biocrates
The future of research and health

Zooming into your favorite metabolic pathway: Combining broad and targeted metabolite profiles for a deeper understanding of the metabolome

Abstract

Metabolomics and lipidomics face two main challenges: comprehensive coverage and interpretation of the results in a broader context. Comprehensive targeted metabolomics solutions go beyond broad coverage and provide reliable, reproducible, and quantitative analysis. However, even when these requirements are met, interpretation and biological relevance can remain a challenge. For an experiment to move beyond analytical measurement, metabolites must be placed in context through pathway analysis. Through incorporating multiple metabolites across various pathways, results are not limited to the analysis of individual metabolite concentrations. Rather, pathway integration enables results to be interpreted in the broader context of diverse, and often interconnected, pathophysiological processes. Here, we suggest a workflow maximizing the output of metabolomics experiments by using broad and targeted profiling approaches synergistically with innovative approaches for functional data interpretation.

As no single method can quantify the complete metabolome, a multiplexed method covering up to 630 metabolites and lipids from 26 compound classes (MxP® Quant 500 kit) offers an attractive solution for high-throughput hypothesis generation. Functional interpretation of results using the MetaboINDICATOR™ software tool allows for the inclusion of 234 pre-defined sums and ratios, as well as user-defined sums and ratios, into the statistical analysis, providing immediate links to alterations in pathophysiological processes (e.g. inflammation, gut microbial dysbiosis, etc.). This initial broad, hypothesis-generating analysis covers key metabolites and can reveal elevated and decreased levels of various metabolites, allowing for further "zooming" into individual pathways. These individual pathways can be subsequently analyzed with specific assays (e.g. for bile acids, tryptophan metabolites, acylcarnitines) to verify and strengthen the generated hypotheses. Through the combination of broad and pathway-specific targeted assays, biocrates addresses the two main challenges of metabolomics. Specifically, biocrates' kit technology offers improved analytical sensitivity and biocrates' MetaboINDICATOR™ software aids in the interpretation of results within a broader context.

Speaker Bio

Dr. Marissa Jones earned her Ph.D. at Vanderbilt University where she focused on analytical chemistry and mass spectrometry under the direction of Prof. Richard Caprioli. During her time at Vanderbilt, her research focused on developing multimodal imaging tools including mass spectrometry and various forms of microscopy to investigate lipids in the spleen that are integral to adaptive immunity. Dr. Jones is currently part of biocrates life sciences as a business development manager for the Midwest region with the goal of connecting scientists to cutting-edge metabolomics technologies to help them excel in their clinical and multi-omics research.