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METABOLIC PROFILING OF SERUM FROM PATIENTS WITH CHRONIC KIDNEY DISEASE BY GC-MS

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Abstract

Chronic kidney disease (CKD) is a worldwide public health problem with an increasing incidence, poor outcomes and high cost. Patients with CKD suffer from a progressive loss of glomerular filtration. The kidneys lose the capacity to remove potentially toxic compounds from the blood stream into the urine, resulting in their accumulation in the body. The accumulation of these toxins has a negative impact on many body functions. Consequently, CKD is a complex disease that often affects multiple organ systems and coexists with numerous associated conditions of which cardiovascular disease is a highly important one. Unfortunately, CKD is usually detected in one of its later stages. In the search for CKD biomarkers we developed a serum based GC-MS platform. A derivatization method using oximation and silylation was optimized and applied to extracts originating from 49 patients in the different CKD stages and 10 healthy controls. The resulting data were treated with XCMS followed by multivariate statistical analysis and metaXCMS. Differentiation was achieved between the metabolic profile of the CKD patients and controls. The biomarker candidates have to be investigated and confirmed in prospective studies.

Keywords: GC-MS, metabolomics, chronic kidney disease, uremic toxins, biomarkers