J Neurogastroenterol Motil, Vol. 28 No. 2 April, 2022
pISSN: 2093-0879 eISSN: 2093-0887
https://doi.org/10.5056/jnm22021
Journal of Neurogastroenterology and Motility

Editorial

A Step Toward Discovering the New World of Esophageal Microbiota

Chan Hyuk Park

Department of Internal Medicine, Hanyang University Guri Hospital, Hanyang University College of Medicine, Guri, Gyeonggi-do, Korea

Article: Esophageal microbiota and nutritional intakes in patients with achalasia before and after peroral endoscopic myotomy
Jung DH, Youn YH, Kim DH, et al
(J Neurogastroenterol Motil 2022;28:237-246)

Due to the development of next-generation sequencing techniques, microbiota in healthy or diseased gastrointestinal mucosa have been thoroughly investigated.[1,2] The impact of the new sequencing technique is synonymous with developing a new navigation tool in the age of exploration. We have known about normally existing bacterial taxa in the esophagus consisting of *Streptococcus, Haemophilus, Neisseria, Prevotella,* and *Veillonella*.[2] The composition of esophageal microbiota differs depending on disease states, such as gastroesophageal reflux disease (GERD), Barrett's esophagus, esophageal adenocarcinoma, esophageal squamous cell carcinoma, and eosinophilic esophagitis. For example, in patients with GERD or Barrett's esophagus, the abundance of *Streptococcus* decreases whereas that of *Haemophilus, Neisseria, Prevotella*, and *Veillonella* increases.[3,4] In esophageal adenocarcinoma, the abundance of *Streptococcus* decreases while that of *Lactobacillus, Enterobacteriaceae*, and *Akkermansia* increases.[5,6] Although the reason for the change has not been clearly elucidated, there are 2 potential sources of the esophageal microbiota: one is the swallowed oropharyngeal microbiota, and the other is intragastric microbiota refluxed from the stomach. A previous study found that Streptococci, bacteria abundantly found in the esophagus of healthy and individuals with GERD or esophageal adenocarcinomas, are commonly observed in the oropharynx.[7] *Streptococcus* in the esophagus may be originated from the oropharynx and outside the body. Other bacteria such as *Veillonella*, which typically increases in esophageal mucosa exposed to refluxed gastric acid, may have been refluxed from intragastric microbiota. However, there is still a possibility that microbiota in diseased esophageal mucosa originates from the oral cavity. For instance, *Prevotella*, Fusobacteria phylum, *Neisseria*, and *Corynebacterium*, may be increased in patients with esophageal squamous cell carcinoma or eosinophilic esophagitis, despite the lack of reflux.[2]

Esophageal microbiota is a new world that is yet to be discovered. The reason for the changes in esophageal microbiota is still not fully understood. As such, the study on esophageal microbiota in patients with esophageal achalasia, published in this issue of the *Journal of Neurogastroenterology and Motility*, is very interesting.[8] In this study, Jung et al[8] analyzed microbiota in the esophageal mucosa and retention fluid from 29 patients with esophageal achalasia. Pathophysiologically, esophageal achalasia is the opposite of GERD. Esophageal microbiota in patients with esophageal achalasia may be affected by saliva and diet rather than refluxed gastric contents.

Received: February 18, 2022 Revised: None Accepted: March 3, 2022

*Correspondence: Chan Hyuk Park, MD, PhD
Department of Internal Medicine, Hanyang University Guri Hospital, Hanyang University College of Medicine, 153 Gyeongchun-ro, Guri, Gyeonggi-do 11923, Korea
Tel: +82-31-560-2230, Fax: +82-31-553-7369, E-mail: yesable7@gmail.com

Therefore, we can assess the impact of the external environment on esophageal microbiota by analyzing the esophageal microbiota in patients with achalasia. Although Jung et al[8] did not include healthy individuals, the relative abundance of *Streptococcus* in participants was low (< 40%), similar to patients with GERD. Interestingly, the composition of esophageal microbiota in the mucosa and retention fluid differed. For example, *Lactobacillus* and Enterobacteriaceae, generally associated with esophageal adenocarcinoma, were found more abundantly in esophageal mucosa than retention fluid. These bacterial taxa may be targets for future research on esophageal carcinogenesis. Similarly, *Veillonella*, which is known to be associated with GERD, was more abundant in the retention fluid than in the esophageal mucosa. Given that gastric acid reflux is minimal in patients with esophageal achalasia, the increased abundance of *Veillonella* may be due to poor clearance of esophageal fluid. In GERD, *Veillonella* may be present due to swallowing the content and poor esophageal clearance rather than refluxed gastric acid. More importantly, Jung et al[8] demonstrated that esophageal microbiota did not differ between pre- and post-peroral endoscopic myotomies. If reflux was the main reason for esophageal dysbiosis, the microbiota composition should differ between the pre- and post-myotomy in patients with esophageal achalasia since the procedure increases acid reflux.[9]

As the authors already stated, the study by Jung et al[8] is limited due to insufficient sample size and lack of healthy controls. Nevertheless, this study is the first to describe the esophageal microbiota compositions in patients with esophageal achalasia. It provides a better understanding of the esophageal microbiota and provides hope to achieve a greater understanding of the esophageal microbiota in the near future.

Financial support: None.

Conflicts of interest: None.

References

1. Chen CC, Liou JM, Lee YC, Hong TC, El-Omar EM, Wu MS. The interplay between *Helicobacter pylori* and gastrointestinal microbiota. Gut Microbes 2021;13:1-22.
2. Park CH, Lee SK. Exploring esophageal microbiomes in esophageal diseases: a systematic review. J Neurogastroenterol Motil 2020;26:171-179.
3. Yang L, Lu X, Nossa CW, Francois F, Peek RM, Pei Z. Inflammation and intestinal metaplasia of the distal esophagus are associated with alterations in the microbiome. Gastroenterology 2009;137:588-597.
4. Liu N, Ando T, Ishiguro K, et al. Characterization of bacterial biota in the distal esophagus of Japanese patients with reflux esophagitis and Barrett's esophagus. BMC Infect Dis 2013;13:130.
5. Elliott DRF, Walker AW, O'Donovan M, Parkhill J. A non-endoscopic device to sample the oesophageal microbiota: a case-control study. Lancet Gastroenterol Hepatol 2017;2:32-42.
6. Snider EJ, Compres G, Freedberg DE, et al. Alterations to the esophageal microbiome associated with progression from Barrett's esophagus to esophageal adenocarcinoma. Cancer Epidemiol Biomarkers Prev 2019;28:1687-1693.
7. Park CH, Seo SI, Kim JS, et al. Treatment of non-erosive reflux disease and dynamics of the esophageal microbiome: a prospective multicenter study. Sci Rep 2020;10:15154.
8. Jung DH, Youn YH, Kim DH, et al. Esophageal microbiota and nutritional intakes in patients with achalasia before and after peroral endoscopic myotomy. J Neurogastroenterol Motil 2022;28:237-246.
9. Park CH, Jung DH, Kim DH, et al. Comparative efficacy of per-oral endoscopic myotomy and Heller myotomy in patients with achalasia: a meta-analysis. Gastrointest Endosc 2019;90:546-558, e3.