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Helicobacter pylori Infection and Predictors Risk Factors among Patients undergoing Gastro-duodenal Fibroscopy in Yaoundé, Cameroon

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ABSTRACT

***Background:* Helicobacter pylori (*H. pylori*) infection affects more than half people worldwide particularly in African countries such as Cameroon. This study aimed to investigate the prevalence of *H. pylori* infection and predictors risk factors among patients undergoing gastro-duodenal fibroscopy at the Centre Medical, la Cathédrale of Yaoundé.**

***Methods:* A facility-based descriptive cross-sectional study involving 147 patients was conducted from October 2015 to April 2016. A structured questionnaire was used to collect information on socio-demographic factors and predictors of *H. pylori* infection. Gastric biopsies specimens were collected from the antrum and corpus using an Olympus GIF – Q30 fully immersible gastroscope respectively. The biopsies were screened for the presence of *H. pylori* by targeting the *glmM* gene using polymerase chain reaction (PCR). Statistical analysis was performed using SPSS v. 20 with p-value<0.05 considered statistically significant.**

***Results:* The mean age was 47.19 ±16.64 years and female were more represented with 88/147 (59.8%) versus (vs.) 59/147(40.1%) for male. The overall prevalence of *H. pylori* infection was 50/147 (34.01%; 95% CI: 26.41% - 42.28%). The prevalence of *H. pylori* infection was 22/59 (37.29%) in male vs. 28/88 (31.82%) in female and this prevalence increased with age and peaked among 30-50 years. Bivariate logistic regression analysis identified that, the regional group, particularly the Centre region (OR 2.55, p= 0.007) and West region (OR 2.67, p=0.005), the level of education (OR 1.18, p=0.001), source of income (OR 0.95, p=0.004), and alcohol consumption (OR 1.41, p=0.0001) were predictors risk factors of *H. pylori* infection.**

***Conclusions:* Our findings indicate a relatively high prevalence of *H. pylori* infection in Yaoundé. Factors such as regional group, level of education, source of income, and alcohol consumption predisposed the subjects to *H. pylori* infection.**

Keywords: *H. pylori* infection, predictors risk factors, gastro-duodenal fibroscopy, Yaoundé.

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I. Introduction

H. pylori is a micro-aerophilic Gram-negative bacteria that colonizes the gastric mucous layer and the epithelial lining of the stomach [1]. More than half of the world population is infected by the bacterium which is responsible for chronic infections [2]. To date, 20 strains of H. *pylori* have been recognized [3] and evidence has shown their implication in many diseases including duodenal ulcers, gastric ulcers, adenocarcinoma of the distal stomach, and mucosa-associated lymphoid tissue (MALT) and lymphoma [1].

High density crowding, poor sanitary practices, family income, educational level, age, occupation, religion, and poor water supply have been documented as important predictors of *H. pylori* infection [4]-[6]. There is an uncertainty surrounding the actual route of transmission of *H. pylori* infection. Some authors have mentioned houseflies [7] as possible transmission route. Water contaminated with faeces and fecal-ora transmissions are considered as predisposing factors for *H. pylori* infection [7], [8]. The most vulnerable group to infection is children below five years of age. Once, the infected child usually remains asymptomatic and in the absence of appropriate medical care the infection remains lifelong [9]. Water, sanitation, and hygiene (WASH) interventions could be an indispensable variable to reduce both the risk of disease and the risk of transmission of *H. pylori.*

The prevalence of *H. pylori* varies geographically with a higher prevalence occurring in the developing countries than western world [1]. Recent statistic pegged the *H. pylori* prevalence at 79.1% in Africa, 54.7% in Asia, compared to 37.1% Northern America and 24.4% Oceania [10]. Available methods have been used for the detection of *H. pylori*. The invasive methods consist of pathological anatomy, culture, PCR, rapid urease test used gastric biopsies. However, non-invasive such as labeled urea breath test, antigen detection in stool, serology is also used for the diagnosis of *H. pylori* [9, 11] Endoscopic biopsy of gastric tissue is recommended for patients suffering for ulcer or for follow-up suspected case of MALT lymphoma or gastric ulcer [12].

The high prevalence of *H. pylori* may pose additional burden on health care system in sub-Saharan countries. Studies have indicated the prevalence of *H. pylori* in several settings in Cameroon. Ndip et al. [13] has reported *H pylori* prevalence of 52.27% using stool antigen test. In the same vein, Ebule et al. [14] working at the Tombel District Hospital, obtained *H. pylori* prevalence of 79.82%, while Agbor et al [15] in Melon, recorded a 43.4 % prevalence both using an enzyme immunoassay-based method. Information on the prevalence of *H. pylori* infection and associated risk factors are scanty in Cameroon using molecular method. The aim of the study was to investigate the prevalence of *H. pylori* and predictors risk factors in patients admitted for upper gastrointestinal endoscopy (UGE). The findings from this study will contribute to improve the management of patients with *H. pylori* infection and provide an epidemiological profile of the infection among patients in Yaoundé.

II. Methodology

A. Study Design and Population

This descriptive cross-sectional study was conducted at the Centre Medical la Cathédrale, a referral private health facility in Yaoundé, Centre Region of Cameroon. One hundred and forty-seven consecutive patients of both sexes, referred for endoscopy between October 2015 and April 2016, were recruited for the study. The aims and purpose of the study was explained to the adults' patients and parental or guardian for children. Inclusion's criteria consist of patients who had not received treatment with broad spectrum antibiotics, non-steroidal anti-inflammatory drugs or proton pump inhibitors in the previous 3 months, and who did not have a history of dysphagia, gastric surgery or upper gastro intestinal bleeding and patients who have signed the consent form were enrolled.

B. Ethics Approval and Consent to Participate

The Ethical clearance was obtained from the Centre Regional Delegation of Public Health (Reference: CE 032 N°/CRERSHC/2015). A written informed consent from adult, parental or guardian for children (age under 21years old) was sought from patients after details of the study were explained to them. Emphasis was laid on the voluntary nature of participation and that they could withdraw at any time without any explanation. Confidentiality was secured by the use of unique identification codes attributed to each study participant.

C. Sample Collection

The resident gastroenterologist carried out a complete physical examination of all selected patients and their medical history recorded. A structured questionnaire made up of socio-demographic data (sex, age, marital status, level of education, nationalities with regional background), socioeconomic factors (household population, source of income) health determining behaviors (cigarette and alcohol consumption), and clinical signs was used to collect participants characteristics. So, two gastric biopsy specimens (antrum and corpus) were collected from each of the patients using an Olympus GIF – Q30 (International Medical Equipment Inc, US) fully immersible gastroscope. The two biopsies were introduced into a container with 2ml of TRIS EDTA buffer for detection of the *glmM* gene using PCR.

D. Sample Processing

Genomic deoxyribonucleic acid (DNA) was extracted from the tissue samples using ReliaPrep genomic DNA miniprep kit (Promega, Southampton UK), according to the manufacturer's instructions. DNA quality was checked by reading at 260/280 nm using Eppendorf Bio photometer Plus (Eppendorf, Germany). The DNA elute was labeled and stored at -20°C until required.

The presence of the *glmM* gene was detected by PCR using primers, the reaction mixture {(2x PCR Master mix (dNTPs [0.4 mM of each dATP, dCTP, dGTP, dTTP], 0.05u/µl Taq DNA polymerase, reaction buffer) and Nuclease-free water}, and thermal cycling [Perkin-Elmer. thermal cycler]. A set of primers (forward primer, 5`-AGG CTT TTA GGG GTG TTA GGG GTT T-3`; and reverse primer, 5`-AAG CTT ACT TTC TAA CAC TAA CGC-3`)

were used to amplify the *glmM* gene (294 bp) [16]. To each PCR tube the following were added (final volume, 25µL): 6µL of the extracted DNA, 12.5 µL of master mix, 1.5 µL of forward primer, 1.5 µl of reverse primer, and 3.5 µL of nuclease free H2O. Water was used as negative control and *E. coli* DNA sample as positive control. The tubes were transferred to the thermal cycler for amplification. The PCR mixture was subjected to 35 amplification cycles. PCR conditions were as follows: An initial denaturation (94°C, 2min), followed by 35 cycles of denaturation (94°C, 2min), annealing (55°C, 2min), and extension (72°C, 2min), with a final extension (72°C, 10 min). The amplicons were analyzed with 2% (wt./vol) ethidium bromide-stained agarose gel. The DNA bands were visualized on a 302 nm UV transilluminator (Applied Biological Materials inc, Canada) and photographed.

E. Statistical Analysis

The data were entered, cleaned, edited and coded, using Excel database, and then exported to SPSS v. 20.0 for analysis. The chi-square and Fischer exact tests were used to establish the association between the prevalence of *H. pylori* and socio-economic variables. Logistic regression analysis was used to measure the association between the risk factors and the Prevalence of *H. pylori* infection. The differences were considered to be statistically significant when the p-value obtained was less than 0.05.

III. Results

The association between *H. pylori* infection and baseline characteristics risk factors is shown in Table I. To ascertain the presence of *H. pylori* in the 147 patient's samples referred for endoscopy, the infection was confirmed in 50/147 (34.01%; 95% CI: 26.41-42.28%) by the *glmM* PCR analysis. The results reveals that the *glmM* gene was detected in 28/88 (31.82%) of female and 22/59 (37.29%) of male (p= 0.49). Analysis by age groups showed that the prevalence of *H. pylori* infection was highest in the age group >30≤50 (40.63%) and lowest in the age group>50 (26.67%). With regards to regional group, coming from Centre (p=0.007) and West regions (p=0.005) were predictors of *H. pylori* infection.

A. Risk Factors Associated with the Prevalence of H. pylori Infection

The prevalence of *H. pylori* infection associated with risk factors is shown in Table II. Smoking and the family size were predisposing factors of *H. pylori* infection. Patients who drink alcohol were 1.41 times more likely to be associated *H. pylori* infection than non-drinkers.

B. Clinical Signs Associated with the Prevalence of H pylori Infection

The relationship between clinical signs of the participants and the presence of *glmM* gene is shown in Table III. The examination of the 147 patients revealed that the most common clinical signs were: epigastralgia 93/147 (63.27%), followed by chronic epigastralgia 17/147 (11.57%), and dyspepsia 10/147 (6.80%). Of the 93 presented with epigastralgia, the *glmM* gene was detected 32/93 (34.41 %) samples. The presence of the *glmM* gene was observed in 07/17 (41.18 %) patients with Chronic epigastralgia, and 01/10 (10.00 %) patients with Dyspepsia. Surprising, no significant relationship was found between the clinical sighs and the presence of the *glmM* gene analyzed by PCR.

TABLE I: ASSOCIATION BETWEEN *H. PYLORI* INFECTION AND BASELINE CHARACTERISTICS RISK FACTORS

Variables	*glmM* (+ve) N=147 n (%)	OR	95%CI	p-value
Gender				
Female	28 (31.82)	0.78	0.39-1.56	0.49
Male	22 (37.29)			
Age (years)				
>10 ≤30	08 (34.78)	1.04	0.40-2.65	0.93
>30 ≤50	26 (40.63)	1.68	0.84-3.34	0.13
>50	16 (26.67)	0.56	0.27-1.16	0.11
Regional group				
Africa (excluding Cameroon)	04 (36.36)	1.11	0.31-4.01	0.87
Centre region	29 (46.03)	2.55	1.27-5.15	0.007**
Far north region	03 (27.27)	0.71	0.17-2.80	0.87
West region	29 (46.77)	2.67	1.32-5.40	0.005**
Level of education				
Primary	19 (38.54)	1.18	0.58-2.41	0.001**
Secondary	14 (28.83)	0.62	0.28-1.39	
Post-Secondary	19 (38.00)	1.23	0.61-2.49	
Source of income				
Primary	14 (28.00)	0.95	0.44-2.04	0.004**
Secondary	08 (16.00)	0.83	0.33-2.08	
Tertiary	28 (56.00)	1.14	0.57-2.27	

N: total number of patients, +ve: positive, %: percentage, OR: Odds Ratio, CI: Confidence Interval, **: significant.

TABLE II: PREVALENCE OF *H. PYLORI* INFECTION ASSOCIATED WITH RISK FACTORS

Variables	*glmM* (+ve) N=147 n (%)	OR	95%CI	p-value
Alcohol				
Yes	30 (36.14)	1.41	0.70-2.83	0.0001**
No	20 (31.25)			
Smoke				
Yes	06 (33.33)	0.96	0.33-2.79	0.94
No	44 (34.11)			
Family size				
>3persons/room	06 (33.09)	0.96	0.33-2.79	0.94
<3 pesons/room	44 (44.44)			

N: total number of patients, +ve: positive, %: percentage, OR: Odds Ratio, CI: Confidence Interval, **: significant.

IV. Discussion

The present study was conducted to investigate the prevalence of *H. pylori* and predictors risk factors among patients at the Centre Medical, la Cathédrale of Yaoundé, Cameroon. The overall prevalence of *H. pylori* was 34.01% (95% CI: 26.41-42.28%) using molecular method. This low prevalence is in contradiction with other study conducted in the Littoral and West region of Cameroon [15], [17]. The low prevalence of *glmM* gene observed in this study may be attributed to a high polymorphism and diversity of the *glmM* in different species of *H. pylori*. Several mechanisms, such as point mutations, intragenic recombination and introduction of foreign alleles may enhance this strain diversity. Similar results were reported by Lage et al. [18] where 38.5% of *glmM* gene was detected in 38.5% on dyspeptic patients. Similar results were found by Brooks et al. [19] in biopsy specimens from 44% of their patients. However, Lim et al. [20] detected 48.8% of *glmM* genes in of the cases studied.

TABLE III: RELATIONSHIP BETWEEN CLINICAL SIGNS OF THE PARTICIPANTS AND THE PRESENCE OF *GLMM* GENE

Clinical signs	n=147 (%)	*glmM* (+ve)	OR	(95%CI)	p-value
ATCD gastric	01 (0.68)	01 (100)			0.73
Balance HTP	04 (2.72)	02 (50.00)	1.97	(0.27-14.48)	0.88
Lefthypochondrial pain	01 (0.68)	0 (0.00)			0.73
Dyspepsia	10 (6.80)	01(10.00)	0.19	(0.02-1.62)	0.18
Dysphagia	05 (3.40)	02(40.00)	1.30	(0.21-8.07)	0.84
Epigastralgia	93 (63.27)	32(34.41)	1.04	(0.51-2.13)	0.89
Chronic epigastralgia	17 (11.57)	07(41.18)	1.41	(0.50-3.97)	0.50
Gastralgia	05 (3.40)	01 (20.00)	0.47	(0.05-4.36)	0.84
Low digestivehemorrhage	03 (2.04)	0 (0.00)			0.52
High digestive hemorrhage	03 (2.04)	02 (66.67)	4.00	(0.35-45.22)	0.55
Precordialgia	01 (0.68)	0 (0.00)			0.73
Heartburn	02 (1.36)	01 (50.00)	1.95	(0.12-31.99)	0.78
RGO	02 (1.36)	01 (50.00)	1.95	(0.12-31.99)	0.78

N: total number of patients, +ve: positive, %: percentage, OR: Odds Ratio, CI: Confidence Interval.
ATCD: chromoendoscopy in premalignant gastric lesions. RGO: Reflux gastro-esophageal.

According to socio-demographic characteristics, our findings indicated that male (37.29%) than female (31.82%) were infected by *H. pylori.* However, no significant association was found between gender and *H. pylori*. Similar data were obtained in study carried out in Cameroon [15, 17]. The current study found no significant variation between, age groups, patient's income and *H. pylori* infection. Several studies have also reported not significant association in the presence of *H. pylori* by sex [17]. Several have observed that the prevalence of *H. pylori* increases with the age [21]. Our findings indicated that the prevalence decreases from 40.63% at the age 30-40 to 26.67% at >50. This contradicts the report by [17].

Our data on gender agrees with those of other studies, which indicated that the males were associated with a higher risk of acquiring *H. pylori* infection than the females [13], because the males are naturally more active and less hygienic than females, considering that the prevalence of *H. pylori* infection and sanitation condition are inversely related [22].

The prevalence of *H. pylori* was significantly higher for patients who resided in the Center (p= 0.007), and Western Regions (p= 0.005). This prevalence can be explained by the fact that the collected site is located at the center region, also because people from the western region are known as traders, hard workers, and travelers.

The prevalence was dependent on level of education with a higher prevalence in those less educated. This may imply a lack of knowledge, attitude, and practices, which predisposes them more to infection as they aged. According to Ahmed et al [23], this may reflect infection acquired in childhood and borne throughout life, which is also consistent with other studies [24]-[27].

There was statistically significant difference (p=0.004) with the source of income and *H pylori*infection. This finding corroborates a previous result [22] where source of income was a risk factor for *H. pylori* infection. Our study showed a statistically significant effect of alcohol consumption on *H. pylori* prevalence (p=0.0001); no association was recorded for living conditions, which is in line with a previous study [28]. The relationship between clinical signs of the study population and *H. pylori* infection shows that, 34.41% (32/93) of our subjects presented with epigastralgia were infected with *H pylori*. Several studies have reported a high prevalence of *H. pylori* among patients with epigastralgia [17], [29].

V. CONCLUSION

This study revealed a prevalence of *H. pylori* infection of 50/147 (34.01%) using molecular method. This prevalence was more represented in males than the females and increased with age. Risk factors such as regional group particularly Centre and West regions, level of education, source of income, and alcohol consumption predisposed the subjects to *H. pylori* infection. Despite the small sample size, these results have epidemiological and clinical significance and calls for intervention to mitigate the situation.

VI. RECOMMENDATION

The overall prevalence of *H. pylori* infection in the current study was 34.01% (50/147) using molecular biology technique, from that one can associate the use of molecular biology for the diagnostic of *H. pylori* infection. The study needs to be expanded on a wide population to other areas in the country as well as the inclusion of healthy individuals as a control group.

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