

Identification of markers for dietary intake and health status by GC-MS based metabolite profiling approaches

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ABSTRACT

Metabolomics and metabolite profiling approaches increasingly gain significance for marker discovery. Identification of dietary markers will complement and verify traditional dietary assessment methods, which will improve investigations of associations between diet and health(1). Metabolomics and metabolite profiling approaches also enable a more comprehensive investigation of markers for diagnosis, prognosis and monitoring of diseases, such as type 2 diabetes mellitus. Within this work, the application of GC-MS based metabolite profiling approaches (volatile organic compounds and sugar compounds) was evaluated for identification of markers of dietary intake using urine samples from a cross-sectional study with 300 participants, and for markers of health status using plasma samples from a human intervention study with diabetic, prediabetic and healthy participants.

So far, dietary markers were mostly identified from among the non-volatile metabolites. An analysis of the urinary volatilome using an untargeted HS-SPME-GC×GC-MS method revealed candidate markers of coffee consumption and further correlations with general dietary intake. The volatilome was highlighted as an interesting source of new dietary markers.

In most studies, only well-known sugar compounds are analyzed in human body fluids due to analytical issues. Our newly developed semitargeted GC-MS sugar profiling method revealed a more complex sugar profile in urine and plasma than expected(2). The sugar profiling method enabled the identification and confirmation of several new and known marker candidates (e.g. for consumption of avocado, dairy products and alcohol). After an oral glucose tolerance test, the plasma sugar profiles of healthy, prediabetic and diabetic volunteers could be clearly distinguished and a variety of sugar compounds (e.g. trehalose) showed marked postprandial differences dependent on health status. Transferring the one-dimensional method into a two-dimensional GC×GC-MS method further improved sensitivity and separation of sugar compounds, enabling detection of 84 sugar compounds in urine. Overall, results from application of the sugar profiling illustrate the benefit of a comprehensive analysis of sugar compounds in body fluids.

We demonstrated that the GC-MS based metabolite profiling approaches for volatile and sugar compounds are promising approaches for the identification of markers of dietary intake and health status. Future work needs to address identification of unknown compounds, quantification of sugar compounds, and validation of the discovered marker candidates. Moreover, the elucidation of the origin and underlying biological mechanisms for several sugar compounds should be prioritized.

1. Scalbert A, Brennan L, et al. (2014) Am J Clin Nutr 99, 1286-1308.
2. Mack CI, Weinert CH, et al. (2018) Am J Clin Nutr 108, 502-516.

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