KSN-17-O095 [한국교와하코기린 신진연구비]

Tonsillar and fecal microbiome in IgA nephropathy

Ji in PARK[1], Tae yoon KIM[2], Hyunjeong BAEK[1], Hae hyuk JUNG[1], Hyun-jeong CHO[3], Hajeong LEE[3], Dong ki KIM[3], Seung hee YANG[3], Bumjo OH[4], Je hee LEE[5], Jongsik CHUN[5], Bong-soo KIM[2], Jung pyo LEE[6], *Yon su KIM[3]

[1]Internal medicine, Kangwon National University Hospital, Korea,South, [2]Life Science, Hallym University, Korea,South, [3]Internal Medicine, Seoul National University Hospital, Korea,South, [4]Family Medicine, Seoul National University Boramae Hospital, Korea,South, [5]Chunlab, Korea,South, [6]Internal Medicine, Seoul National University Boramae Hospital, Korea,South

Objectives : Mucosal immune system plays a role in pathogenesis of Immunoglobulin A nephropathy (IgAN); however, little has been known about the relationship between IgAN and the microbiome reside in tonsil and intestine.

Methods : We prospectively enrolled 30 biopsy-proven IgAN patients at 3 centers and collected tonsil swabs and fecal specimens at the time of renal biopsy. Tonsil swabs and feces from different groups of thirty healthy volunteers were used as control. The composition of microbiota was analyzed using extracted metagenomic DNA from the feces and tonsil swabs by Illumina MiSeq system.

Results : The fecal microbiota of both IgAN and control group were dominated by two bacterial phyla, Firmicutes and Bacteroidetes. Compared to control group, fecal microbiota of IgAN patients showed significantly lower OTUs and Shannon diversity index. The relative abundances of Firmicutes were higher, whereas those of Bacteroidetes were lower in IgAN patients than healthy subjects.

The microbiota of tonsil swabs were also analyzed. Bacterial diversity was higher in IgAN patients than control group. The proportions of Firmicutes and Bacteroidetes were higher, whereas those of Proteobacteria were lower in IgAN patients than control group. When we matched age between IgAN and control groups, twelve patients and 12 healthy persons were selected, and the relative abundance of Bacteroidetes were still significantly higher in IgAN patients.

Conclusions : The fecal and tonsillar microbiota of IgAN patients differed from those of control group. Such differences might be related with pathogenesis of IgAN.

Keywords : IgA nephropathy, microbiome