

Altered microbiome prevalent in the diseased esophagus

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Gastroesophageal reflux diseases , or GERD, affects about 10 million people in the United States, yet the cause and an unexpected increase in its prevalence over the last three decades remains unexplainable. Now, researchers have discovered that GERD is associated with global alteration of the microbiome in the esophagus. The findings, reported in the August 1, 2009 issue of *Gastroenterology*, may provide for the foundation for further study of the condition as a microecological disease with new treatment possibilities.

The findings of an altered microbiome may have profound implications for treating diseases of the esophagus, among the most common disorders affecting Western populations. In fact, about 40% of adults experience heartburn symptoms at least once a month. [Chronic inflammation](#) associated with GERD can lead to the development of Barrett's esophagus, precancerous condition. The incidence of cancer of the esophagus has increased six-fold since the 1970s--the fastest increasing cancer in the Western world.

"These findings have opened a new approach to understanding the pathogenesis of reflux-related disorders," states Zhiheng Pei, MD, PhD, assistant professor of pathology and medicine at NYU Langone Medical Center and lead author of the study. "At this time, we don't yet know whether the changes in bacterial populations are triggering GERD or are simply a response to it. But if changes in the bacterial population do indeed cause reflux, it may be possible to design new therapies with antibiotics, probiotic bacteria or prebiotics."

Researchers collected and sequenced bacteria from the esophagus of 34 patients, both healthy and those suffering from GERD (specifically [esophagitis](#) and Barrett's esophagus). They found a high concentration of [Streptococcus](#) in the esophagus of healthy patients. In contrast, an altered type of microbiome dominated by Gram-negative bacteria was contained in greater proportions in those patients with esophagitis and Barrett's [esophagus](#).

The human microbiome is comprised of all the microorganisms that reside in or on the human body, as well as all their DNA, or genomes. Microbial cells in the human body are estimated to outnumber human cells by a factor of ten to one. These communities, or microbiomes, however remain largely unstudied, leaving almost entirely unknown their influence upon human development, physiology, immunity and nutrition.

Source: New York University School of Medicine ([news](#) : [web](#))

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