ASSOCIATION BETWEEN HELICOBACTER PYLORI INFECTION AND GASTROESOPHAGEAL REFLUX DISEASE: MENDELIAN RANDOMIZATION STUDY

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UEG Week Copenhagen 2023 | Poster

Stomach & H. Pylori

October 15, 2023

A Mendelian randomization study using data from FinnGen and UK Biobank found no evidence for a causal relation between Helicobacter pylori infection and the risk of gastroesophageal reflux disease.

KEY POINTS

- Eighteen single nucleotide polymorphisms associated with Helicobacter pylori IgG and six specific antibodies (UreA, CagA, VacA, Catalase, OMP, and GroEL) were used as genetic instruments to examine causal associations with GERD risk.
- Genetically predicted Helicobacter pylori IgG antibody levels were not associated with GERD risk in either FinnGen (OR=0.992, 95%CI 0.961-1.025) or UK Biobank (OR=0.999, 95%CI 0.998-1.001).
- Genetically predicted levels of the six Helicobacter pylori specific antibodies were not associated with GERD risk, except for UreA antibody in the MR-Egger method only, for which pleiotropy was indicated.
- Multivariable Mendelian randomization analysis also found no associations between Helicobacter pylori specific antibody levels and GERD risk.
- This work addresses inconsistent findings from previous epidemiological studies and may interest researchers and clinicians evaluating the role of Helicobacter pylori in GERD pathogenesis.

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