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Summary

PRIMARY CHOLEDOCHOLITHIASIS OCCURRENCE AND RECURRENCE IS SYNERGETCALLY MODULATED BY THE BILE MICROBIOME AND METABOLOME ALTERNATIONS

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Hepatobiliary

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Multiomics analysis of bile samples from 50 patients reveals reduced microbial diversity, altered metabolic pathways, and specific bacterial taxa associated with primary choledocholithiasis formation and recurrence risk.

KEY POINTS

- Bile microbiome diversity was significantly reduced in patients with primary choledocholithiasis compared to those with benign biliary stricture, with five alpha diversity indices significantly decreased and 49 differential bile flora identified between groups.
- Pathway analyses showed significant enrichment of bacterial infections, microbiota-derived amino acid metabolites, and secondary bile acid-related pathways in the stone-formation group.
- The relative abundances of 6 bacteria were associated with choledocholithiasis relapse conditions during 24-month follow-up, with reduction in Actinomycetes phylum identified as having predictive value for recurrence.
- The authors conclude that bile host-microbial dysbiosis modulates abnormal metabolite accumulation, potentially disrupting calcium homeostasis and promoting stone formation through synergistic effects with impaired bile duct epithelial cell function.

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