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Summary

ALTERATIONS IN THE BILIARY STENT MICROBIOME IN PATIENTS WITH OBSTRUCTIVE BILIARY DISEASE

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Hepatobiliary

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A novel protocol using biliary stents enabled characterization of the bile duct microbiome in 123 patients, revealing three distinct microbial clusters associated with disease phenotypes and clinical parameters.

KEY POINTS

- The study analyzed 245 biliary stents and 17 bile samples from 123 patients (53 with malignant disease, 70 with non-malignant disease including post-operative stenosis) using 16S rRNA gene sequencing.
- 4339 phylotypes from 321 genera and 14 phyla were detected, with Enterococcus, Lactobacillus, and Escherichia/Shigella as the most abundant genera.
- Three distinct microbial clusters were identified that differed significantly at clinical and microbial levels and correlated with CRP, bilirubin, and stent indwelling time.
- Stent microbiome composition was significantly correlated with indwelling time, with Escherichia/Shigella and Dialister showing positive correlations and Enterococcus phylotypes showing negative correlations.
- Patients with early unplanned stent dysfunction (mean 21 days) showed significant microbiome differences at the genus level compared to those with non-dysfunctional stents.

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