Analysis of oral pathogenic bacteria in the patients of eosinophilic esophagitis

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Background＆Aim: We have reported that oral pathogenic bacteria including *Porphyromonas gingivalis* (*P.g*) and *Streptococcus mutans* (*S.m*) accelerates systemic diseases. In our present study, we focused on eosinophilic esophagitis (EoE), a refractory rare disease, and analyzed oral bacteria in EoE patients to find relationship between EoE and infection of bacteria.

Method: Twenty four healthy control volunteers, 52 EoE subjects who were diagnosed by Shimane university and 22 subjects of reverse esophagitis (RE) were recruited. Oral bacteria were collected by mouse washing with 1.5 mL of distilled water. Bacterial DNA was extracted and analyzed by next generation sequencer. In addition, popular pathogenic oral bacteria including *P.g* and *S.m* were detected by PCR.

Resutls: Population of *Prevotella* genus was smaller in EoE and RE compared to that in healthy control. Same tendency was observed in four *Prevotella* spieces. On the other hand, *S.m* and *S.m*-derived collagen-binding protein (*cnm*), through which *S.m* induces dysfunction of tissues or organs, were detected more frequently both in EoE and RE than healthy control.

Conclusion: Oral bacterial flora in EoE subjects are likely to be different from that in healthy subjects, and infection to *S.m* is correlates with prevalence of EoE.