

ENRICHMENT OF POLYSTYRENE-DEGRADING MICROBES IN THE UPPER GASTROINTESTINAL TRACT OF FUNCTIONAL DYSPESIA PATIENTS

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Poster

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Re-analysis of duodenal microbiome data reveals differential abundance of predicted plastic-degrading genes in functional dyspepsia patients compared to controls, with some genes enriched in patients and others in controls.

KEY POINTS

- Two 16S rRNA datasets were analysed (study 1: 17 FD, 11 controls; study 2: 61 FD, 38 controls) using consistent bioinformatics and PICRUSt2 functional prediction to assess plastic-degrading microbial capacity
- In the first dataset, no significant differences in predicted polyethylene terephthalate utilization pathways were found in duodenal mucosa, but partial TCA cycle pathways were increased in gastric mucosa of FD patients
- In the second dataset, the gene 3-oxoadipate enol-lactonase was significantly increased in FD patients, while two other polyethylene-associated degradation genes were significantly increased in controls
- The authors conclude that PET-degrading microbes are significantly enriched in the upper gastrointestinal tract of FD patients and suggest these findings highlight potential microbial biomarkers warranting further investigation

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