Gut microbiota according to the stages of chronic kidney disease

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Objectives: Recent evidences suggest that the microbiome profile is altered in patients with chronic kidney disease (CKD) compared to healthy population. However, there had been no study reporting fecal microbiota according to the renal function. We evaluated differences in the composition of fecal microbiota according to the stages of CKD.

Methods: We prospectively enrolled 113 patients with CKD who underwent kidney biopsy or expecting kidney transplantation and 35 healthy subjects who was supposed to donate their kidneys in three centers. Fresh feces were collected from the subjects and frozen at -80℃. The composition of microbiota was analyzed using extracted metagenomic DNA from the feces by Illumina MiSeq system. Estimated GFR (eGFR) was calculated using CKD-EPI equation.

Results:
Total of 148 subjects was enrolled and divided into 6 groups according to the CKD stage; 35 healthy control, 24 CKD stage 1, 24 stage 2, 21 stage 3, 16 stage 4 and 5ND, and 28 stage 5D. The mean eGFR of the groups were 103, 105, 78, 45, and 12 mL/min/1.73 m², respectively, and not estimated in stage 5D.

The fecal microbiota was dominated by two bacterial phyla, Firmicutes and Bacteroidetes. Though the difference was not significant, the abundances of Bacteroidetes and Proteobacteria showed decreasing tendency in the higher stage of CKD, whereas those of Firmicutes showed an increasing tendency. Acinetobacter was significantly higher in CKD stage 3 compared to healthy subjects or stage 5D (p=0.008). At Genus level, the abundances of Oscillibacter were significantly higher (p=0.029) but those of Lachnospira was lower (p=0.010) in the advanced CKD stages.

Conclusions: The fecal microbiota of CKD patients showed difference according to the CKD stage. This might be related to uremia and systemic inflammation of CKD. Future study would be needed to reveal the connection.