

論 文 要 旨

Colorectal Cancer Patients Have Four Specific Bacterial Species in Oral and Gut Microbiota in Common – A Metagenomic Comparison with Healthy Subjects

大腸がん患者は口腔・腸内細菌叢に共通して
4種の特異な菌種を有する
—メタゲノム解析による健常者との比較—

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Abstract: Oral microbiota is reportedly associated with gut microbiota and influences colorectal cancer (CRC) progression; however, the details remain unclear. This study aimed to evaluate the role of oral microbiota in CRC progression. Fifty-two patients with CRC and 51 healthy controls were included. Saliva and stool samples were collected, and microbiota were evaluated using 16S rRNA analysis and next-generation sequencing. Comparative analysis was performed on both groups. Linear discriminant analysis effect size (LEfSe) revealed the presence of indigenous oral bacteria, such as *Peptostreptococcus*, *Streptococcus*, and *Solobacterium* spp., at a significantly higher relative abundance in saliva and stool samples of CRC patients compared with controls. Next, CRC patients were divided into early stage (Stage I, II; $n = 26$; 50%) and advanced stage (Stage III, IV; $n = 26$; 50%) disease. LEfSe revealed that *S. moorei* was present at a significantly higher relative abundance in the advanced-stage group compared with the early-stage group, again consistent for both saliva and stool samples. Among bacterial species with significantly higher relative abundance in CRC patients, *P. stomatis*, *S. anginosus*, *S. koreensis*, and *S. moorei* originated from the oral cavity, suggesting indigenous oral bacteria may have promoted initiation of CRC carcinogenesis. Furthermore, *S. moorei* may influence CRC progression.