

**FROM HELICOBACTER PYLORI TO THE GASTRIC MICROBIOME:  
BASELINE FINDINGS IN CHRONIC GASTRITIS AND GASTRIC CANCER**

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Gastric cancer remains a leading cause of cancer-related mortality worldwide, and *Helicobacter pylori* is recognized as a major driver of chronic gastric inflammation and carcinogenesis. Growing evidence indicates that, beyond *H. pylori*, broader alterations of the gastric and intestinal microbiome contribute to progression from chronic gastritis to gastric cancer. This study aims to characterize the clinical and *H. pylori* serological profile of gastritis and cancer patients, as a baseline for further investigation of the gut microbiome's role in diagnosis and treatment of gastric diseases.

A cross-sectional study is enrolling patients with chronic gastritis, gastric cancer, and healthy controls. Demographic, lifestyle, and laboratory data (blood count, biochemistry, coagulation, urinalysis, *H. pylori* IgG ELISA, viral hepatitis markers) were collected for 64 patients with chronic gastritis (mean age 48.3 years), 53 with gastric cancer (mean age 61.5 years), and 31 controls. Gastric biopsies and fecal samples are being collected for subsequent 16S rRNA metagenomic sequencing.

*H. pylori* IgG seropositivity was found in 30/55 (54.5%) tested gastritis patients, whereas all 53 tested gastric cancer patients were seronegative. Cancer patients were older than gastritis patients (61.5 vs 48.3 years) with a male predominance (66% vs 45%).

The decline in *H. pylori* seropositivity from gastritis to cancer is consistent with bacterial loss following gastric atrophy and supports a multifactorial, microbiome-driven model of gastric carcinogenesis beyond *H. pylori* alone. These baseline findings support the ongoing 16S rRNA-based microbiome analysis to identify novel diagnostic and therapeutic biomarkers for gastric diseases.