

Antimicrobial peptide expression and gastric bacteria associated with *Helicobacter pylori* infection in patients with gastritis

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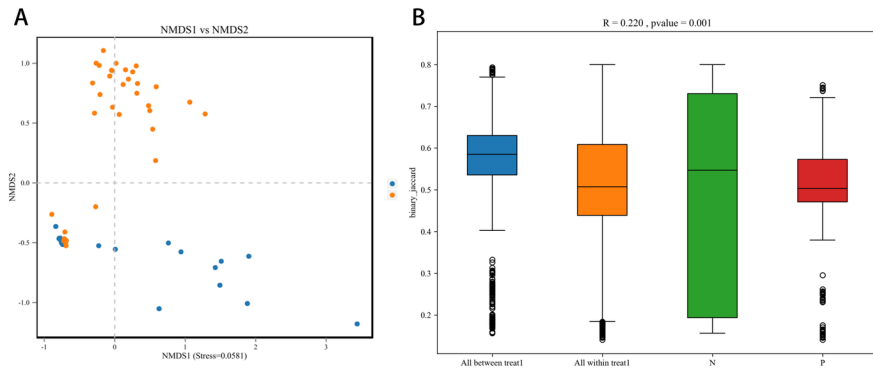
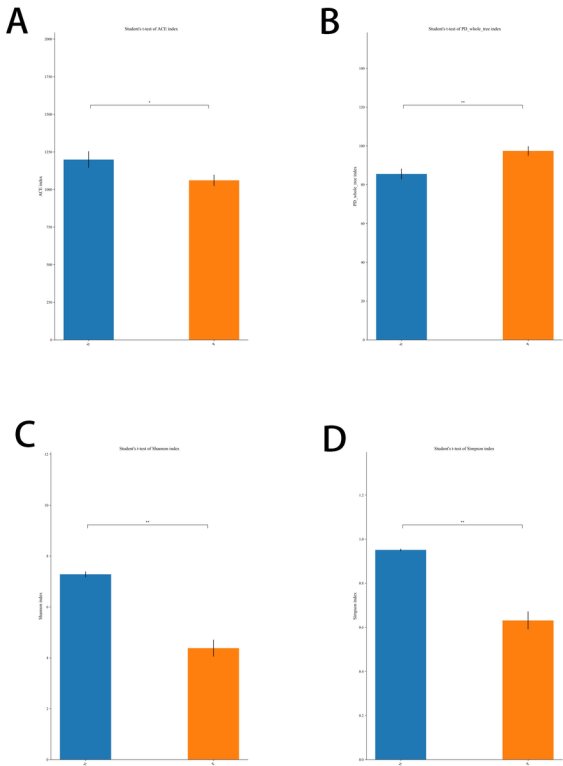
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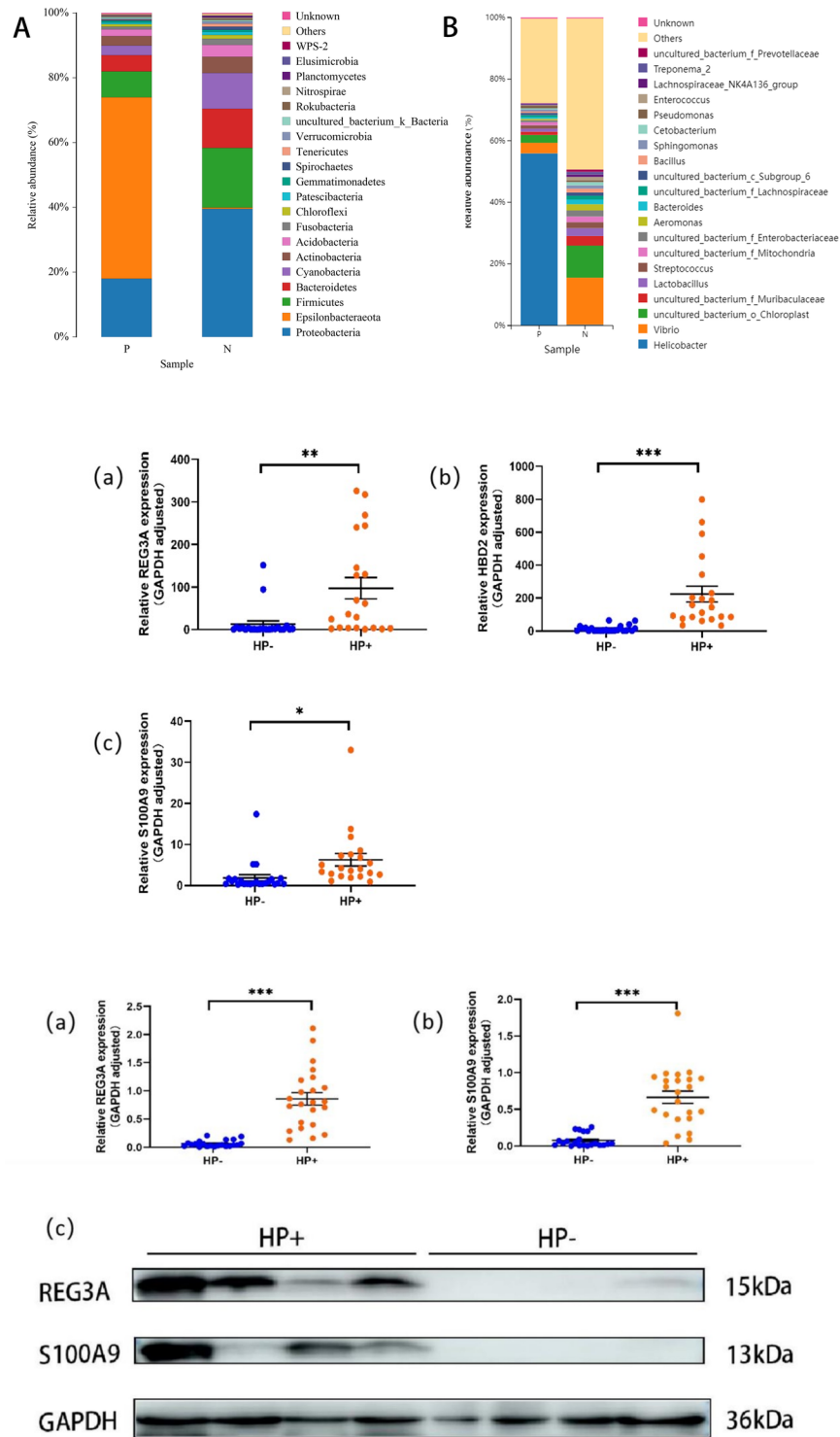
Abstract

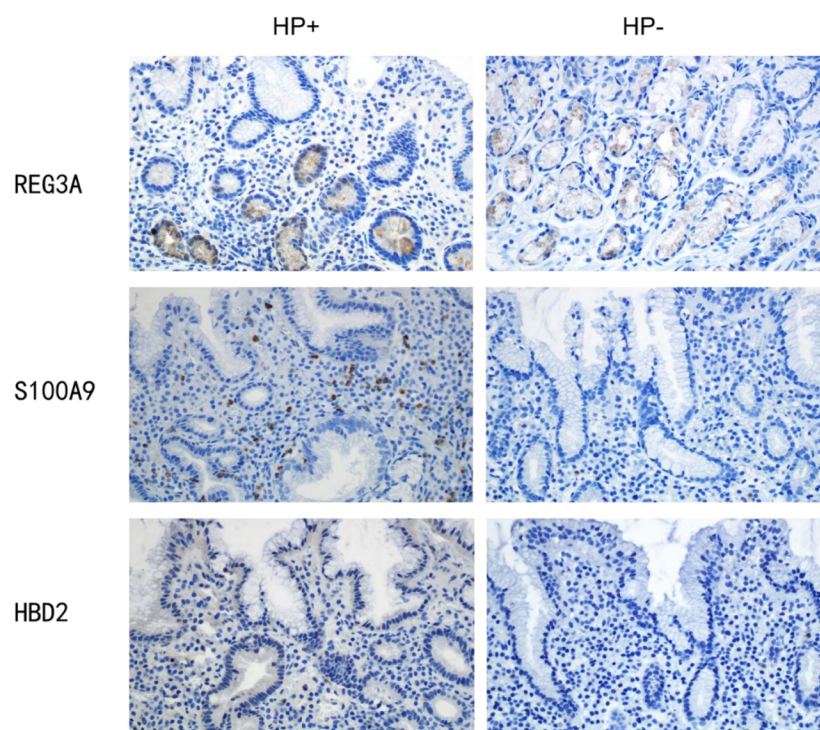
Background: The complex interplay between the continuous infection of *Helicobacter pylori* (Hp) in gastric mucosa and the development of Hp-associated gastritis remains poorly understood. The interaction between the gastric epithelium and the immune response induced by Hp may be an important contributing factor. Antimicrobial peptides (AMPs) can protect the gastric mucosa from bacteria. This study aimed to investigate the effects of Hp on the gastric flora, AMP (e.g., REG3A, HBD2 and S100A9) expression and the mucosal ultrastructure in Hp-positive (Hp+) patients with gastritis. **Methods:** The bacterial composition was analyzed in 63 patients with gastritis using 16S rRNA sequencing. The altered expression levels of AMPs (REG3A, HBD2 and S100A9) were analyzed by RT-qPCR for quantification of AMP mRNA levels. Western blotting and immunohistochemical staining were used to investigate AMPs expressions in the gastric biopsies. Observation of the gastric ultrastructure was performed by transmission electron microscopy (TEM). **Results:** HP infection significantly reduced the abundance of bacteria. REG3A, S100A9, and HBD2 were highly expressed in Hp+ patients. The destruction of the epithelial cell membrane and the entry of mucus particles into the gastric lumen were observed by TEM in Hp+ patients. **Conclusion:** The findings reported here confirm the dysbiosis of gastric microecology and AMPs expression in gastritis patients infected with Hp. This study provides information on the complex and dynamic ecosystem and may be helpful for further research to find a treatment alternative in the post-antibiotic era to eradicate multidrug-resistant Hp strains.

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