Maldi-tof ms and 16s rna identification of culturable gastric microbiota: Variability associated with the presence of helicobacter pylori

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Abstract
Helicobacter pylori is the main bacteria associated with gastroduodenal diseases. Recent studies have reported that gastric microbiota might be modified by the H. pylori colonization, favoring gastric lesions’ development. In Chile, the region of La Araucanía concentrates a high risk of gastric cancer associated with Helicobacter pylori colonization, rurality, poverty, and Mapuche ethnicity. Hence, we aimed to identify the culturable gastric microbiota and characterize its variability at different stages of epithelial injury, based on its H. pylori colonization in dyspeptic patients from this Chilean region. Microaerophilic bacteria strains were isolated from antrum biopsies of 155 dyspeptic patients’ biopsies and identified using MALDI-TOF MS or 16sRNA gene sequencing for non-pylori species identification, and UreC gene amplification for H. pylori confirmation. We found 48 species from 18 families, mainly belonging to Neisseriaceae (21.3%), Streptococcaceae (20.0%), Actinomycetaceae (9.0%), Enterobacteriaceae, and Lactobacillaceae (4.5%); however, Streptococcaceae and Actinomycetaceae families showed a significant reduction in samples infected with H. pylori, along with a considerably lower diversity of species. Our results revealed a microbiota modification due to H. pylori colonization associated with the gastric epithelial state, suggesting a potential microbiota role for developing and progressing gastric diseases.

Author keywords
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