

論 文 要 旨

Gallbladder microbiota composition is associated with pancreaticobiliary and gallbladder cancer prognosis

胆嚢微生物叢と膵胆管・胆嚢がんの予後との関連

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Background: The microbial population of the intestinal tract and its relationship to specific diseases has been extensively studied during the past decade. However, reports characterizing the bile microbiota are rare. This study aims to investigate the microbiota composition in patients with pancreaticobiliary cancers and benign diseases by 16S rRNA gene amplicon sequencing and to evaluate its potential value as a biomarker for the cancer of the bile duct, pancreas, and gallbladder.

Results: We enrolled patients who were diagnosed with cancer, cystic lesions, and inflammation of the pancreaticobiliary tract. The study cohort comprised 244 patients. We extracted microbiome-derived DNA from the bile juice in surgically resected gallbladders. The microbiome composition was not significantly different according to lesion position and cancer type in terms of alpha and beta diversity. We found a significant difference in the relative abundance of *Campylobacter*, *Citrobacter*, *Leptotrichia*, *Enterobacter*, *Hungatella*, *Mycolicibacterium*, *Phyllobacterium* and *Sphingomonas* between patients without and with lymph node metastasis.

Conclusions: There was a significant association between the relative abundance of certain microbes and overall survival prognosis. These microbes showed association with good prognosis in cholangiocarcinoma, but with poor prognosis in pancreatic adenocarcinoma, and vice versa. Our findings suggest that pancreaticobiliary tract cancer patients have an altered microbiome composition, which might be a biomarker for distinguishing malignancy.