Lipidomics profiling and fingerprinting methodology

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Organisation

Name of the organisation Ghent University (UGent)

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Country Belgium

Geographical Area Flemish Region

SCOPE OF THE METHOD

The Method relates to	Animal health, Environment, Human health
The Method is situated in	Basic Research, Translational - Applied Research
Type of method	In chemico: Lipidomics

DESCRIPTION

Method keywords

metabolomics

lipidomics

Lipids

profiling

fingerprinting

feces
urine
mass spectrometry
Liquid chromatography
cell culture
colon tissue

Scientific area keywords

analytical chemistry
metabolic disorders
inflammation
biofluids
food allergy
cancer research

Method description

Our lipidomics profiling and fingerprinting methodology enables the analysis of all lipids within a biological matrix. These lipids can then be compared between an individual or condition with a specific metabolic state and healthy controls to find biomarkers or pathways that can be related to diseases. It applies ultra-high performance liquid chromatography coupled to hybrid quadrupole-Orbitrap high-resolution mass spectrometry. Both the instrumental method, as well as generic extraction protocols for colon tissue, cell cultures, blood, urine and feces have been extensively validated in both a targeted as well as an untargeted fashion. The lipidomics workflow consists of a sample preparation, followed by the UPHLC-HRMS analysis, after which multivariate statistical analysis will be performed to identify potential biomarker candidates or altered pathways, associated with a specific metabolic state.

Lab equipment

UHPLC ;
HR-Orbitrap-MS.

Method status

History of use

Internally validated

Published in peer reviewed journal

PROS, CONS & FUTURE POTENTIAL

Advantages

Lipids are involved in a plethora of biological processes, including energy homeostasis, immune response, membrane architecture, enzyme activity, inflammation, cellular signaling and transduction of cellular events. Evidently, a dysregulated lipid metabolism has been implicated in a variety of pathological conditions. Therefore, the measurement of this lipidome, which is at the end of the genome-transcriptome-proteome cascade, will provide the most holistic image of the phenotype of a patient. Additionally, it provides both a qualitative as well as a quantitative functional read-out. Therefore, it can be considered the method of choice for hypothesis testing and hypothesis generation.

Challenges

Multi-step procedure => Long analysis time, extensive sample preparation.

Big data handling.

Modifications

The method can be adapted to other matrices or other animal species when necessary.

REFERENCES, ASSOCIATED DOCUMENTS AND OTHER INFORMATION

References

Van Meulebroek et al (2017)

Analytical Chemistry Rombouts et al (2019)

Analytica Chimica Acta De Spiegeleer et al (2019) submitted

Associated documents

Van Meulebroek et al. 2017.pdf

Rombouts et al, 2019.pdf

Links

Van Meulebroek et al, 2017

Rombouts et al, 2019

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