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Summary

PREVALENCE OF HELICOBACTER PYLORI INFECTION AND VIRULENCE GENES IN PATIENTS WITH UPPER GASTROINTESTINAL DISEASES FROM SOUTHWEST OF IRAN

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Stomach & H. Pylori

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Study of 426 patients in Khuzestan province found H. pylori in 44.13% by histopathology and identified significant associations between specific vacA and hrgA genotypes and different upper gastrointestinal diseases.

KEY POINTS

- H. pylori was detected in 33.8% of patients by rapid urea test and 44.13% by histopathology, with histopathology described by authors as more specific, especially in gastric ulcer bleeding cases.
- The cagA genotype was present in 93.3% of isolates, vacAs1 in 71.6%, vacAm2 in 70.1%, and hrgA in 67.2%, with vacAs1m2 the most prevalent allelic variant at 45.5%.
- Statistically significant associations were found between vacAs1m2 and gastric ulcer (P = 0.004), vacAs2m2 and non-ulcer dyspepsia (P = 0.017), and hrgA and duodenal ulcer (P = 0.043).
- Non-ulcer dyspepsia was the most common endoscopic finding at 56.7%, followed by erosive gastritis at 20.9% and gastric ulcer at 13.4%.
- This study may interest clinicians and researchers investigating H. pylori virulence factors and their relationship to upper gastrointestinal disease presentation.

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