

Observational Study

Prevalence and associated risk factors of *Helicobacter pylori* infection in community households in Lanzhou city

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Specialty type: Gastroenterology and hepatology**Provenance and peer review:** Unsolicited article; Externally peer reviewed.**Peer-review model:** Single blind**Peer-review report's classification****Scientific Quality:** Grade A, Grade C, Grade C**Novelty:** Grade B, Grade B, Grade C**Creativity or Innovation:** Grade A, Grade B, Grade C**Scientific Significance:** Grade A, Grade B, Grade C**P-Reviewer:** Kirkik D; Rao RSP; Vyshka G**Received:** May 24, 2024**Revised:** September 12, 2024**Accepted:** September 23, 2024**Published online:** December 21, 2024**Processing time:** 185 Days and 17.8 Hours**Ju-Kun Zhou**, The First Clinical Medical College, Lanzhou University, Lanzhou 730000, Gansu Province, China**Ju-Kun Zhou, Ya Zheng, Yu-Ping Wang, Rui Ji**, Department of Gastroenterology, The First Hospital of Lanzhou University, Lanzhou 730000, Gansu Province, China**Ju-Kun Zhou, Ya Zheng, Yu-Ping Wang, Rui Ji**, Gansu Province Clinical Research Center for Digestive Diseases, The First Hospital of Lanzhou University, Lanzhou 730000, Gansu Province, China**Co-corresponding authors:** Rui Ji and Ya Zheng.**Corresponding author:** Rui Ji, PhD, Chief Doctor, Full Professor, Department of Gastroenterology, The First Hospital of Lanzhou University, Donggang West Road, Lanzhou 730000, Gansu Province, China. jir@lzu.edu.cn**Abstract****BACKGROUND***Helicobacter pylori* (*H. pylori*) infection exhibits a familial clustering phenomenon.**AIM**To investigate the prevalence of *H. pylori* infection, identify associated factors, and analyze patterns of transmission within families residing in the community.**METHODS**From July 2021 to September 2021, a total of 191 families (519 people) in two randomly chosen community health service centers in the Chengguan District of Lanzhou in Gansu Province, were recruited to fill out questionnaires and tested for *H. pylori* infection. Individuals were followed up again from April 2023 and June 2023 to test for *H. pylori* infection. The relationship between variables and *H. pylori* infection was analyzed using logistic regression and generalized linear mixed models.**RESULTS**In 2021, the individual-based *H. pylori* infection rate was found to be 47.0% (244/519), which decreased to 38.1% (177/464) in 2023. Additionally, the rate of individual-based *H. pylori* new infection was 22.8% (55/241). The family-based *H. pylori* infection rate in 2021 was 76.9% (147/191), which decreased to 67.1%

(116/173) in 2023, and the rate of family-based *H. pylori* new infection was 38.6% (17/44). Individual *H. pylori* infection was positively correlated with age, body mass index (BMI), eating food that was excessively hot, frequent acid reflux, bloating, and halitosis symptoms, and negatively correlated with family size and nut consumption. New individual *H. pylori* infection was positively correlated with BMI, other types of family structures, drinking purified water, and frequent heartburn symptoms, while negatively correlated with the use of refrigerators and following a regular eating schedule. A larger living area was an independent protective factor for *H. pylori* infection in households. Frequently consuming excessively hot food and symptoms of halitosis were independent risk factors for *H. pylori* infection in individuals; frequent consumption of nuts was an independent protective factor for *H. pylori* infection. Other types of family structure, drinking purified water, and frequent heartburn symptoms were independent risk factors for new individual *H. pylori* infection; the use of a refrigerator was an independent protective factor for new *H. pylori* infections.

CONCLUSION

The household *H. pylori* infection rate in Lanzhou is relatively high and linked to socio-demographic factors and lifestyles. Eradication efforts and control of related risk factors are recommended in the general population.

Key Words: *Helicobacter pylori*; Household; China; Prevalence; Risk factors

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Core Tip: *Helicobacter pylori* (*H. pylori*) is characterized by family cluster infection. However, studies investigating the status of *H. pylori* infection and patterns of intra-household transmission are scarce. In our study, the individual *H. pylori* infection rate in the Chengguan District of Lanzhou was found to have decreased from 47.0% in 2021 to 38.1% in 2023. The rate of new individual infection is currently 22.8%. Similarly, the proportion of households with at least one infected member has decreased from 76.9% in 2021 to 67.1% in 2023. These results suggest that family-based prevention and treatment are more conducive to the management of *H. pylori*.

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INTRODUCTION

Helicobacter pylori (*H. pylori*) is a spiral-shaped gram-negative bacterium. A recent systematic review and meta-analysis found that the estimated global prevalence of *H. pylori* infection decreased from 58.2% in the 1980-1990 period to 43.1% in the 2011-2022 period[1]. Although the prevalence of *H. pylori* infection in China is high, most patients do not present with obvious symptoms or complications. However, almost all *H. pylori*-infected individuals undergo inflammatory changes in their gastric mucosa 25%-30% of cases develop a variety of gastrointestinal and extra-gastrointestinal disorders[2-4]. Studies on familial *H. pylori* clustering infections have increased in recent years. In a large-scale study of *H. pylori* in 29 provinces in mainland China in 2021, 10735 families (31098 individuals) were included, and the average individual-based *H. pylori* infection rate was 40.66%. Among these, 43.45% were adults and 20.55% were children and adolescents. The average family-based infection rate was 71.21%. The rate of familial *H. pylori* infection is much higher than that of individuals, and the infection rates are higher in northwest China[5]. Zhang *et al*[6] found that the use of a family-based strategy to screen for *H. pylori* infections exhibited an improvement of 4.02% in the ability to detect infection. This approach is a cost-effective strategy that enables an optimized allocation of screening resources[7].

Several studies have shown that *H. pylori* is mainly transmitted through oral-oral and fecal-oral contact, as well as through water sources[8,9]. Infection is also caused by close contact with *H. pylori*-positive family members[10,11]. This may explain persistent, recurrence and reinfection of *H. pylori*. Parents, especially mothers, infected with *H. pylori*, have been found to play a crucial role in transmitting the bacteria to their children[12,13]. The infection rate of *H. pylori* in children significantly increases with an increase in the parental infection rate[14]. Although a Japanese study initially showed support for this, it also highlighted the importance of mother-to-child transmission, making it difficult to clarify the spread of *H. pylori* in these families[15]. The transmission of *H. pylori* is also evident between spouses and among siblings. Studies on *H. pylori* infection in spouses have highlighted a degree of consistency in infection among spouses, wherein one spouse's infection could increase the other's risk of becoming infected[16]. As the duration of marriage increases, the infection rate of *H. pylori* in spouses has also been found to increase significantly, indicative of potential cross-infection between couples[17]. In a previous study conducted in Spain, a remarkably high consistency of *H. pylori* transmission among siblings was observed, further confirming that sibling-to-sibling transmission is a route of *H. pylori* infection in children. Additionally, living with non-siblings in extended families may increase the risk of infection, but

only in families where *H. pylori* infection is prevalent in all family groups[18]. Therefore, familial clustering and the high prevalence of *H. pylori* are among the most important reasons for the failure of *H. pylori* treatment. This is because it can lead to transmission among family members during the treatment process and increase the recurrence rate of *H. pylori* in patients after eradication.

Previous large clinical studies and guideline consensus recommend tests and treatments, as well as screening and treatment strategies for the individual-based management of *H. pylori* infection in various infected populations[2-4,19]. Due to the familial clustering of *H. pylori* infections, whole-family *H. pylori* infection control and management is clinically significant for the prevention of related diseases[20]. In China, a newly proposed strategy of family-based *H. pylori* infection control and management provides an advanced clinical approach for controlling the intrafamilial transmission and infection of *H. pylori*[8,17]. However, relatively few studies have investigated the status of family-based infections, associated factors, and patterns of intrafamilial transmission in the general population.

In this study, a cross-sectional comparison of infections before and after 20 months was conducted to evaluate household infections, risk factors, and transmission routes of *H. pylori* in families in the community of Lanzhou, in northwest China. We also assessed the willingness of *H. pylori*-infected individuals to undergo co-treatment with their entire family and conducted post-treatment follow-up. This study provides empirical evidence relating to familial *H. pylori* infection and contributes to the development of improved strategies for family co-treatment.

MATERIALS AND METHODS

Study population and design

This family-based survey was conducted in the Chengguan District of Lanzhou in Gansu Province, China from July 2021 to September 2021. After considering factors such as area, water source, cost, accessibility, testing facilities, and coronavirus disease 2019 (COVID-19), we randomly selected the Zhangye Road Guangwumen Community Health Service Center and the Yanchang Road Caochang Street Community Health Service Center from which to recruit volunteers by distributing introductory brochures or information booklet for this study and posting posters at community health service centers to inform residents of the risk of *H. pylori* infection and the need for eradication treatment. We offered free testing to those who volunteered to participate on a family basis, without any incentives. At the research site, our experienced doctors provided relevant consultation services. Community workers were responsible for helping to recruit community family members for onsite registration.

Participants included in the study were defined as individuals who had resided in the same household for a period exceeding 10 months within the past five years. The exclusion criteria encompassed the use of medications, including antibiotics, herbal medicines with antimicrobial properties, proton pump inhibitors, bismuth, probiotics, and other pharmaceuticals that could potentially impact the outcomes of the test if consumed within the preceding four weeks. In total, 519 individuals from 191 households (family size ≥ 2 persons) participated in the complete survey. All members of the included households participated, carefully fulfilling the *H. pylori* testing and completing the relevant questionnaire. After the completion of initial testing, the active intent-to-treat population was provided with a first-line bismuth-containing quadruple regimen for *H. pylori* eradication, and followed up again from April and June 2023 to test for *H. pylori* infection. However, due to the global COVID-19 pandemic since 2019, the treatment population has been unable to undergo timely follow-up examinations.

The study was approved by the Ethics Committee of the First Hospital of Lanzhou University (No. LDYYLL2021-146), and all participants provided written informed consent. For participants who were minors, written informed consent was obtained from a legal guardian.

Questionnaires for family members

Our questionnaire was rigorously designed based on the existing literature. Before initiating the study, we conducted a small-scale pilot experiment to ensure that participants could understand the reliability and accuracy of the questions and answers. For each eligible household, all members were asked to complete a questionnaire online or on-site. Well-trained physicians and community workers were on hand to guide and help individuals with the registration process and the filling out of the questionnaires. All participants were informed that their information would be treated as confidential and only used for statistical analysis. Community workers at the health centers with knowledge of the families assisted in checking the questionnaires to avoid the inclusion of careless answers. According to the purpose of this study, the questionnaire included the following items: (1) General information (*e.g.* age, gender, body mass index (BMI), the number of family members, occupation, marital status, income, and housing areas); (2) Family hygiene and living habits; (3) Dietary habits; (4) Exercise and sleep status; (5) Chronic diseases; (6) Gastrointestinal symptoms; and (7) Family history of gastrointestinal diseases.

H. pylori testing for all family members

According to the manufacturer's instructions, a specially trained clinical physician or laboratory technician used the ^{13}C -urea breath test (UBT) reagent kit to evaluate all participating family members for *H. pylori* infection. All study participants were tested in the morning after fasting for at least 6 hours. After collecting an initial breath sample with the sample collection container bag during normal respiration, the participants were orally administered 80 mL of a pre-prepared orange juice-flavored solution containing 50 mg of ^{13}C -urea. Thirty minutes later, a second breath sample was collected. We analyzed the samples using a ^{13}C breath detector (Guangzhou Huayou Mingkang Optoelectronics Technology Co., Ltd., China). A delta over baseline $\geq 4.0\%$ was considered positive for *H. pylori*, and a delta over baseline

< 4.0‰ was considered negative. An infected household was defined as a household with at least one *H. pylori*-infected family member. The definition of a new infection of *H. pylori* was that of an individual who was not infected in 2021 but was infected in 2023. The definition of new infected households was that of families where all family members were negative in 2021 and at least one positive member was infected in 2023. All tests were conducted in adherence to the manufacturer's instructions, with calibration and verification completed using samples of known gas concentrations supplied by the analyzer manufacturer before the start of the study.

Statistical analysis

Statistical analyses were conducted with Statistical Package for the Social Sciences 27.0.1. Categorical data were presented as frequencies and percentages. Univariate logistic regression analysis was used to examine the correlation between the study variables and *H. pylori* infection. When analyzing at the family level, a binary logistic regression model was used due to the independence between families. At the individual level, a generalized linear mixed model was utilized to account for the nested nature of individuals within households in the collected data. Variables with statistical significance in the univariate analysis were included in the multivariate logistic regression and generalized linear mixed models to investigate the association between risk factors and *H. pylori* infection. The results indicated odds ratios (OR) and 95% CI. $P < 0.05$ was considered statistically significant.

RESULTS

General information on enrolled families and individuals

Details of family enrollment are provided in [Figure 1](#). A total of 519 individuals from 191 families signed informed consent and received ¹³C-UBT testing for analysis of prevalence and risk factors. In 2023, 18 families (55 individuals) were lost to follow-up testing, and 173 families (464 individuals) completed the ¹³C-UBT.

The average age of the 519 individuals in 2021 was 45.3 years. Of these individuals, 222 (42.8%) were male, 297 (57.2%) were female, 404 (77.8%) were married, and 55 (10.6%) were children and adolescents. The average family size of the 191 participating families was 3.0 persons. A total of 173 families (464 individuals) followed up in 2023, comprising 194 (41.8%) males, 270 (58.1%) females, and 49 (10.5%) children and adolescents ([Table 1](#)).

Household *H. pylori* infection status and risk factors

The family-based *H. pylori* infection rate in 2021 was 76.9% (147/191). All members were infected in 19.8% (43/191) of the enrolled families, in 54.5% (104/191) of the families at least one member was infected, and in 23.0% (44/191), there were no infections. The family-based infection rate in 2023 was 67.1% (116/173). All members were infected in 13.3% (23/173) of the enrolled families. In 51.4% (89/173) of the families, at least one member was infected, and in 32.3% (57/173) of the families, there were no infections ([Figure 2A-B](#)).

Information on the infection and risk factors of the family members in the 191 registered households is provided in [Table 2](#). A larger living area (*e.g.*, sixty and above: OR: 0.10, 95%CI: 0.01-0.77) was an independent protective factor for household infections ($P < 0.05$). Other factors in this study did not affect the risk of household infections ($P > 0.05$), including family size and structure, annual household income level, household hygiene, eating habits, and the sharing of cups, dental implements, towels, dishes, and drinking sources.

Individual-based *H. pylori* infection status and risk factors

In 2021, the individual-based *H. pylori* infection rate was found to be 47.0% (244/519), which decreased to 38.1% (177/464) in 2023 ([Figure 2A](#)). Initially, the consideration of individuals infected with *H. pylori* was designated as the dependent variable, and a generalized mixed model was employed to establish a two-level zero model with individuals at level 1 and families at level 2. The findings indicated a significant clustering of *H. pylori* infection within households ($P < 0.05$). Age, BMI, family size, eating excessively hot food, consumption of nuts, and having symptoms of acid reflux, bloating, and halitosis were all found to be associated with *H. pylori* infection in individuals ($P < 0.05$) ([Supplementary Table 1](#)).

In a multivariate analysis, eating excessively hot food daily or often (OR: 2.11, 95%CI: 1.09-4.11) and frequent or occasional symptoms of halitosis (OR: 0.60, 95%CI: 0.39-0.93) were independent risk factors for individual infection ($P < 0.05$). However, the daily or frequent consumption of nuts (OR: 0.60, 95%CI: 0.39-0.93) was an independent protective factor for individual *H. pylori* infection ([Table 3](#), $P < 0.05$).

Individual-based *H. pylori* new infection status and risk factors

The individual-based *H. pylori* new infection rate was 22.8% (55/241). In the 2023 follow-up, 92 out of 244 individuals infected with *H. pylori* in 2021 opted for eradication treatment using the bismuth quadruple. BMI, family structure, source of drinking water, use of a refrigerator at home, following a regular eating schedule, and heartburn symptoms were associated with new *H. pylori* infection ($P < 0.05$) ([Supplementary Table 2](#)).

In a multivariate analysis, family structure (*e.g.*, others: OR: 7.18, 95%CI: 1.83-28.13), source of drinking water (*e.g.*, purified water, OR: 3.08, 95%CI: 1.34-7.10), and frequent or occasional symptoms of heartburn (OR: 3.21, 95%CI: 1.35-7.64) were independent risk factors for new individual *H. pylori* infection ($P < 0.05$). However, the use of a refrigerator at home (OR: 0.11, 95%CI: 0.02-0.75) was an independent protective factor for new *H. pylori* infections ([Table 4](#), $P < 0.05$).

Table 1 Demographic information and *Helicobacter pylori* infection status of enrolled individuals, *n* (%)

Variables	<i>H. pylori</i> -infected ¹	<i>H. pylori</i> uninfected	^a P value	New <i>H. pylori</i> -infected ²	New <i>H. pylori</i> uninfected	^b P value
Gender						
Female	105 (47.3)	117 (52.7)		18 (18.0)	82 (82.0)	
Male	139 (46.8)	158 (53.2)	0.829	37 (26.2)	104 (73.8)	0.100
Age (years)						
≤ 18	14 (25.5)	41 (74.5)		5 (13.5)	32 (86.5)	
≤ 39	79 (46.2)	92 (53.8)	0.010	19 (23.5)	62 (76.5)	0.251
≤ 59	77 (49.0)	80 (51.0)	0.004	18 (25.0)	54 (75.0)	0.167
≥ 60	74 (54.4)	62 (45.6)	0.001	13 (25.5)	38 (74.5)	0.233
Body mass index (kg/m ²)						
< 18.5	15 (29.4)	36 (70.6)		3 (9.1)	30 (90.0)	
18.5-23.9	132 (46.6)	151 (53.4)	0.034	30 (23.3)	99 (76.7)	0.105
24-27.9	76 (50.7)	74 (49.3)	0.017	18 (26.9)	49 (73.1)	0.048
> 28	21 (60.0)	14 (40.0)	0.011	4 (33.3)	8 (66.7)	0.117
Nationality						
The Han nationality	238 (46.9)	269 (53.1)		49 (20.0)	186 (79.1)	
Others	6 (50.0)	6 (50.0)	0.721	6 (100.0)	0 (0.0)	0.986
Marital status						
Unmarried	46 (40.0)	69 (60.0)		11 (17.7)	51 (82.3)	
Married	198 (49.0)	206 (51.0)	0.127	44 (24.6)	135 (75.4)	0.248
Education level						
Junior high school and below	65 (47.1)	73 (52.9)		16 (24.6)	49 (75.4)	
High school or technical school	59 (47.2)	66 (52.8)	0.994	14 (25.0)	42 (75.0)	0.757
Junior college	59 (47.2)	66 (52.8)	0.790	15 (25.4)	44 (74.6)	0.977
College and above	61 (46.6)	70 (53.4)	0.975	10 (16.4)	51 (83.6)	0.295
Occupation						
Blue collar	46 (43.8)	59 (56.2)		18 (32.7)	37 (67.3)	
White collar	78 (45.3)	94 (54.7)	0.765	15 (19.2)	63 (80.8)	0.116
Student	14 (26.9)	38 (73.1)	0.057	4 (11.8)	30 (88.2)	0.057
Unemployed people	106 (55.8)	84 (44.2)	0.069	18 (24.3)	56 (75.7)	0.494
Family size						
2	103 (54.8)	85 (45.2)		14 (17.7)	65 (82.3)	
3	82 (42.7)	110 (57.3)	0.035	18 (18.8)	78 (81.3)	0.952
Four and above	59 (42.4)	80 (57.6)	0.049	23 (34.8)	43 (65.2)	0.088
Family structure ³						
Couple's family	62 (54.4)	52 (45.6)		5 (10.4)	43 (89.6)	
Nuclear family	35 (40.2)	52 (59.8)	0.081	6 (13.6)	38 (86.4)	0.795
Immediate family	51 (45.5)	61 (54.5)	0.243	12 (25.5)	35 (74.5)	0.149
United States family	34 (47.9)	37 (52.1)	0.433	10 (28.6)	25 (71.4)	0.109
Others	62 (45.9)	73 (54.1)	0.270	22 (32.8)	45 (67.2)	0.022

Household income (renminbi)						
< 10000	62 (48.1)	67 (51.9)		9 (15.5)	49 (84.5)	
10000-30000	78 (52.0)	72 (48.0)	0.569	19 (29.7)	45 (70.3)	0.158
> 30000	104 (43.3)	136 (56.7)	0.466	27 (22.7)	92 (77.3)	0.567
Annual household living area (m ²)						
≤ 30	51 (46.4)	59 (53.6)		8 (15.1)	45 (84.9)	
30-60	88 (47.6)	97 (52.4)	0.810	18 (20.7)	69 (79.3)	0.422
≥ 60	105 (46.9)	119 (53.1)	0.822	29 (28.7)	72 (71.3)	0.092

^a*P* value was calculated by univariate logistic regression of the infected individuals, *P* < 0.05 indicates that infection risk increased/decreased significantly compared with the reference groups.

^b*P* value was calculated by univariate logistic regression of the new infected individuals, *P* < 0.05 indicates that new infection risk increased/decreased significantly compared with the reference groups.

¹*H. pylori*-infected: *Helicobacter pylori* (*H. pylori*)-infected individuals were infected in 2021.

²New *H. pylori*-infected: New *H. pylori*-infected individuals were not infected in 2021 but were infected in 2023.

³Family structure refers to the relationships between the family members who make up the family. The couple's family is composed of only two individuals: A husband and a wife. The nuclear family is a family composed of parents and unmarried children. Immediate family is a family consisting of two or more generations of married couples, with no more than one couple per generation and no intergenerational gap between them. A United States family refers to a family in which any generation contains two or more couples. Others include single-parent families, intergenerational families, cohabiting families, homosexual families, and single families.

H. pylori: *Helicobacter pylori*.

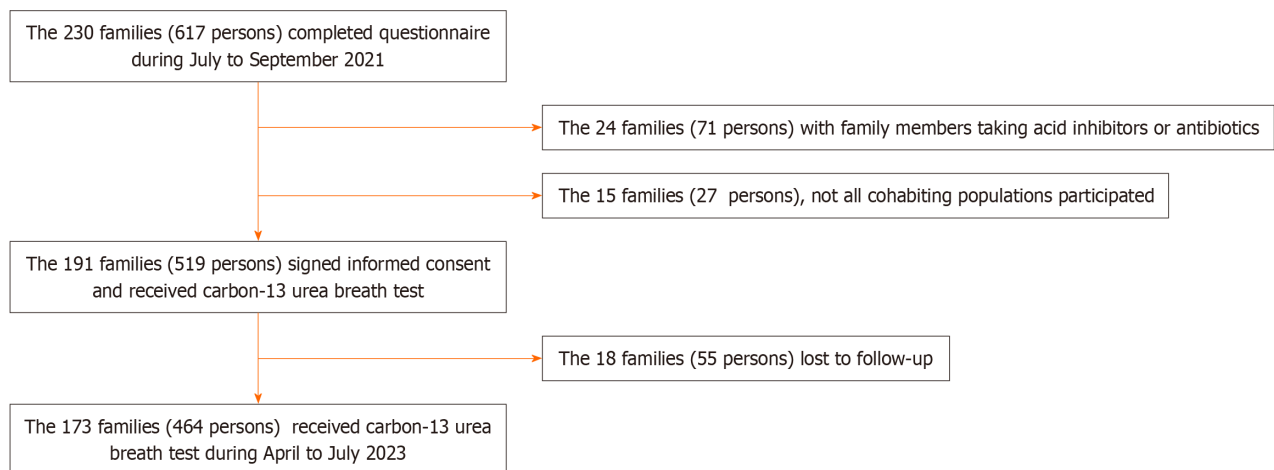


Figure 1 Flow chart of household and individual enrolment processes. An infected household is defined as a household with at least one *Helicobacter pylori* (*H. pylori*) infected family member. The new infection of *H. pylori* occurred in individuals who were not infected in 2021 but were infected in 2023.

DISCUSSION

Our study investigated the prevalence of *H. pylori* infection within households and individuals within the community of Lanzhou in Gansu Province, China, for which cross-sectional comparisons were conducted after 20 months. The results revealed that the rate of family-based *H. pylori* infections was significantly higher than individual-based infections, indicative of the existence of an inter-family of *H. pylori* infection, possibly due to the high prevalence of *H. pylori* in the general population and communal dining habits in China. In the present study, the assessment of *H. pylori* test outcomes before and after a 20-month period revealed a reduction in the prevalence of individual infection from 47.0% (244/519) to 38.1% (177/464), as well as a decrease in the prevalence of household infection from 76.9% (147/191) to 67.1% (116/173). There are several potential explanations for this phenomenon: (1) A shift in poor living and dietary habits among participants following an increased awareness of *H. pylori* infection through health education; (2) Some infected people voluntarily chose eradication treatment, and although some of them did not undergo eradication treatment for *H. pylori* infection, they tested negative for ¹³C-UBT in 2023, potentially due to the widespread antibiotic use during the COVID-19 pandemic[21]; and (3) Due to the limitations of this study's sample size.

Nevertheless, infected family members were recommended to undergo quadruple treatment. However, a 22.8% rate for new infections was observed in this study, which may be due to the combination of a high incidence of *H. pylori* infection and communal dining habits in China. In 2021, only 37.3% (92/244) of infected individuals voluntarily received eradication treatment *via* the bismuth quadruple therapy, and they did not follow up in a timely during the medication

Table 2 Household *Helicobacter pylori* infection status and risk factors, n (%)

Variables	Infected household (147) ¹	Uninfected household (44) ²	Crude OR	95%CI	^a P value	Adjusted OR	95%CI	^b P value
Family structure ³								
Couple's family	43 (75.4)	14 (24.6)	Reference					
Nuclear family	22 (78.6)	6 (21.4)	1.19	0.40-3.54	0.749			
Immediate family	26 (81.3)	6 (18.8)	1.41	0.48-4.13	0.530			
United States families	16 (88.8)	2 (11.1)	2.61	0.53-12.76	0.238			
Others	40 (71.4)	16 (28.6)	0.81	0.35-1.88	0.630			
Family size								
2	69 (73.4)	25 (26.6)	Reference					
3	49 (76.6)	15 (23.4)	0.38	0.12-1.19	0.097			
Four and above	29 (87.9)	4 (12.1)	0.45	0.14-1.49	0.191			
Household income (renminbi)								
< 10000	41 (80.4)	10 (19.6)	Reference					
10000-30000	49 (76.6)	15 (23.4)	0.80	0.32-1.96	0.621			
> 30000	57 (75.0)	19 (25.0)	0.73	0.31-1.74	0.479			
Annual household living area (m ²)								
≤ 30	29 (96.7)	1 (3.3)	Reference			Reference		
30-60	61 (72.6)	23 (27.4)	0.09	0.01-0.71	0.022	0.09	0.01-0.71	0.022
≥ 60	57 (74.0)	20 (26.0)	0.10	0.01-0.77	0.027	0.10	0.01-0.77	0.027
Household hygiene								
Good	100 (76.3)	31 (23.7)	Reference					
Fair or poor	47 (78.3)	13 (21.7)	1.12	0.54-2.34	0.761			
Eating habits								
Individual dining	8 (80.0)	2 (20.0)	Reference					
Dish sharing	83 (73.5)	30 (26.5)	0.69	0.14-3.44	0.653			
Both of the above	56 (82.4)	12 (17.6)	1.17	0.22-6.20	0.856			
Use cleaning agents or detergent to clean tableware								
Frequently	39 (79.6)	10 (20.4)	Reference					
Everyday	108 (76.1)	34 (23.9)	0.81	0.37-1.80	0.613			
Sharing drinking cup								
Rarely	111 (76.0)	35 (24.0)	Reference					
Frequently	36 (80.0)	9 (20.0)	1.26	0.55-2.87	0.581			
Sharing dental equipment								
Rarely	135 (77.1)	40 (22.9)	Reference					
Frequently	12 (75.0)	4 (25.0)	0.89	0.27-2.91	0.846			
Sharing towels								
Rarely	130 (76.5)	40 (23.5)	Reference					
Frequently	17 (81.0)	4 (19.0)	1.31	0.42-4.11	0.646			
Sharing tableware								
Rarely	69 (73.4)	25 (26.6)	Reference					

Frequently	78 (80.4)	19 (19.6)	1.49	0.75-2.93	0.252
Source of drinking water					
Tap water	73 (73.7)	26 (26.3)	Reference		
Purified water	74 (80.4)	18 (19.6)	1.46	0.74-2.90	0.273
Storage methods for leftover food					
Put it in the fridge	120 (76.9)	36 (23.1)	Reference		
Room temperature	17 (81.0)	4 (19.0)	1.28	0.40-4.03	0.679
Throw away	10 (71.4)	4 (28.6)	0.75	0.22-2.54	0.643

^a*P* value was calculated by univariate logistic regression, *P* < 0.05 indicates that infection risk increased/decreased significantly compared with the reference groups.

^b*P* value was calculated by multivariate logistic regression and was adjusted with items of *P* < 0.05 in univariate logistic regression.

¹Infected household is defined as a household with at least one *Helicobacter pylori* (*H. pylori*)-infected family member.

²Uninfected household is defined as a household without any *H. pylori*-infected family member.

³Family structure refers to the relationships between the family members who make up the family. The couple's family is composed of only two individuals: A husband and a wife. The nuclear family is a family composed of parents and unmarried children. Immediate family is a family consisting of two or more generations of married couples, with no more than one couple per generation and no intergenerational gap between them. A United States family refers to a family in which any generation contains two or more couples. Others include single-parent families, intergenerational families, cohabiting families, homosexual families, and single families.

OR: Odds ratio; *H. pylori*: *Helicobacter pylori*.

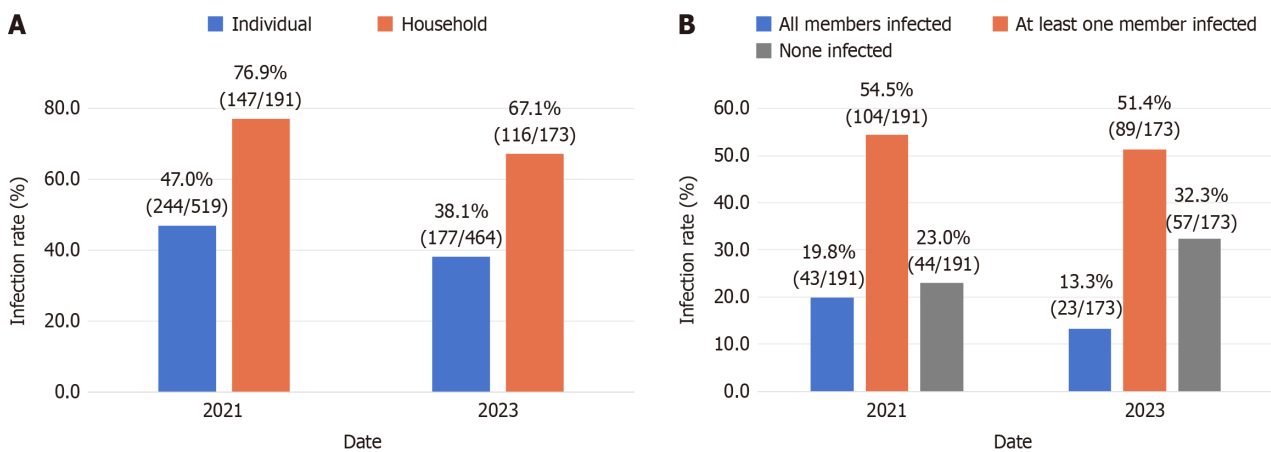


Figure 2 Individual and household *Helicobacter pylori* infection rates. A: Individual and household *Helicobacter pylori* infection rates in 2021 and 2023; B: Proportion of households with different numbers of infected family members.

period, potentially resulting in insufficient compliance. According to the questionnaire, in families where participants tested positive for *H. pylori*, fewer of the infected members in these families followed up with treatment together after health education. This was partly because a small percentage of enrolled participants were unable or unwilling to receive treatment. Some infected members of the family selected eradication treatment, while other infected family members were at increased risk of reinfection and recurrence if they did not undergo eradication treatment[22]. These findings highlight the need to provide treatment to all family members who have been infected together.

Sampling for this study was conducted at Community Health Service Centers, which services over 10 communities, and evaluated the impact of different household factors, such as occupation, education levels, and different income levels, on the rates of infection. The results suggested that a larger living area per capita was an independent protective factor for household *H. pylori* infection. This is in line with previous research that living in crowded living conditions is associated with higher rates of *H. pylori* infection[9,23]. Nevertheless, factors such as family size and structure, income levels, hygienic conditions, and shared use of living goods were not found to be significantly correlated with household infections. In this study, as individuals began to realize the importance of personal hygiene and living standards in disease prevention, fewer living goods were shared, with the exception of dishes and chopsticks. Previous studies have shown a strong correlation between *H. pylori* infection in family members and their lifestyle choices, as well as the significance of intra-household transmission of the infection in family members. *H. pylori* is adapted to live in the stomach and can enter the mouth through the reflux of gastric juice. As a result, *H. pylori* can be transmitted through the sharing of tableware or cups, or by chewing or tasting children's food[24]. A study of children in China found that eating in unster-

Table 3 Multivariate analysis of factors associated with individual-based *Helicobacter pylori* infection

Model	Intercept and variables	Odds ratio	95%CI	P value
Fixed effect	Intercept	0.53	0.21-1.35	0.184
	Age (years)			
	≤ 18	Reference		
	≤ 39	1.68	0.75-3.75	0.207
	≤ 59	1.74	0.76-4.02	0.193
	≥ 60	1.97	0.82-4.71	0.127
	Body mass index (kg/m ²)			
	< 18.5	Reference		
	18.5-23.9	2.25	0.80-6.31	0.123
	24-27.9	1.28	0.56-2.95	0.557
	> 28	1.19	0.55-2.61	0.656
	Family size			
	2	Reference		
	3	0.69	0.43-1.12	0.134
	Four and above	0.64	0.37-1.11	0.114
	Eating too hot food			
	Never	Reference		
	Occasionally	1.14	0.73-1.79	0.563
	Every day or often	2.11	1.09-4.11	0.027
	Consumption of nuts			
	Never	Reference		
	Occasionally	0.56	0.36-0.88	0.013
	Every day or often	0.45	0.22-0.92	0.03
	Heartburn			
	Never or rarely	Reference		
	Often or occasionally	1.00	0.64-1.57	0.993
	Abdominal distension			
	Never or rarely	Reference		
	Often or occasionally	1.07	0.64-1.80	0.791
	Halitosis			
Never or rarely	Reference			
Often or occasionally	1.70	1.06-2.72	0.028	
Random effect	Level 2			0.055
	Level 1 (scale parameters)			

P value was calculated by multivariate analysis utilizing generalized linear mixed models and was adjusted with items of $P < 0.05$ in univariate logistic regression.

ilized conditions, sharing towels, communal meals, maternal chew-feeding, artificial feeding, lack of hand hygiene, overcrowded housing, and a family history of gastrointestinal disease were associated with a significantly increased risk of infection[24]. Some studies have identified low levels of household income and education[5,17], infection in family members, larger family size, and family history of gastric cancer as risk factors for household *H. pylori* infection[5].

Our findings highlight a noteworthy association between age and *H. pylori* infection, with a higher prevalence of *H. pylori* infection observed in individuals over the age of 60 years. This susceptibility in older individuals can be

Table 4 Multivariate analysis of factors associated with new individual-based *Helicobacter pylori* infection

Model	Intercept and variables	Odds ratio	95%CI	P value
Fixed effect	Intercept	0.13	0.01-1.56	0.107
	Body mass index (kg/m ²)			
	< 18.5	Reference		
	18.5-23.9	2.80	0.64-12.27	0.171
	24-27.9	4.33	0.89-21.06	0.069
	> 28	6.71	0.87-51.80	0.068
	Family structure			
	Couple's family	Reference		
	Nuclear family	1.53	0.29-7.98	0.612
	Immediate family	3.43	0.80-14.71	0.097
	United States family	3.61	0.78-16.78	0.101
	Others	7.18	1.83-28.13	0.005
	Source of drinking water			
	Tap water	Reference		
	Purified water	3.08	1.34-7.10	0.008
	Using a refrigerator at home			
	No	Reference		
	Yes	0.11	0.02-0.75	0.025
	Eating regularly and on time			
	Often or occasionally	Reference		
Every day	0.47	0.22-1.02	0.056	
Heartburn				
Never or rarely	Reference			
Often or occasionally	3.21	1.35-7.64	0.009	
Random effect	Level 2			0.062
	Level 1 (scale parameters)			

P value was calculated by multivariate analysis utilizing generalized linear mixed models and was adjusted with items of $P < 0.05$ in univariate logistic regression.

attributed to age-related declines in physiological function, resistance, and immunity. Nevertheless, studies have indicated a decrease in *H. pylori* infection rates in individuals aged 40-50 years[25,26], possibly due to younger and middle-aged individuals being more likely to come into contact with infected individuals while dining out and socializing. Furthermore, cytokines are essential in combating *H. pylori*, and variations in immune responses across age groups further influence infection rates[27]. There may be a bi-directional association between BMI and *H. pylori* infection [28]. Our research revealed a positive association between BMI and the prevalence of *H. pylori* infection in individuals, with overweight individuals showing a heightened risk of new infections. Previous research has established a positive correlation between *H. pylori* infection and BMI in developing countries[29-31], while a negative association has been observed in developed nations[32]. This was supported by the significant rise in body weight observed after the successful eradication of *H. pylori*, which may be attributed to the improvement of gastrointestinal dyspepsia symptoms following the elimination of the infection[33]. The mechanisms underlying the relationship between *H. pylori* infection and obesity are unclear. There was a suggestion that gastrointestinal hormone regulation may play a role. Individuals infected with *H. pylori* were found to exhibit decreased serum leptin levels, which can lead to delayed satiety and an increased susceptibility to obesity[34]. An additional potential mechanism contributing to the development of obesity in individuals infected with *H. pylori* was the observed association with increased insulin resistance[35]. Furthermore, compromised gastrointestinal immune function in individuals with obesity may promote the persistence of *H. pylori*[36].

Family size and structure were linked to individual *H. pylori* infections in this study, with infection rates decreasing as the number of family members increased. This contradicts previous findings that larger families have a higher risk of

infection[4,5], possibly because many two-person families in this study were couples who were in close contact with each other. Previously, studies have found that couples in which one partner is infected face a heightened risk of infection, and that couples exhibiting symptoms of reflux are more susceptible to infection[37,38]. In this study, other family structures, including sibling, single-parent, or intergenerational families, exhibited a greater susceptibility to new infections compared to husband-and-wife families. This finding contradicted the prevailing notion that households with spouses are more closely contact-transmissible and therefore at higher risk, indicative of a potentially complex pattern underlying the intrafamilial transmission of *H. pylori*.

A significant correlation was observed between the frequent consumption of excessively hot food and an elevated incidence of infection. This association may be attributed to the irritant effects of hot food on the gastric mucosa, leading to a reduction in gastrointestinal resistance and increased susceptibility to infection. This finding aligns with the outcomes of a multicenter randomized study conducted by Razuka-Ebela *et al*[39] in Latvia, Eastern Europe. The study involved 1855 participants aged 40-64 years and examined the presence of antibodies for *H. pylori*. The results indicated that the consumption of excessively hot food or beverages was identified as a risk factor for *H. pylori* infection (OR: 1.32, 95%CI: 1.03-1.69). We also found that the consumption of nuts was an independent protective factor for *H. pylori* infection in individuals. In a study conducted by Shu *et al*[40] on Chinese adults aged 40 years to 59 years, a diet rich in nuts was associated with a reduced prevalence of *H. pylori* infection. Phytochemicals obtained from nuts have been shown to inhibit *H. pylori* infection and influence metabolic and gut bacteria[41]. Consequently, the moderate consumption of nuts may help prevent *H. pylori* infection. Following a regular eating schedule was also found to be an independent protective factor for new individual *H. pylori* infections. Overeating and irregular prolonged meal times were associated with an increased risk of *H. pylori* infection[42,43]. These results suggest that eating regular meals, including avoiding oversaturation or excessive hunger, could help to prevent gastric mucosal damage and dysfunction resulting from abnormal gastric acid secretion, thereby reducing the risk of *H. pylori* infection.

A significant positive association was observed between individuals experiencing frequent symptoms of acid reflux, bloating, and halitosis and *H. pylori* infection, as well as a positive association between frequent heartburn symptoms and new *H. pylori* infection. These findings aligned with those of previous studies indicating a link between *H. pylori* infections and gastrointestinal dysfunction[44]. However, some studies have found that chronic dyspepsia does not predict *H. pylori* infection[45]. A study even identified a significant negative correlation between frequent symptoms of reflux and the presence of *H. pylori* antibodies[46]. Thus, halitosis could be a risk factor for *H. pylori* infection in individuals. In cases of *H. pylori* infection, there is a notable decrease in pressure in the lower esophagus, leading to the reflux of stomach contents and the subsequent transmission of strains to the oral cavity, resulting in halitosis. However, *H. pylori* infection was not found to be an independent risk factor for halitosis. Several studies have demonstrated the presence of *H. pylori* in saliva, the dorsum of the tongue, and dental plaque in the oral cavity of individuals with periodontal disease[47,48].

In summary, the prevalence of household *H. pylori* infection in families living in Lanzhou is significantly higher than the rate of individual infection. In response to the fact that *H. pylori* is characterized by familial clustering, in 2021, China proposed measures for the “family-based prevention and control of *H. pylori* infection” as an important strategy to effectively stop the infection and spread of *H. pylori*[8]. This is applicable in areas unaffected by the incidence of *H. pylori* infection and gastric cancer, and in some high-prevalence areas, is economically beneficial, reducing both the social and economic burden[49]. It is extremely important to raise public awareness of *H. pylori* through lectures on lifestyle and dietary habits. In this respect, the following measures could be taken: (1) Address unhealthy lifestyles, improve personal hygiene (*e.g.* wash hands before meals), adopt healthy habits (*e.g.* quit smoking and drinking), and practice physical exercise; (2) Pay attention to dietary habits, avoid consuming high-risk foods and raw foods, do not share chopsticks and spoons, and improve the dietary structure; (3) Monitor screening, especially for previously infected individuals, the family members of infected individuals, and other high-risk groups, such as those with halitosis, periodontal disease, *etc.*; and (4) *H. pylori*-infected individuals and their family members should undergo joint eradication treatment, and accurate testing and evaluation should be carried out before eradication. For children and the elderly, accurate testing and a comprehensive evaluation should be mainly based on their age, symptoms, and tolerance level before deciding whether to treat.

This study has several limitations. These include the lack of a timely review post-treatment for *H. pylori*-infected patients in 2021 and the inability to determine eradication failure or re-infection in individuals with positive ¹³C-UBT test results in 2023. In addition, although three-quarters of the infected families were willing to receive treatment together, not many families ultimately chose to be co-treated on a family basis, making it difficult to compare the eradication rate of co-treatment between families and individuals. These findings highlight the continued need for health education and the promotion of lifestyle changes. In addition, the small size of the study limits the representation of *H. pylori* infections in Lanzhou. Furthermore, the absence of bacterial strain culture and DNA data prevented the precise assessment of *H. pylori* genotypes in infected individuals.

CONCLUSION

In summary, the household *H. pylori* infection rate in Lanzhou is relatively high and linked to socio-demographic factors and lifestyles. Eradication efforts and control of related risk factors are recommended in the general population.

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