Decreased diversity of nasal microbiota and their secreted extracellular vesicles in patients with chronic rhinosinusitis based on a metagenomic analysis

Seok Hyun Cho, MD

Otorhinolaryngology-Head and Neck Surgery, Hanyang University Hospital, Seoul, Korea

Introduction: Chronic rhinosinusitis (CRS) is an inflammatory process in the nasal cavity and paranasal sinuses, and bacteria have been considered to be a cause. Indeed, recent evidence indicates that bacteria-derived extracellular vesicles (EV) appear to be an important causative agent of inflammatory diseases. Here, we aimed to evaluate the diversity of nasal microbiota and their secreted EV in patients with CRS.

Method: Nasal lavage (NAL) fluid samples were obtained from five patients with CRS with polyposis, three patients with CRS without polyposis, and three non-CRS controls. After preparation of bacteria and EV from samples using differential centrifugation, genomic DNA was extracted and 16S-rDNA amplicons were subjected to high-throughput pyrosequencing on a Roche 454 GS-FLX platform.

Results: Metagenomics showed that bacteria composition

was positively correlated with EV composition. Samples from patients with CRS had greater bacterial abundance and lower diversity, both from bacteria and the EV portion of samples, compared with non-CRS samples. At each phylogenetic level, Bacteroidetes decreased while Proteobacteria increased in the CRS group at the phylum level. At the genus level, Prevotella spp. decreased in the CRS group, while Staphylococcus spp. increased from both bacteria and EV. Moreover, Staphylococcus aureus and its secreting EV compositions were higher in samples from CRS with polyps compared with CRS without polyps.

Conclusion: These results suggest that patients with CRS have altered nasal microbiota and decreased diversity in bacterial compositions as well as increased *S. aureus* abundance in those patients with polyps.