

BACTERIOPHAGES OF *HELICOBACTER PYLORI* IDENTIFIED IN GASTRIC CANCER SAMPLES FROM THE STATE OF PARÁ

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Introduction: Gastric cancer (GC) remains one of the most lethal malignancies worldwide, with over one million new cases diagnosed annually. Gastric carcinogenesis is a multifactorial process involving a complex interplay between environmental and host factors. Emerging evidence suggests that alterations in the gastric microbiome, including infection with *Helicobacter pylori*, contribute to cancer development. Notably, bacteriophages (phages) may influence tumorigenesis by modulating microbial communities, promoting the proliferation of oncogenic bacteria, and altering host–microbiota interactions. Moreover, early diagnosis of GC remains a major challenge, significantly impacting treatment efficacy and increasing mortality rates. Phages have been proposed as potential biomarkers for diseases associated with dysbiosis, due to the correlation between disease states and changes in the virome, which in turn reflect bacterial alterations. Therefore, it is crucial to deepen our understanding of the interaction between phages and the human bacteriome, as this relationship may be exploited for the early diagnosis of GC and the monitoring of carcinogenesis in the gastrointestinal tract. **Objectives:** This study aimed to characterize the *Helicobacter pylori* phage community in gastric tumor samples from patients diagnosed with GC. **Methods:** Tumor fragments (0.5 cm) were collected from 11 *H. pylori*-positive GC patients admitted to oncology reference hospitals in Pará, Brazil. RNA was extracted and sequenced using the Illumina NextSeq 500 platform. Low-quality reads and adapter sequences were removed using Trimmomatic, and read quality was assessed with FastQC. Taxonomic classification was performed using Kraken against a custom database of 31 complete *H. pylori* phage genomes obtained from GenBank. **Results:** A total of 11 *H. pylori* phages from the genus *Schmidvirus* were identified. The most abundant was prophage Pt-4472-G (51% of reads), followed by Pt-1293-U (14%) and Fr-B58-M (5%). Other phages included COL-23-PUJ (4%), Fr-GC43-A (3%), Pt-1846-U (2%), Pt-22899-G (2%), Pt-B92-G (2%), Pt-B89-G (1%), KHP40 (1%), Pt-5771-G (1%), and additional *Schmidvirus* phages (13%), demonstrating significant phage diversity within the tumor microenvironment. **Conclusion:** The presence and taxonomic diversity of *H. pylori* phages in gastric tumors suggest a complex virome–bacteriome interaction with potential implications for GC pathogenesis and progression. The modulation of the gastric microbiome by phages highlights their potential as biomarkers for tumor-associated dysbiosis and as candidates for the early diagnosis and monitoring of gastric cancer.

Keywords: Gastric cancer; Bacteriophages; *Helicobacter pylori*.