

A novel interplay between intestinal bacteria and metabolites in IgA nephropathy identified via integrated microbiome and metabolome approaches.

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Abstract

Immunoglobulin A nephropathy (IgAN) is the most common form of primary glomerulonephritis. Intestinal bacteria and their metabolites have been implicated in various diseases. Improved understanding of the gut microbiota and its metabolic capabilities will facilitate development of diagnostic, therapeutic, and prognostic methods for IgAN. We identified gut microbiota and metabolite biomarkers of IgAN by analyzing microbiomes and metabolomes of fecal and serum samples of IgAN patients and healthy controls using 16s ribosomal RNA gene sequencing and liquid chromatography-tandem mass spectrometry, respectively, and bioinformatics approaches. We found that relative abundances of *Streptococcus* and *Enterococcus* were higher in IgAN patients, whereas *Bacteroidetes* and *Bacteroides* were lower. The changes in gut microbiota affected metabolism and absorbance of microbiota-associated metabolites of IgAN patients, in particular polyunsaturated fatty acids, free amino acids and oligopeptides, and activated the phenylalanine metabolism pathway. Also, 5-hydroxyeicosatetraenoic acid and 5-hydroxy-6E,8Z,11Z-eicosatrienoic acid were proved to be associated with the classification of segmental glomerular sclerosis but not 24h urine protein and

estimated glomerular filtration rate. Our findings demonstrate an interplay between intestinal bacteria

and metabolites in IgAN. The identified metabolites may have diagnostic and therapeutic applications.

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Biography:

Hongwei Wu is doing his PhD study in Jinan University. He is the doctor of The First Affiliated Hospital of Jinan University and major in nephritis. He has published 3 papers in professional journals.