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An Evidence-based Approach for Eradication of Helicobacter pylori

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Introduction

Helicobacter pylori is a bacterium that infects half of the world's population and is an underlying cause in the pathogenesis of peptic ulcer disease, chronic gastritis, and gastric cancer. The current treatment regimens are being selected empirically despite high failure rates, which are continuing to promote antibiotic resistance. Creating an individualized therapeutic approach will help reduce resistance rates and improve patient outcomes.

Materials & Methods

- Based on an extensive literature survey, we compiled a list of factors involved in the antibiotic resistance of H. pylori and collected data from >2000 patients for each of these factors.
- Inclusion criteria: Patients treated for H. pylori infection at the CUH from 12-31-10 to 12-31-15.
- Exclusion criteria: Patients lost to follow up, patients with incomplete course of treatment or inadequate documentation regarding the diagnosis or treatment course of H. pylori.
- We created an algorithm for customized therapies for H. pylori using statistically analyzed data.

Accuracy of the algorithm was confirmed by analyzing patients stool samples using RT-PCR based biprobe assay that detects the known clarithromycin mutations in the 23S rRNA gene.

Results

- Our data showed a clear pattern of H. pylori prevalence and antibiotic resistance in our low-income patient population 80% and 62% of patients over the age of 40 and women, respectively.
- The prevalence of infection was higher in the African American (30%) and Hispanic populations (36%).
- Patients with a median income of less than $54,000 and smokers had a 19% and 19.5% decrease chance of eradication, respectively.
- Previous omeprazole use increased the chance of eradication two-fold.
- Cefepime and past H. pylori decreased the chance of eradication by 70% and 90% respectively.
- Results of the stool testing supported the predictions from the algorithm.

Table 1. Predicted and actual outcomes for sensitivity/resistance to clarithromycin in H. pylori patients.

Conclusion

- Our algorithm is based on a number of environmental factors, variations in patient attributes and data from a large number of patients.
- Accuracy of algorithm was confirmed using patient stool samples. Inclusion of gut microbiome data will make the algorithm comprehensive and will significantly enhance its practical value.
- The implementation of our algorithm will allow individualized treatment of patients based on risk factors for antibiotic resistance, which will help reduce antibiotic resistance and increase the chance of eradication of H. pylori.

Ongoing Work

- Recently, it was also shown that infection with H. pylori causes changes in gut microbiome of the patients and these changes also are influenced by the ethnicity of the patients.
- Our data showed that our patient population has a high risk of H. pylori colonization, as well as antibiotic resistant infection: We thus aims to evaluate the gut microbiota of H. pylori patients to fine-tune our algorithm.
- We are currently collecting samples for gut microbiome analysis.

References