Polar metabolomics profiling and fingerprinting methodology

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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: Metabolomics
This method makes use of	Animal derived cells / tissues / organs

DESCRIPTION

Method keywords

metabolomics

mass spectrometry

Liquid chromatography

metabolic profiling

Metabolism

metabolic fingerprinting

biofluids

urine

feces

saliva

blood

cell culture

colon tissue

Scientific area keywords

analytical chemistry
metabolic disorders
inflammation
biofluids
cancer research
food allergy

Method description

Our polar metabolomics profiling and fingerprinting methodology 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, urine, feces, plasma and saliva have been extensively validated in both a targeted as well as an untargeted fashion. The metabolomics 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

HPLC ;
HR-Orbitrap-MS.

Method status

Internally validated
Published in peer reviewed journal

PROS, CONS & FUTURE POTENTIAL

Advantages

The metabolome is considered as the endpoint of metabolism and is therefore influenced by amongst others the genes, the diet, the environment and the residing

microbiome. As such, the measurement of the metabolome provides 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

Vanden Bussche et al (2015)
Analytical Chemistry, 87, 10927-10934 De Paepe et al (2018)
Analytica Chimica Acta, 1033, 108-118 Rombouts et al (2019)
Analytica Chimica Acta, 1066, 79-92 Wijnant et al (2019) submitted
De Spiegeleer et al (2019) submitted

Associated documents

De Paepe et al, 2018.pdf
Rombouts et al, 2019.pdf
Vandenbussche et al, 2015.pdf

Links

Rombouts et al, 2019
De Paepe et al, 2018
Vanden Bussche et al, 2015

PARTNERS AND COLLABORATIONS

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