Mucosal dysbiosis in patients with gastrointestinal follicular lymphoma.

Abstract
Because the pathogenesis of gastrointestinal follicular lymphoma (GI-FL) remains unclear, no standardized treatment strategy has been established. Of the gastrointestinal lymphomas, gastric mucosa-associated lymphoid tissue (MALT) lymphomas are strongly associated with H. pylori; hence, the microbiota may be involved in GI-FL pathogenesis. However, the association between GI-FL and the microbiota remains uninvestigated. Therefore, we compared the mucosal microbiotas of GI-FL patients with those of controls to identify microbiota changes in GI-FL patients. Mucosal biopsy samples were obtained from the second portion of the duodenum from 20 GI-FL patients with duodenal lesions and 20 controls. Subsequent 16S rRNA gene sequencing was performed on these samples. QIIME pipeline and LEfSe software were used to analyze the microbiota. The GI-FL patients had significantly lower alpha diversity (P = 0.049) than did the controls, with significant differences in the microbial composition (P = 0.023) evaluated by the beta diversity metrics between the two groups. Comparing the taxonomic compositions indicated that the genera Sporomusa, Rothia and Prevotella and the family Gemellaceae were significantly less abundant in the GI-FL patients than in the controls. GI-FL patients presented altered duodenal mucosal microbial compositions, suggesting that the microbiota might be involved in the GI-FL pathogenesis. This article is protected by copyright. All rights reserved.

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