

中文題目：腎臟衰竭末期病人之腸道微菌與慢性發炎間的關係

英文題目：The relationship between gut microbiota and chronic inflammation in patients with end-stage kidney disease

作者：吳秉勳^{1,2}，林憶婷^{2,3}，林定筠⁴，洪思群⁴，劉勃佑⁵，洪薇鈞⁶，郭美娟^{1,2}，邱怡文^{1,2}

服務單位：高雄醫學大學中和紀念醫院內科部腎臟內科¹；高雄醫學大學醫學院醫學系²；高雄醫學大學中和紀念醫院家庭醫學科³；台北慈濟醫院腎臟內科⁴；中央研究院生物多樣性研究中心⁵；高雄醫學大學醫學院醫學系基礎醫學科微生物暨免疫學科⁶

Background:

Chronic inflammatory processes are common in individuals with chronic kidney disease, especially end-stage kidney disease (ESKD). Gut microbial dysbiosis may contribute to systemic inflammation. Several gut microbial-associated factors could explain the development of systemic inflammation in ESKD, such as cytokine excretion and uremic toxins production. Herein, we investigated the association between gut microbial compositions in different CRP levels in patients receiving hemodialysis.

Methods:

Among 194 hemodialysis patients, fecal samples were obtained to analyze the gut microbiome using 16S RNA amplicon sequencing. The amplicon library was constructed by amplifying the variable regions 3 and 4 (V3-V4) of the 16S rRNA gene, and 16S amplicons were sequenced with Illumina MiSeq sequencer. We compared the microbial composition between patients stratified by tertile baseline C-reactive proteins (CRP) levels. Differences in the microbial composition were assessed using linear discriminant analysis effect size (LEfSe) analysis.

Results:

The species richness or evenness (α -diversity) was higher among hemodialysis patients with lower CRP levels. A distinct inter-individual diversity (β -diversity) between CRP tertile groups was found. In LefSe analysis, hemodialysis patients with a lower CRP level increased microbial composition in the *Clostridia* class, including *Clostridiales* order, *Peptostreptococcaceae* family, *Christensenellaceae* family, and *Ruminococcaceae* family. In contrast, subjects with a higher CRP level predominantly *Streptococcaceae* family and *Streptococcus* genus.

Conclusion:

In ESKD patients, the microbial species richness or evenness were negatively associated with CRP levels. Patients stratified by tertile CRP levels presented a distinct microbial composition. Importantly, we identified an increased *Clostridia* class among patients with lower CRP levels and an increase in the *Streptococcaceae* family among patients with higher CRP levels. These findings suggested a contribution of chronic inflammation by the gut microbiome in ESKD patients.