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Prevalence and Risk Factors of *Helicobacter pylori* Infection in Patients with Dyspepsia: A Cross-Sectional Study in Gerash, Iran (2023)

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ABSTRACT

Background: *Helicobacter pylori* is a gram-negative, microaerophilic bacterium and a major etiological agent of various gastrointestinal disorders, including gastritis, peptic ulcer disease, and gastric cancer. Given the high prevalence of this infection in Iran, identifying factors influencing its transmission is crucial.

Methods: This descriptive cross-sectional study was conducted in 2023 on 71 patients presenting with dyspepsia at the Amir-al-Momenin Educational and Treatment Center in Gerash, Iran. The initial diagnosis was performed using the Urea Breath Test (C14), with molecular confirmation by PCR. Gene expression analysis of *vacA* and *fliA* was conducted using SYBR Green Real-Time PCR. Data were analyzed with SPSS version 25 using the t-test and Chi-square test.

Results: Among 71 participants, 51 (71.8%) were infected with *H. pylori*. Prevalence was significantly higher in individuals aged 40 years or older and in those of lower socioeconomic status (P<0.05). High consumption of fast food and sweets was also associated with increased infection risk. Molecular analysis revealed high expression of the *vacA* gene in 82% and of the *fliA* gene in 76% of infected patients, indicating the presence of highly pathogenic strains in this region.

Conclusion: The findings suggest that lower socioeconomic status, unhealthy dietary habits, and increasing age are significant contributors to the high prevalence of *H. pylori* in Gerash. Implementing educational initiatives, improving sanitary conditions, and promoting dietary modifications could effectively reduce the burden of this infection.

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Introduction

Helicobacter pylori is a gram-negative, microaerophilic bacterium that colonizes the gastric and duodenal mucosa in humans. It is recognized as a primary causative agent of several gastrointestinal diseases, including gastritis, gastric and duodenal ulcers, and gastric cancer. First identified by Warren and Marshall in 1983, their discovery was later awarded the Nobel Prize in Medicine [1]. *H. pylori* remains one of the most common chronic human infections globally, with an estimated prevalence in approximately half of the world's population [2]. The infection is particularly prevalent in developing countries and regions with suboptimal public hygiene. Persistent infection can lead to chronic gastritis and, if untreated, may progress to gastric cancer, a leading cause of cancer-related mortality in many developing nations, for which *H. pylori* is classified as a Group I carcinogen [3].

In Iran, *H. pylori* is a frequent cause of gastrointestinal morbidity. Studies report high infection rates across the country, especially in the southern and central regions. For instance, research by Ziaei et al. (2020) in southern Iran indicated a prevalence of 24.8% among children [4], highlighting the role of inadequate sanitary conditions and limited healthcare access. The prevalence in adults is reportedly even higher, reflecting disparities in hygiene and socioeconomic factors compared to Western nations [5].

Multiple risk factors contribute to *H. pylori* acquisition, including low socioeconomic status, poor hygiene, and contaminated water sources [6]. Dietary habits, such as high intake of fatty foods, fast food, processed sweets, and foods rich in added sugars and trans fats, may also promote bacterial colonization by inducing gastric inflammation and compromising immune responses [7, 8]. Additional factors such as age, gender, and family history have been implicated, with higher infection rates observed in individuals over 40 years [9].

Diagnosis typically involves clinical tests such as the Urea Breath Test, endoscopy with biopsy, and molecular methods like PCR and quantitative reverse transcription PCR (RT-qPCR), which allow for precise detection and virulence gene profiling [10, 11].

This study aimed to investigate the molecular prevalence of *H. pylori*, assess expression levels of its virulence genes (*vacA* and *fliA*), and identify associated risk factors among dyspeptic patients in Gerash, Iran. By elucidating local epidemiological and molecular characteristics, this research seeks to inform targeted prevention strategies and improve clinical management in high-prevalence regions.

Materials and Methods

Study Design and Setting

This cross-sectional study was conducted in 2023 at the Amir-al-Momenin Educational and Treatment Center in Gerash, Iran. Consecutive patients presenting with dyspeptic symptoms who underwent Urea Breath Testing were invited to participate.

Participants

A convenience sample of 71 symptomatic patients (56 women, 15 men) was enrolled. Inclusion criteria comprised adults (≥18 years) with symptoms such as epigastric pain, bloating, dyspepsia, or nausea. Patients who had taken antibiotics or proton pump inhibitors within five days prior to testing were excluded.

Data Collection

A structured questionnaire administered by a physician or health specialist collected data on demographics, socioeconomic status, medical history, dietary habits, and personal hygiene.

H. pylori Detection

Urea Breath Test (C14): Used for initial non-invasive diagnosis.

Molecular Confirmation: DNA was extracted from gastric samples using a commercial kit. Conventional PCR targeted *16S rRNA* and *ureA* genes for confirmation.

Gene Expression Analysis: Total RNA was extracted, reverse transcribed to cDNA, and analyzed by SYBR Green Real-Time PCR. Expression of *vacA* and *fliA* was quantified using the ΔΔCt method, with *GAPDH* as the endogenous control.

Statistical Analysis

Data were analyzed using SPSS version 25. Categorical variables were compared using the Chi-square test, and continuous variables with the independent t-test. Logistic regression identified independent risk factors. A P-value <0.05 was considered statistically significant.

Results

Prevalence of H. pylori

Of 71 patients, 51 (71.8%) were positive for *H. pylori*. Prevalence was significantly higher in patients aged >40 years (84.1%) compared to younger individuals (59.4%; P=0.047). Demographic and clinical characteristics are summarized in Table 1.

Risk Factor Analysis

Infection rates did not differ significantly by gender (P=0.915). Lower economic status was associated with higher prevalence (52.0% in low-income vs. 33.3% in high-income groups). High weekly consumption of

fast food and sweets was correlated with increased infection risk. Multiple logistic regression identified age (OR: 1.035, 95% CI: 1.00–1.071) and non-separate toilet type (OR: 2.83, 95% CI: 0.984–8.180) as independent predictors (Table 2).

Molecular Findings

PCR confirmed *H. pylori* in 84.9% of UBT-positive cases. High expression of *vacA* and *fliA* was observed in 82% and 76% of infected patients, respectively (Tables 3 & 4).

Table 1. Comparison of demographic and clinical characteristics in patients with and without peptic ulcer disease. (a: Independent t-test, b: Chi-square)

Variables	Total Population N(%)	Peptic Ulcer Disease Yes, N (%)	Peptic Ulcer Disease No, N(%)	P-value
Age (Year)				
Mean ± SD	16.55 ± 44.28	14.73 ± 40.94	17.72 ± 47.35	0.104[a]
Gender				
Male	(21.1) 15	(46.7) 7	(53.3) 8	0.915[b]
Female	(78.9) 56	(48.2) 27	(51.8) 29	
Education				
Non-university	(93.0) 66	(45.5) 30	(54.5) 36	0.136[b]
University	(7.0) 5	(80.0) 4	(20.0) 1	
Economic Status				
Weak	(35.2) 25	(52.0) 13	(48.0) 12	0.711[b]
Medium	(56.3) 40	(47.5) 19	(52.2) 21	
Good	(8.5) 6	(33.3) 2	(66.7) 4	
Excellent	(0.0) 0	(0.0) 0	(0.0) 0	
Toilet Type				
Separate	(60.6) 43	(39.5) 17	(60.5) 26	0.081[b]
Combined	(39.4) 28	(60.7) 17	(39.3) 11	
Fast Food Intake				
One	(85.9) 61	(49.2) 30	(50.8) 31	0.143[b]
Two	(11.3) 8	(25.0) 2	(75.0) 6	
Three	(2.8) 2	(100.0) 2	(0.0) 0	
<Three	(0.0) 0	(0.0) 0	(0.0) 0	
Salt Intake				
Low	(49.3) 35	(51.4) 18	(48.6) 17	0.564[b]
Medium	(39.4) 28	(50.0) 14	(50.0) 14	
High	(4.2) 3	(33.3) 1	(66.7) 2	
Very high	(7.0) 5	(20.0) 1	(80.0) 4	
Sweets Intake				
One	(69.0) 49	(51.0) 25	(49.0) 24	0.746[b]
Two	(8.5) 6	(50.0) 3	(50.0) 3	
Three	(5.6) 4	(25.0) 1	(75.0) 3	
<Three	(16.9) 12	(41.7) 5	(58.3) 7	
Soda Intake				
No consumption	(39.4) 28	(42.9) 12	(57.1) 16	0.945[b]
One	(26.8) 19	(47.4) 9	(52.6) 10	
Two	(8.5) 6	(50.0) 3	(50.0) 3	
Three	(2.8) 2	(50.0) 1	(50.0) 1	
<Three	(22.5) 16	(56.3) 9	(43.8) 7	
Alcohol				
Yes	(7.0) 5	(60.0) 3	(40.0) 2	0.574[b]
No	(93.0) 66	(47.0) 31	(53.0) 35	

Continued Table 1. Comparison of demographic and clinical characteristics in patients with and without peptic ulcer disease. (a: Independent t-test, b: Chi-square)

Variables	Total Population N(%)	Peptic Ulcer Disease Yes, N (%)	Peptic Ulcer Disease No, N(%)	P-value
Spicy Foods				
Yes	(84.5) 60	(46.7) 28	(53.3) 32	0.631[b]
No	(15.5) 11	(54.5) 6	(45.5) 5	
Autoimmune Disease				
Yes	(11.3) 8	(37.5) 3	(62.5) 5	0.532[b]
No	(88.7) 63	(49.2) 31	(50.8) 32	
History of *H. pylori* Rx				
Yes	(18.3) 13	(53.8) 7	(46.2) 6	0.634[b]
No	(81.7) 58	(46.6) 27	(53.4) 31	
Clinical Symptoms				
Pain				
Yes	(83.1) 59	(45.8) 27	(54.2) 32	0.427[b]
No	(16.9) 12	(58.3) 7	(41.7) 5	
Diarrhea				
Yes	(14.1) 10	(40.0) 4	(60.0) 6	0.590[b]
No	(85.9) 61	(49.2) 30	(50.8) 31	
Fever				
Yes	(12.7) 9	(55.6) 5	(44.4) 4	0.622[b]
No	(87.3) 62	(46.8) 29	(53.2) 33	
Flatulence				
Yes	(71.8) 51	(49.0) 25	(51.0) 26	0.760[b]
No	(28.2) 20	(45.0) 9	(55.0) 11	
Headache				
Yes	(56.3) 40	(52.5) 21	(47.5) 19	0.377[b]
No	(43.7) 31	(41.9) 13	(58.1) 18	

Table 2. Multiple logistic regression for peptic ulcer disease (Method: Backward logistic regression)

Variables	OR (95% CI)	P-value
Age	(1.071 - 1.00) 1.035	0.047
Toilet Type		
Separate	Reference	0.054
Combined	(8.180 - 0.984) 2.83	

Table 3. Molecular diagnosis results of H. pylori

Patient No.	Urea Breath Test Result	*16S rRNA* PCR Result	*ureA* PCR Result
1	Positive	Positive	Positive
2	Negative	Negative	Negative
3	Positive	Positive	Positive
4	Positive	Positive	Positive
5	Negative	Negative	Negative

Table 4. Expression results of vacA and fliA genes

Patient No.	*vacA* Expression Level	*fliA* Expression Level	Real Time PCR Result
1	High	High	Positive
2	Low	Low	Negative
3	High	High	Positive
4	High	Low	Positive
5	Low	Low	Negative

Discussion

This study revealed a notably high prevalence of *H. pylori* infection (71.8%) among dyspeptic patients in Gerash, Iran. This rate exceeds those reported in many other regions of Iran and globally, including a reported prevalence of 24.8% among children in Shiraz [4]. Such disparities likely reflect regional variations in environmental, socioeconomic, and lifestyle factors. The elevated burden observed in Gerash may be attributed to several interconnected determinants, primarily suboptimal sanitary infrastructure and socioeconomic constraints common in southern Iran. Challenges such as limited access to clean water, use of contaminated sources, and inadequate wastewater management are established facilitators of fecal-oral transmission for *H. pylori* [6]. Consequently, public health interventions targeting sanitation and water quality could substantially reduce the transmission dynamics of this infection in similar settings.

A central finding of this study is the significant association between lower socioeconomic status and a higher prevalence of *H. pylori* infection. Individuals from economically disadvantaged backgrounds exhibited greater susceptibility, likely mediated through crowded living conditions, compromised hygiene, and limited access to healthcare and nutritious food. This correlation is consistent with epidemiological patterns observed in other developing nations, including Pakistan and regions in Africa, where poverty is a key driver of *H. pylori* endemicity [12, 13].

Dietary habits emerged as another significant modifiable risk factor. High consumption of fast food and sweets was positively correlated with *H. pylori* infection. This aligns with existing evidence suggesting that diets rich in processed foods, trans fats, and refined sugars may alter gastric physiology and the local immune response, potentially creating a more favorable environment for bacterial colonization and persistence [14, 15]. Such foods often contain pro-inflammatory additives and lack protective nutrients, possibly weakening mucosal defense mechanisms [16]. Therefore, public health initiatives promoting dietary modification towards whole foods and balanced nutrition could serve as a viable preventive measure against *H. pylori* acquisition and related morbidity.

Furthermore, age was identified as an independent predictor of infection, with individuals over 40 years exhibiting significantly higher prevalence. This finding is consistent with the natural history of *H. pylori*, which is typically acquired in childhood and persists as a chronic infection [17]. The cumulative duration of infection increases the risk of developing significant gastroduodenal pathology, including atrophic gastritis, peptic ulcer disease, and gastric cancer [18]. An age-related decline in immune efficacy may also contribute to higher bacterial load and increased detection in older adults [9]. This highlights the importance of early detection and eradication therapy, particularly in high-prevalence regions, to prevent long-term sequelae.

At the molecular level, our analysis revealed high expression of the virulence genes *vacA* and *fliA* in 82% and 76% of infected patients, respectively. The *vacA* gene encodes a potent cytotoxin responsible for vacuolization and epithelial damage, while *fliA* is a key regulator of flagellar biosynthesis and bacterial motility, crucial for colonization [19]. The predominant expression of these genes indicates the circulation of highly pathogenic strains within this population, which may correlate with an increased risk of severe clinical outcomes, such as peptic ulceration and gastric inflammation [20]. These molecular insights are critical for understanding local strain pathogenicity and could guide future research into genotype-phenotype correlations and tailored therapeutic approaches.

Globally, the prevalence of *H. pylori* remains markedly higher in developing countries compared to developed nations, a disparity largely driven by socioeconomic determinants [21]. Studies from India and Pakistan, for instance, report high infection rates strongly linked to poor living conditions and low household income [22, 23], mirroring our observations in Gerash. This consistent pattern across diverse geographic contexts underscores the universal role of socioeconomic development and public health infrastructure in controlling *H. pylori* transmission.

Conclusion

H. pylori infection remains a significant public health challenge in southern Iran, strongly associated with lower socioeconomic status, unhealthy

dietary patterns, and older age. The high virulence gene expression observed suggests an elevated risk of severe gastric pathology. Comprehensive interventions including health education, sanitation improvements, and early detection programs are essential to reduce the transmission and disease burden of *H. pylori* in this region.

Ethical Considerations

The study was approved by the Ethics Committee of Gerash University of Medical Sciences (Code: IR.GERUMS.REC.1402.006). Written informed consent was obtained from all participants, and data were anonymized.

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