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Prevalence of Helicobacter Pylori and Molecular Detection of the cagA Gene in Adults with gastrointestinal Symptoms

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ABSTRACT

Background: Helicobacter pylori (*H. pylori*) is a known gastrointestinal disease-related pathogen. The cytotoxin-associated gene A (cagA) emerged as H. pylori virulence factors, used to identify the pathogenicity and clinical outcomes. The noninvasive technique (stool-based testing) and molecular detection of *Chaga* are widely used to detect for H. pylori in epidemiological studies.

Objective: To assess the prevalence of H. pylori in adult patients presenting with gastrointestinal symptoms in Iraq and to reveal the existence of the cagA gene employing polymerase chain reaction (PCR) from stool samples.

Methods: A cross-sectional study was conducted to analyze data of adult patients presented with gastrointestinal symptoms at Baquba Teaching Hospital, Diyala, Iraq. Stool specimens were collected and eventually tested for *H. pylori* using a rapid stool antigen test (SAT), followed by molecular detection of the *cagA* gene via PCR. The Chi-square tests and binary logistic regressions were employed to assess the relationship between *cagA* positivity and demographic features.

Results: Out of 123 examined stool samples, 14.6% (18/123) diagnosed with H. Pylori. Among these, 61.1% (11/18) were cagA-positive. Higher prevalence of H. Pylori was seen among female gender (15.9%) and residents of rural regions (18.2%) compared to males (13.3%) and those residents in urban region (10.8%). There were significant associations between cagA positivity and individuals in the age group 41–60 years ($p = 0.033$). However, findings of multivariate logistic regression revealed that age (Adjusted OR = 2.9, 95% CI: 1.1–7.7, $p = 0.031$) and rural residency (Adjusted OR = 2.5, 95% CI: 1.0–6.4, $p = 0.042$) were the independent predictors for cagA positivity.

Conclusion: In conclusion, moderate prevalence of *H. pylori* and high occurrence of the *cagA* gene were reported among infected Iraqi adults. Community -based health care interventions and early detection of H. pylori with affordable approaches are crucial control infection and prevent the gastric cancers.

INTRODUCTION

Despite the harsh acidic media of the stomach, Helicobacter pylori (H. pylori) have the ability to withstand for a long time in the mucous membrane of the stomach promoting the development of severe stomach injuries such as chronic gastritis, digestive ulcers, and stomach cancer [1]. Several virulence agents might be related with the H. Pylori; however, the cytotoxin-associated gene A (cagA) was highlighted as a decisive sign of diseases. The discovery of the CAGA genes in H. Pylori has attracted the researchers' attention to understand its role in the development of the disease [1,2]. The researchers found that the severity of the clinical findings is more likely related to the difference in geographical spread of H. Pylori's positive cagA. Therefore, the possibility of acute gastritis, duodenal ulcers, and stomach cancer are higher among the individuals with positive strains of CagA compared to those with negative strains [2],[3].

Traditionally, diagnosis of H. pylori depends on culture methods, biopsies, and urease tests. However, these approaches suffered from some limitations, including the need for invasive sampling techniques and the difficult technical procedure used to handle and culture the organism according to laboratory conditions [4]. The more advanced technology (polymerase chain reaction; PCR) provided more sensitive and specific molecular diagnosis of H. pylori and its associated virulence factors like Chaga [5].

Gastric biopsies represent the ideal choice for H. pylori detection. The extracted samples contribute to perform direct histological examination and building a reliable source for future molecular studies which are targeting Chaga [6]. Many studies have reported the benefit of PCR in detection of cagA from stomach biopsy samples. However, the invasive nature and limited resource made the use of endoscopy as a challenge [7],[8],[9].

Culture media provides typical chance to isolate H. pylori and cagA, in addition to an opportunity to check the antibiotic susceptibility and to examine virulence factors. However, the strict conditions required for culturing H. Pylori may reduce the desired benefit, especially in routine diagnoses [10]. Moreover, the convenience, non-invasive and reliable diagnostic instruments such as stool antigen examination and PCR-based H. pylori detection in fecal samples provide an alternative method that have significantly participated in diverse clinical settings [11].

In this context, a comprehensive approach to detecting cagA in fecal samples is essential to clarify the pathophysiological role of H. pylori in gastric illnesses. Such investigations are particularly relevant in the high-prevalence areas with high H. pylori and significant morbidity associated with peptic ulcers and gastric cancer [12]. The consolidation of molecular diagnostics into clinical practice can enhance our understanding of H. pylori pathogenesis, improve patient management, and contribute to the development of targeted interventions [13]. This study aimed to detect the H. pylori cagA in fecal samples of Iraqi patients.

MATERIALS AND METHODS

STUDY SUBJECTS

A cross-sectional study was executed from 1st April to 30th September 2024 at the internal medicine outpatient clinic of Baquba Teaching Hospital, Diyala, Iraq. Each patient presented with dyspeptic

symptoms suggestive of H. pylori infection during the outpatient routine visits was informed in detail about the possible diagnosis and the objectives of the study.

INCLUSION AND EXCLUSION CRITERIA

All patients with history of gastric pain, both gender, aged 18 years old and more, signed the consent form with verbal approval were included in the study. Exclusion criteria constitute patients presented with gastrointestinal bleeding for any reason, known malignancy, those who had undergone to bismuth-based therapy or colonoscopy one week before collection of stool samples, history of gastrectomy, antibiotic use during the last four weeks, the severely ill and elderly patients unable to collect the stool specimens independently.

SAMPLE COLLECTION

According to inclusion and exclusion criteria 123 participants were recruited from both urban and rural regions across Diyala Governorate, Iraq. The eligible patients were instructed to use a sterile and labeled container when they provide the fresh stool sample. The collected specimens transferred to the laboratory on the same day in dry ice and kept at –80°C until the DNA extraction and PCR analysis were performed.

STOOL ANTIGEN TESTING (SAT)

Initially, a "One-Step H. pylori Antigen Test" (Plasmatec, UK) was recruited to screen for H. pylori antigen in the patients' stool.

DNA ISOLATION

The fresh and frozen stool samples which has been tested positive for H. pylori antigen were recruited to rapid extract DNA using the commercial QIAamp DNA stool minikit (QIAGEN) according to the manufacturer's instruction. The final eluate was stored at -20oC until analysis. The amount of total DNA isolated from stool samples were 55.2-190.5 ng/µL.

POLYMERASE CHAIN REACTION (CAGA GENE EXTRACTION)

Amplification of the cagA gene was carried out using specific primers: forward (5′-AATACACCAACGCCTCCAAG-3′) and reverse (5′-TTGTTGCCGCTTGCTCTC-3′) (Interactiva, England), targeting a 400 bp fragment. The PCR procedure was conducted using a GeneAmp PCR System 9700 (Applied Biosystems, Perkin Elmer, Norwalk, USA). The thermal cycling conditions included an initial denaturation at 94°C for 4 minutes, followed by 35 cycles consisting of denaturation at 94°C for 1 minute, annealing at 59°C for 1 minute, and extension at 72°C for 1 minute, with a final extension step at 72°C for 10 minutes.

Subsequently, 10 µL of the amplified products were analyzed by electrophoresis on a 2% agarose gel prepared in Tris-acetate-EDTA (TAE) buffer and stained with ethidium bromide. The amplified fragments were visualized alongside a 100 bp DNA ladder (Boehringer Mannheim, Germany) to determine product size.

STATISTICAL ANALYSIS

Sociodemographic information including the age, sex, and place of residency was gathered through using a semi-structured questionnaire. Frequency and percentage analysis were used to describe the variables. In bivariate analysis the Chi-Square test was employed to explore the association between H. Pylori and cagA with various sociodemographic variables. Binary logistic regression was performed to determine the independent predictors of cagA gene presence. The value of $P < 0.05$ was considered a statistical sign. The SPSS version 16 used to analyze the data

considering the statistically significant to be less than 0.05.

In figure 1 showed the molecular assay for detection of cagA gene of H. pylori.In gastrointestinal symptomatic adult by polymerase chain reaction that showed the positions of the forward and reverse primers generating a ~400 bp amplicon conceived under UV transluminator

ETHICAL CONSIDERATIONS

This study was approved by the Institutional Review Board of Diyala University. Written informed consent was obtained from all participants.

RESULTS

More than half (51.2 %) of respondents were females lived in urban areas (52.8 %), and about one-third (31.7%) of them were in the age group 41-60 years. These properties provide a balanced sample across the sociodemographic features (Table 1).

The prevalence of Helicobacter pylori and the cagA virulence marker was highlighted across the different demographic groups in table 2. In term of genders, the prevalence of H. pylori among females (15.9%) was slightly exceeded that of males (13.3%). Almost similar cagA positivity rates (50.0%) were seen among all age groups with exception of age group (41–60 years) where the highest H. pylori prevalence (20.5%) and the highest cagA positivity (75%) were noted, indicating a potential age-related increase in virulent strains. Based on residency, infection of H. Pylori was more among individuals from rural areas (18.2%) compared to those residents in the urban (10.8%), and the positivity of cagA was slightly higher among patients in rural regions (63.6% vs. 57.1%). These results suggest sociodemographic variations in H. pylori and cagA prevalence.

Table 3 displays the findings of the chi-square test examining the association between cagA positivity and selected demographic variables. There was significant association between the cagA positivity and the age group ($\chi^2 = 4.52$, $p = 0.033$) and residence ($\chi^2 = 3.84$, $p = 0.049$), suggesting that cagA positivity different significantly across various age groups and between rural and urban regions. In contrast, there was no significant association between cagA positivity and gender ($p = 0.794$), indicating that age of patient and where they live may influence the likelihood of carrying cagA-positive H. pylori strains.

Table 4 presents the findings of the binary logistic regression analysis showing the predictors of cagA positivity among H. pylori patients. The patients in age group 41–60 years and rural residence were significantly associated with higher odds of cagA positivity (Adjusted OR = 2.9, 95% CI: 1.1–7.7, $p = 0.031$) and (Adjusted OR = 2.5, 95% CI: 1.0–6.4, $p = 0.042$), respectively. However, female gender shows no significant association ($P = 0.81$). These results indicate that age and living in rural regions are independent predictors of cagA carriage.

DISCUSSION

In this study, H. Pylori infection was reported in 14.6 % of total sampled patients, with 61.1 % of the infected sample carry a CAGA gene. This rate is compatible with previously published studies suggesting continuous endemicity of H. Pylori in Iraq [15],[16]. It also confirms what previous studies announced about a decrease in H.

Pylori prevalence rates compared to previous years [16],[17],[18],[19].

However, the findings of this study showed a relatively moderate prevalence of H. Pylori in the area of study compared to the known historical information of other regions [20],[21], which may reflect improvement in the general health awareness among the population or as a result of successful interventions to enhance health care services and improved sanitation. However, the high CAGA positive rate among the H. Pylori patients remains concerning, given its essential role in the formation of ulcers and stomach cancer later [22],[23].

This study revealed that infection rates or cagA expression were not related to gender, which is in line with the results of Akeel et al. [24] in the Kingdom of Saudi Arabia, but it contradicts the information from Iraq and Libya, where the dominance of males was reported [24],[26].

The non-significant difference among genders in this study supports the hypothesis that adopted lifestyle and the surrounding environmental factors may exceed the biological differences in the mode of H. pylori transmission [27],[28].

The significant predictors of cagA positivity in multivariate regression analysis were the patients living in rural areas and those in the age group 41–60 years. Several risk factors such as limitation to access clean water, and unhealthy living conditions including the overcrowded and poor hygiene significantly contribute in rising the likelihood of getting H. Pylori, particularly in rural areas. These results consistent with data from some studies from UK [29], and Venezuela [30], where rural residence has been associated with the burdens of the higher incidence of H. pylori. While other countries showed similar trend such Vietnam [31].

In addition, the 41-60 age group showed the highest percentage of cagA, which consistent with the concept that continuous exposure and chronic infection over long period may rise the likelihood of gaining more virulent strains [32]. This is particularly important because the emergence of complications such as digestive ulcers and stomach cancers increases with the age and the duration of chronic injury [33].

Indeed, using of stool antigen testing, and PCR detection of cagA considered a noninvasive and valid methods to diagnose infection and virulence profiling. It also helps avoidance the endoscopy-related possible discomfort and high costs, making it especially suitable for community-based screening in health resource-limited approaches [8].

The current results shed light on the necessity to engage the molecular diagnostic tools in routinely applied public health screening of H. pylori. The accurate identifying of cagA-positive strains can help directing the higher risk group of patients for the disease severity and guiding them for targeted eradication therapy. This study suffers from some limitations such as the sample size and cross-sectional design, which prevents establishing cause effect. Moreover, PCR sensitivity can be reduced by the previous use of antibiotics, although exclusion criteria aim to reduce it.

CONCLUSION

The study demonstrates that H. pylori and its cagA virulent marker were more common among female gender, elderly individuals (especially 41–60 years), and those living in rural areas. Analysis of data

revealed significant associations between cagA positivity and both age group and place of residence. Binary logistic regression confirmed that patients aged 41–60 years and rural residents had significantly higher odds of carrying cagA-positive H. pylori strains, highlighting age and residence as key independent predictors. These results shedding lights so the need for targeted screening and interventions among populations at high-risk to deal with H. pylori-related gastrointestinal health problems, especially in underserved rural communities.

RECOMMENDATION

The study recommends future research to evaluate the antimicrobial resistance settings and to explore more virulence markers such as vacA. Furthermore, a longitudinal study that tracking acquisition of H. pylori, cagA presence, and clinical outcomes. It also may help to provide wider insight about the pathogen's role in exacerbating and progression of gastrointestinal disease in Iraq.

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TABLES

Table 1. Sociodemographic Characteristics of Participants (n=123)

Variable	Categories	N (%)
Gender	Males	60 (48.8)
	Females	63 (51.2)
Age Group	18–30 years	28 (22.8)
	31–40 years	32 (26.0)
	41–60 years	39 (31.7)
	>60 years	24 (19.5)
Residence	Urban	65 (52.8)
	Rural	58 (47.2)

Table 2. Prevalence of H. pylori and cagA by sociodemographic (n=123)

Variable	Categories	H. pylori Positive N (%)	cagA Positive N (%)
Gender	Male (n=60)	8 (13.3%)	5/8 (62.5%)
	Female (n=63)	10 (15.9%)	6/10 (60.0%)
Age Group	18–30 years	2 (7.1%)	1/2 (50.0%)
	31–40 years	4 (12.5%)	2/4 (50.0%)
	41–60 years	8 (20.5%)	6/8 (75.0%)
	>60 years	4 (16.7%)	2/4 (50.0%)
Residence	Urban (n=65)	7 (10.8%)	4/7 (57.1%)
	Rural (n=58)	11 (18.2%)	7/11 (63.6%)

Table 3.Chi-square analysis: cagA positivity by age and residence (n=123)

Variable	χ^2 Value	P-value
Age Group	4.52	0.033*
Gender	0.07	0.794
Residence	3.84	0.049*

Table 4.Logistic regression – predictors of cagA positivity (n=123)

Variable	Adjusted OR	95% CI	p-value
Age (41–60 y)	2.9	1.1–7.7	0.031*
Rural Residence	2.5	1.0–6.4	0.042*
Female Gender	1.1	0.5–2.4	0.81

FIGURES

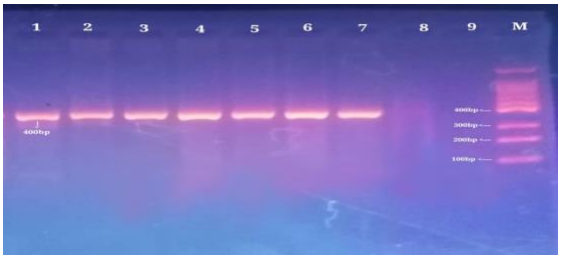

Figure 1. Schematic representation of PCR amplification of the Helicobacter pylori cagA gene in sample 1, 2,3,4,5,6 and 7 with corresponding agarose gel electrophoresis demonstrating a distinct 400 bp band compared with the DNA marker(M), lanes 8 and 9