sciences Facility (GBSF)
451 Health Sciences Drive, Room 1313
Email: ofiehn@ucdavis.edu

Highlights

- Chronic diseases are influenced by gene-environment interactions.
- While the genome has already been characterized, a better understanding of the exposome is necessary to fully understand disease phenotypes.
- Untargeted metabolomics is perfectly suited to handle the complexity and breadth of the chemical exposome, and should be used to complement existing targeted methods.
- Through various mass spectrometric techniques, untargeted metabolomics allows for the detection of both exposure compounds and the phenotypic variation caused by exposure compounds.

Abstract

The exposome is the summary of all chemical and non-chemical exposures over an individual's lifetime that collectively describe all non-genetic factors that may influence phenotype. While advances in genomics have significantly improved the understanding of chronic disease, they have also highlighted the need for better characterization of exposure. Untargeted metabolomics should complement targeted methods for quantitative and reliable analysis of exposome compounds in biological matrices. Using an existing workflow consisting of untargeted instrumental acquisition, analyte annotation using library matching, unknown identification, and data visualization, environmental effects on endogenous metabolites can be assessed by accurate and comprehensive exposure analysis.

Genome wide association studies do not explain complex disease phenotypes

In recent years, it has become clear that the environment has more impact on disease phenotype than originally thought [1]. While the Human Genome Project and the subsequent Genome-wide Association Studies (GWAS) have been successful in elucidating associations between genotype and phenotype [2], much of phenotypic variation remains unexplained for chronic diseases [3]. GWAS studies are designed to get a better understanding of heritability, a measure of the proportion of total phenotypic variability explained by genomic variability.