

FECAL MICROBIOME AND METABOLOME SIGNATURES DISTINGUISH FAMILIAL ADENOMATOUS POLYPOSIS SEVERITY

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Poster

Colorectal

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Gut microbiome and metabolome analysis in 28 FAP patients and 96 controls reveals distinct profiles associated with disease presence and severity, with reduced microbial diversity, elevated Firmicutes/Bacteroidetes ratio, Streptococcus enrichment, and increased taurocholic acid in severe cases.

KEY POINTS

- FAP patients exhibited significantly reduced alpha diversity compared to controls (Shannon Index, $FDR < 0.001$), with severe FAP cases showing further reductions relative to moderate patients ($FDR < 0.1$).
- An elevated Firmicutes/Bacteroidetes ratio was observed in FAP patients versus controls ($FDR < 0.001$) and in severe versus moderate FAP patients ($FDR < 0.01$).
- Streptococcus was enriched in FAP patients compared to controls and further elevated in severe cases, consistent with its known role in colorectal cancer.
- Metabolomic profiles significantly differed by phenotype, with 162 metabolites differing between severe and moderate FAP ($FDR < 0.1$), including taurocholic acid enrichment in severe cases.
- Machine learning classification using metabolic profiles achieved strong predictive capacity between FAP and control samples (balanced accuracy = 0.86, PR AUC = 0.92), suggesting potential use as biomarkers for FAP severity.

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