ALTERATIONS IN THE MICROBIAL METABOLIC LANDSCAPE DIFFERENTIATE CHRONIC PANCREATITIS FROM PANCREATIC CANCER

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A classifier combining eleven rectal microbiota taxa and CA 19-9 distinguished chronic pancreatitis from pancreatic ductal adenocarcinoma with an AUROC of 86.1%, outperforming CA 19-9 alone (82.2%) in a multicenter cohort of 332 patients.

KEY POINTS

- The study analyzed buccal and rectal swabs, plasma, and feces from 332 chronic pancreatitis and pancreatic ductal adenocarcinoma patients recruited from 8 European centers using metagenomic sequencing and targeted metabolomics.
- Significant differences in the rectal microbiota were observed between chronic pancreatitis and pancreatic ductal adenocarcinoma patients.
- Chronic pancreatitis patients showed a decrease in species typically known for short chain fatty acid production capacity.
- Metabolic prediction suggested lower production capacity of short chain fatty acids in chronic pancreatitis, and targeted metabolomics confirmed significantly lower levels of short chain fatty acids in fecal samples of chronic pancreatitis patients.
- The data provide first evidence of a shift in the metabolic landscape of the rectal microbiome between chronic pancreatitis and pancreatic ductal adenocarcinoma.

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