

Metabolomics Reveals TMAO as a Potential Marker and Intervention Target for Chronic Kidney Disease

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Commentary

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ABOUT THE STUDY

Chronic Kidney Disease (CKD) is an important cause of all-cause mortality, with a global prevalence of 9.1% in 2017 and a year-on-year increase in recent years. Since most CKD patients have irreversible kidney damage, CKD patients will gradually progress to End-Stage Renal Disease (ESRD) under the interaction with multiple pathological factors and thus have to receive renal replacement therapy, which not only brings great suffering to patients and their families but also a heavy burden to the society^[1]. Therefore, it is important to reveal the pathogenesis of CKD and find effective interventions to delay the progression. Recently, metabolomics has been widely used to study the pathogenesis of diseases and discover potential biomarkers by qualitatively and/or quantitatively analysing changes in the metabolome during the development of diseases. Metabolomics is a developing research area of nephrology, which has also been well-documented ^[2-4]. Metabolomics can be used as a systematic tool to provide new insights into CKD pathogenesis.

medium, provided the original author and source are credited.

Recently Hu et al, used an LC-MS/MS-based non-targeted metabolomics to analyze the plasma samples from uremic patients and healthy controls, the key findings of which were further quantitatively validated in stage I-V CKD patients, where they found a significant correlation between blood Trimethylamine N-oxide (TMAO) concentrations and CKD progression^[5]. Subsequently, cellular and animal models were used to demonstrate that decreased production of TMAO attenuated kidney injury, at least in part, by mitigating the renal fibrosis involved in the down-regulation of α -Smooth Muscle Actin (α -SMA).

TMAO is a dietary metabolite of choline, L-carnitine, and betaine and has been reviewed as a risk factor for multiple health outcomes, including cardiovascular and cerebrovascular diseases, type II diabetes, hypertension, and renal dysfunction^[6,7]. Recently, attention has been growing on the role of TMAO in the development of CKD. Previous studies have found that plasma TMAO levels are significantly higher in CKD patients than those of controls and that elevated plasma TMAO levels are associated with poorer long-term survival^[8,9]. TMAO levels can be a potential risk factor for the development of CKD, but the role of TMAO in the progression of CKD disease and the underlying mechanisms remain largely unknown. In this article, Hu et al.'s research reveals that 1) plasma TMAO is positively correlated with renal dysfunction in patients with CKD at different stages, and 2) manipulation of TMAO may be a potential approach to retarding CKD progression.

Hu et al.'s study also left many to be further explored, including but not limited to 1) the metabolites other than TMAO identified in the reported cohort, which may also have nephrotoxicity and contribute to CKD progression, were not been studied/discussed; 2) An intensive and systematic study on the underlying mechanism of TMAO promoting CKD progression is lacking; 3) Some unknown metabolites recorded by LC-MS/MS, which may contribute to CKD progression, are not be investigated due to their structures unable to be annotated. Still, the present study extends previous findings by providing a further understanding of the pathogenesis of CKD progression through metabolomics, and reducing the production of TMAO may be a novel strategy to mitigate the progression of kidney injury in CKD patients.

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