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Metagenomic analysis of Bacteria-Derived Extracellular Vesicles in the Serum of Hemodialysis Patients

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Objectives:

Alteration of gut microbiome is found in CKD patient and known to contribute renal progression and complications of CKD.

Bacteria-derived extracellular vesicles (EVs) are spherical and bilayered proteolipids which contain bacteria membrane protein, DNA, RNA and virulent components such as lipopolysaccharide and endotoxins. They are constitutively secreted into the extracellular milieu from bacteria, enter systemic circulation freely through intestinal mucosal membrane, and can act as a key mediator in host-microbe communication to develop diseases.

In this study, we performed metagenomic analysis of bacteria-derived EVs in the serum of maintenance HD patients and healthy controls.

Methods: Serum was collected from 20 HD patients (10 diabetics, 10 non-diabetic) and 20 healthy controls. Bacteria-derived EVs were isolated from serum as described previously. Bacteria DNA was extracted from 1ug of isolated EVs. 16S rRNA gene sequencing was performed using high-throughput 454 pyrosequencing after amplification of the V1–V3 region. Taxonomy assignment was carried out by using UCLUST and QIIME against the 16sRNA sequence database in GreenGenes 8.15.13.

Results:

The alpha-diversity value was lower in HD patients than in controls, which suggests HD patients lose microbiome diversity. The beta-diversity value was significantly different which means the composition was different between two groups. At the level of Phylum, Acidobacteria EVs were significantly higher in HD patients, but Proteobacteria's were lower. At the level of Genus, 29 organisms were elevated and 18 were decreased in HD patients: EVs of Streptococcus, Koribacteraceae(f), Ellin6513(o), and Burkholderia were higher in HD patients, but EVs of Enterobacteriaceae(f), Acinetobacter, Pseudomonas, Proteus and Lactobacillus were lower. There was no significant difference between diabetic and non-diabetic patients.

Conclusions:

Using metagenomic analysis, we observed significant differences in the composition and amounts of bacteria-derived EVs in the serum of HD patients and healthy controls.

Metagenomic analysis of bacteria-derived EVs could be a useful tool to investigate microbial dysbiosis.