LC-MS and GC-MS methods for sweat analysis as alternative biofluid in metabolomics

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Background: Sweat is a promising but still insufficiently studied matrix in the field of metabolomics research. Compared to blood, saliva, hair, or urine sweat appears less complex, since the concentration of proteins (saliva), lipids, phospholipids (blood), or urea (urine) are significantly lower. Therefore, the sample preparation process for mass spectrometry might be simplified. From a diagnostic point of view, the analysis of this alternative biofluid is an opportunity to find yet undiscovered biomarkers. Sweat represents short term ongoing metabolic processes comparable with blood or saliva.[1–3] The sampling allows theoretically the access to samples from people outside of a hospital, without an additional infection risk. This is important to support diagnostics in low-income countries, especially for vulnerable patients such as children. However, one of the challenges of sweat analysis is the low concentration of biomarkers and the low sample volume (25 – 200 µL). Methods for the analysis of sweat using LC-MS and GC-MS have been developed to investigate potential markers for tuberculosis. However, this contribution focusses on the development and execution of the methodical part only.

Method: Sweat samples were collected using an iontophoresis technique combined with pilocarpine. To achieve sufficient statistical data (including technical replicates), the methods were optimized to operate with a sample volume of less than 30 µL. Measurement were performed on a LTQ Orbitrap XL LC-MS and a Leco GC-TOF-MS. For the GC-TOF-MS analysis, a method based on Fiehn (2016)[4] was developed.

Results: By LC-MS, about 6400 features were found. Typical amino acids and even antibiotic drugs have been detected. By GC-TOF-MS 128 metabolites out of about 2800 detected features have been identified by retention time index and electron impact spectra matched with the Fiehn Library.

Conclusion: LC-MS and GC-MS are feasible approaches for sweat analysis if sufficient sample volume is available. The basis for future studies, including specific sampling recommendations, was developed.

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