

MODELING COMMUNITY AND HOUSEHOLD TRANSMISSION DYNAMICS OF *HELICOBACTER PYLORI* IN CHINA, 1990-2021

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Poster

Stomach & H. Pylori

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A novel agent-based household transmission model for *Helicobacter pylori* in China, calibrated with national survey data from 1990-2021, confirms that household transmission is the primary infection route and that most infections occur during childhood.

KEY POINTS

- The model showed that within-household contact rates drive transmission more than community contact, and larger households and three-generation households have higher infection rates than smaller or one- to two-generation households.
- Children's infection probability was 31% with both parents infected, 21% with one infected parent, and 9% with neither parent infected.
- Family clustering of *H. pylori* infection becomes more pronounced in low-prevalence contexts compared to high-prevalence periods.
- This is the first *H. pylori* transmission model to incorporate household-level dynamics, calibrated using Chinese census data and a 2021 national family-based survey.
- The model may be useful for evaluating control strategies and could be extended to include antibiotic resistance dynamics or adapted to other countries.

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