Disruptor taxa, oral microbes, and strict anaerobes in the human small-intestine microbiome

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Video Byte

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Abstract

Past research has already tied our gut microbiome to many diseases. However, most research to date has focused on the large intestine, as collecting stool samples is less invasive than sampling the small intestine. Recently, researchers used standard-of-care endoscopies as an opportunity to collect samples from the first section of the small intestine, the duodenum. Using quantitative sequencing, they evaluated the patients' microbial loads. They found preliminary evidence of microbes traveling from the mouth to the small intestine, as 89% of the microbial taxa found in duodenum samples were also present in saliva samples from the same patient. Within the duodenum, the researchers identified a collection of bacterial taxa that, when present, often dominated the microbial population. These 'disruptor taxa' appeared to replace the strict anaerobes common in the duodenum and were more prevalent in individuals with the serious GI disorder small intestinal bacterial overgrowth (SIBO). Higher loads of disruptor taxa were associated with more severe GI symptoms. Further research is needed to determine how these disruptor taxa behave in people without GI disorders and to examine the origins of disruptor taxa and how they influence major GI symptoms.