

COMPARISON OF THE GUT MICROBIOME FROM PREOPERATIVE FECAL SCREENING SAMPLES BETWEEN PATIENTS WITH OR WITHOUT ANASTOMOTIC LEAKAGE FOLLOWING COLORECTAL SURGERY

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Poster

Colorectal

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Preoperative gut microbiome composition in colorectal cancer patients differed significantly between those who developed postoperative anastomotic leakage and matched controls without leakage in a preliminary Danish biobank study using third-generation sequencing of screening fecal samples.

KEY POINTS

- The study analyzed 16S ribosomal RNA genes from fecal immunochemistry screening samples of 18 colorectal cancer patients who developed anastomotic leakage and 36 matched controls without leakage, using Oxford Nanopore third-generation sequencing technology.
- Gut microbiome composition was significantly different between groups (PERMANOVA $p = 0.01$), with Bacteroidota phylum, Campylobacterales and Bacteroidales orders, and Campylobacteraceae family more abundant in controls ($p < 0.05$ to $p < 0.001$).
- The anastomotic leakage group had significantly more Burkholderiaceae family, Ralstonia, and Burkholderia genera ($p < 0.001$), which the authors suggest may be harmful, while Campylobacter and Oridobacter were more abundant in controls and may be protective.
- The data are preliminary with analysis incomplete, and the authors note that validation studies are needed along with investigation of microbiome changes from bowel preparation and assessment of predictive value.
- This material is relevant for colorectal surgeons and researchers interested in surgical complications and the role of the gut microbiome in anastomotic healing.

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