SPECIFIC GUT MICROBIOTA SIGNATURES ARE ASSOCIATED WITH SYMPTOMATIC LACTOSE MALABSORPTION

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A study using 16S rRNA profiling found distinct gut microbiota signatures in lactose-intolerant patients, with increased biodiversity and elevated Proteobacteria, Bacteroidetes, and specific dysbiosis markers compared to healthy controls.

KEY POINTS

- 28 lactose-intolerant patients showed significantly increased alpha-diversity ($p<0.05$, Shannon and Simpson index) and beta-diversity ($p=0.001$) compared to 29 healthy controls.
- Proteobacteria and Bacteroidetes phyla were significantly elevated ($p<0.05$) in lactose-intolerant patients, with Dialister, Staphylococcus, Streptococcus, Enterobacteriacae, and Bacteroides identified as dysbiosis markers at species level ($p<0.05$).
- Increased intestinal permeability was observed in 88.8% of lactose-intolerant patients versus 6.6% of controls, while altered intestinal transit occurred in 50% of symptomatic patients regardless of lactose malabsorption status.
- The authors suggest these findings indicate a potential prebiotic role for lactose targeting differential microbial elements, though further characterization is needed to elucidate symptom mechanisms.
- This material is most relevant to gastroenterologists and researchers investigating the microbiome's role in functional gastrointestinal disorders and lactose intolerance pathophysiology.

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