

DISTINCT COMPOSITION AND METABOLIC POTENTIAL OF BILIARY MICROBIOTA IN PATIENTS WITH MALIGNANT BILE DUCT OBSTRUCTION

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Poster

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A case-control study of 56 patients identified distinct biliary microbiota composition and metabolic profiles in malignant bile duct obstruction compared to benign choledocholithiasis.

KEY POINTS

- In 25 patients with malignant bile duct obstruction, biliary microbiota composition at phylum level was Firmicutes 40.67%, Proteobacteria 36.44%, Bacteroidetes 11.33%, Actinobacteria 6.81%, and Fusobacteria 3.71%.
- Four genera were exclusively present in the tumor group: Clostridium IV, Halomonas, Rouxiella, and Turicibacter.
- Bile acid levels were significantly lower in the malignant obstruction group compared to the choledocholithiasis control group ($p < 0.05$), except for ursodeoxycholic acid and taurocholic acid.
- Twenty-two metabolic pathways were enriched in the tumor group, and bile samples were analyzed using 16S rRNA sequencing and ultra performance liquid chromatography-tandem mass spectrometry.
- The study enrolled patients prospectively from December 2022 to October 2023 with bile samples collected via ERCP, excluding those with recent antibiotic use or prior gastrointestinal surgery.

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