Docket #: S16-456

Universal metabolomics analysis of biological samples by LC-MS/MS

Researchers at Stanford have developed a simplified LC-MS/MS metabolomics analysis method that requires only a single injection to analyze both polar and non-polar molecules with high resolution of isomeric compounds. Most diseases cause fluctuations in metabolic concentrations. Detection and analysis of these fluctuations can be used for disease diagnosis. Current metabolomics analysis techniques using high resolution mass spectrometry (MS) exist, but are non-optimal as they require 4 injections to separate polar and non-polar molecules. This requires more sample, uses more instrument time and can introduce more error. To overcome these limitations the inventors have developed this LC-MS/MS method. It requires only a single injection of a minute amount of sample and can analyze the full range of polar and non-polar molecules with high resolution of clinically important isomeric compounds. Further, both polar and non-polar molecules can be eluted using an identical gradient. This simplified metabolomics analysis method can be used to improve disease diagnosis and for research.

Stage of research
Initial validation studies show great promise. Additional work is ongoing.

Applications

- Metabolomics analysis for:
    - Disease diagnostics
    - Research

Advantages

- Requires only 1 injection:

    - Minimizes instrument time
    - Requires only small amount of sample
    - Reduces potential for error
    - Reduces redundant data
- Provides high resolution of clinically important isomers
- Can capture both polar and non-polar molecules
- Uses identical gradient to elute both polar and non-polar molecules for analysis

Patents

- Published Application: 20210364498
- Issued: 11,906,510 (USA)

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