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Original Research

Gastric Cancer and *Helicobacter pylori*: Impact of *hopQ*II Gene

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Abstract: The *Helicobacter pylori* (H. pylori) is a Gram-negative, microaerophilic bacterium found usually in the stomach and use a number of mechanisms to survive in the stomach lumen. The presence of these bacteria in the stomach can lead to gastritis and reduction in stomach acid production. Acute inflammation can directly damage to the peripheral cells that are responsible for the secretion of acid. The risk of developing gastric carcinoma is associated to heterogeneity of *Helicobacter pylori* virulence factors. The *hopQ*II is one of the outer membrane proteins involved in bacterial adherence to gastric mucosa and has been suggested to also play a role in the virulence of *H. pylori*. The purpose of the current study was to investigate the association between different *H. pylori* virulence *hopQ*II allele and patients with gastroduodenal disorders. For this purpose 58 stomach biopsies of patients with gastric cancer and 100 saliva samples from healthy individuals were collected. Then genomic DNA was purified and PCR for was done for desired genes via specific primers. The *H. pylori* infections were diagnosed by PCR for *Glm*M gene. Then frequencies of *hopQ*II^{+} and *hopQ*II^{-} genotypes was determined in *H. pylori* infected cases. Statistical analysis showed that there were not significant differences between healthy and diseased ones for genotype *hopQ*II^{+}.

Key words: Gastric cancer, *HopQ*II genotyping, *Helicobacter pylori*.

Introduction

The gastric cancer phenomenon is the most universal lethal cancer with around 738,000 deaths per year (1). Different occurrence of gastric cancer in worldwide can be due to diversity in the genetic conditions, nutritional behaviors and living conditions (2).

The *Helicobacter pylori* is a gram negative and successful gastric pathogen which colonizes more than 50% of the world population (3).

The *H. pylori* infection is the key cause of gastric and duodenal ulcers, as well as a potential risk factor for gastric cancer and mucosa-associated tissue lymphoma (4). Available information indicates a slight association between gastroduodenal diseases and *H. pylori* virulence factors (5).

The *H. pylori* is now recognized to be a significant co-factor in the etiology of non-cardia gastric cancer of both the diffuse and intestinal histological type. The latter type develops via a complex multistage and multifactorial process. The first stage involves progression from superficial gastritis to atrophic pangastritis with intestinal metaplasia and correlated hypochlorhydria. This gastric phenotype may then progress to dysplasia and gastric cancer. Many co-factors are concerned in this progression as well as the strain of *H. pylori*, host genetic factors, host gender and environmental factors. Intestinal colonization with helminthic infection may retard the progression by changing the immune and inflammatory response to *H. pylori* and colonization of the achlorhydric stomach with nitrosating bacteria may promote progression to cancer. *H. pylori* appears to be an necessary co-factor in the etiology of most gastric cancers. Therefore, avoidance of the infection or its eradication in early life should reduce the rate of this widespread and usually fatal tumor (6).

If *H. pylori* infects the gastric epithelium cells, the interleukin-8 should be induced and production of too much amounts of toxic reactive oxygen species (ROS) may be occurred. It may induce the interferon-γ (IFN-γ), tumor necrosis factor-α (TNF-α) and some other interleukins (7). Oxidative stress that caused by ROS is involved in human carcinogenesis (8). ROS generated in normal respiration of cells and during xenobiotics metabolism. It is known as a candidate agent in the growth of cancer and damage to cell membranes, mitochondria and DNA molecule (9).

Several putative virulence factors for *H. pylori* have been identified including *vacA*, *babA*, and *iceA*. The *HopQ* is one of the outer membrane proteins involved in bacterial adherence to gastric mucosa and has been found as a virulence factor of *H. pylori*. In 2005, Cao *et al.,* reported that *H. pylori hopQ* genotypes are associated with an increased risk for peptic ulcer disease (10). The *H. pylori* genomes include about 30 different *hop* genes, which encode outer membrane proteins (11).

LOH *et al.,* (2008) showed that, in certain *H. pylori*, adherence to the gastric epithelial cells are faintly facilitated in strains expressing *hopQ* (12), though they did not present further data about disease specific virulence factor of *hopQ*.

The high rate of *H. pylori* infection in Iran and the increasing number of digestive complaints lead to the current study on whether the presence of *hopQ* (typeII)

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Table 1. Primer sequences and amplified fragment length for *H. pylori* genes.

Gene	Accession No.	Primer sequence	Amplified fragment length
*glm*M	900169	5'-AAGCTTTTAGGGGTGTTAGGGGTTT-3' 5'-AAGCTTACTTTCTAACACTAACGC -3'	294 bp
*hopQ*II	8208107	5'-A*CAG*CCACTCCAATC*CAG*AA-3' 5'-TTGACCAACAACCACAAACCGAAG-3'	160 bp

Table 3. Thermal cycles for PCR reaction for different *H. pylori* genes.

Gene	Thermal cycles for PCR reaction				
	1	2	3	4	5
glmM	94 ºC (5 min)	94 ºC (30 sec)	58 ºC (30 sec)	72 ºC (30 sec)	72 ºC (5 min)
*hopQ*II	94 ºC (5min)	94 ºC (30 sec)	54 ºC (30sec)	72 ºC (30 sec)	72 ºC (5 min)

can affect disease outcome.

The purpose of the current study was to investigate the association between different *H. pylori* virulence *hopQ*II allele (types II) and patients with gastroduodenal disorders among a sample of the Iranian population.

Materials and Methods

Materials, chemicals and reagents

Agarose and polymerase chain reaction (PCR) materials were prepared from Fermentas. Specific primers were synthesized by Cinnaclon, Iran. All chemicals and reagents were prepared from Zagros Bioidea Co, Kermanshah, Iran.

Participants

The population consisted of gastric cancer patients and cancer- free subjects as controls. All desired population was *H. pylori* infected. Gastric biopsies were taken from 58 gastric cancer patients and 100 cancer-free subjectsthat were infected to *H. pylori*. The patients and controls were age and sex matched. The experiment materials included stomach biopsies of the patients with gastric cancer and saliva samples from healthy individuals.

DNA purification and gene amplification

The genomic DNA was purified from stomach biopsies of the patients with gastric cancer according to MORADI *et al.,* 2014 method (13) and saliva samples from buccal epithelial cells of the healthy individuals according to AIDAR, 2007 method (14).

The PCR was done for desired genes via specific primers (Table 1). The *H. pylori* infections were diagnosed by PCR for *glmM* gene. Then frequencies of *hopQ*II+ and *hopQ*II- genotypes were determined in *H. pylori* infected cases. All materials amount and conditions for PCR reactions are shown in tables 2 and 3.

The presence of *H. pylori* and *hopQ*II allele in gastric biopsy specimens and in saliva healthy samples was identified by specific PCR assays.

Statistical analysis

The χ^2 analysis was applied for study of different frequency in patients and healthy people. The SPSS V19 was used for Statistical analysis.

Results

Genomic DNA purification

Genomic DNA from 58 gastric cancer patients and 100 cancer- free subjects was purified successfully (Figure 1). The quality and quantity of purified genomic DNA was studied via spectrophotometery.

Table 2. Materials amount for all PCR reaction in current experiment.

Materials	Amounts
$MgCl_2$	1.5 mM
dNTP	200 mM
PCR Buffer	50 mM
F-Primer	50 pmol
R-Primer	50 pmol
Template DNA	300 ng
Taq DNA Polymerase	1 unit
Double distilled water	16.25µl
Total volume	**25µ l**

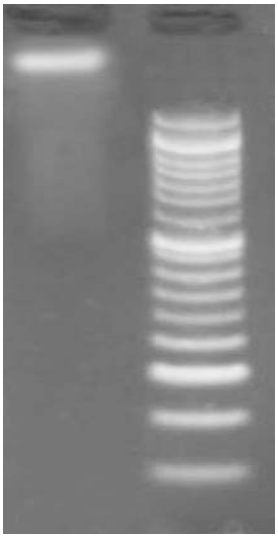

Figure 1. Purified genomic DNA from *H. pylori* infected samples. Lane 1: genomic DNA and Lane 2: Size marker.

Identification of *H. pylori* infected samples via *glmM* gene PCR amplification

The *H. pylori* infections were identified by PCR for *glm*M gene. The PCR reaction for this gene amplified a fragment in 294 bp length in the *H. pylori* infections (Figure 2).

Polymerase chain reaction for *hopQ*II gene detection

The agarose gel electrophoresis for *hopQ*II gene detection in the *H. pylori* infections via PCR has been shown in Figure 3. The PCR reaction for this gene in *hopQ*II+ samples amplified a fragment in 160 bp.

The *hopQ*II gene frequency in the *H. pylori* infections

The frequencies for the *hopQ*I gene frequency in the

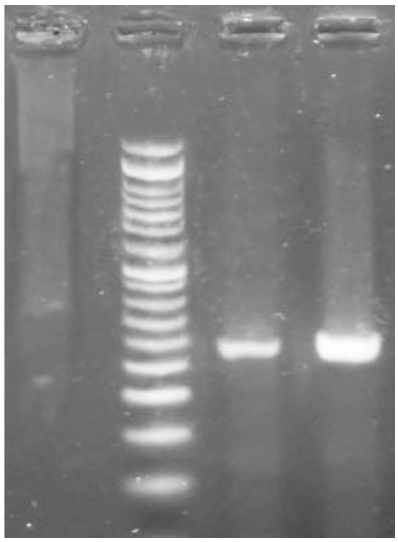

Figure 2. Diagnosis of *H*. pylori from biopsy specimens and normal samples. PCR products and agarose gel electrophoresis for *glm*M gene detection from *H. pylori* infected samples. . Lane 1: Negative control. Lane 2: Size marker Lane. Lane 3: PCR product for *glm*M gene in cancer-free. 4: *glm*M gene amplification in gastric cancer patients.

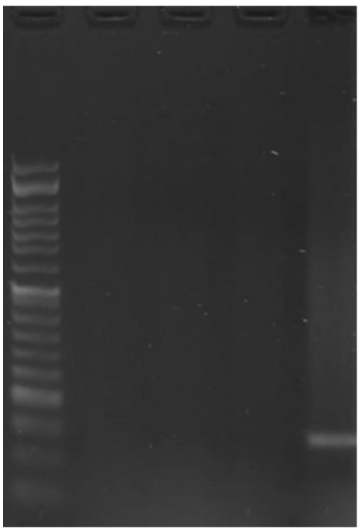

Figure 3. The agarose gel electrophoresis for *hopQ*II gene amplification in the *H. pylori* infections via PCR. Lanes 1: DNA size marker. Lane 2 and 3: *hopQ*II$^-$ strains. Lane 4: Negative control. Lane 5: *hopQ*II$^+$ strains.

H. pylori infections has been shown in table 4. The χ^2 analysis showed that there was not a significant difference between gastric cancer and healthy individuals for presence of allele in their strains (P<0.05).

Table 4. The *hopQ*II gene frequency in the *H. pylori* infections.

	***hopQ*II$^+$ (%)**	***hopQ*II$^-$ (%)**
Case	43.6	56.4
Normal	42.9	57.1

P value =0.555

Discussion

The gastric cancer phenomenon is the most numerous diseases diagnosed in worldwide and it is the most common lethal cancer in Iran. Epidemiologic investigations have reported frequent risk factors for gastric cancer, including genetic factors, environmental, adverse living conditions, dietary habits and the prevalence of *Helicobacter pylori* infection (15).

Helicobacter pylori plays a key role in the pathogenesis of chronic gastritis, peptic ulceration, and noncardia gastric cancer. As it has been shown in Figure 2, the PCR product from gastric cancer patients biopsies (lane 4) was more efficient rather than saliva samples from healthy individuals (lane 3).

Clinical development of *H. pylori* infection is affected by the interaction of numerous virulence factors as well as by the host. The *H. pylori* infection is the key causative agent of superficial gastritis and confirms an expected task in the etiology of peptic ulcer disease (16).

Based on the biologic concepts, achieving successful and long term colonization requires composite adhesion mechanisms for bacteria. Consequently, all potential bacterial products were under focus for investigating the possible contribution in bacterial colonization. The *H. pylori Hop*Q is one of the main outer membrane proteins on the bacterial surface and is the major outer membrane protein family observed in *H. pylori* genome. Determining a link between *H. pylori hopQ* and convinced digestive diseases may provide a start point for answering questions regarding *H. pylori* adherence to gastric cells. This study was designed to determine the frequency of *H. pylori hopQ* genotypes isolated from biopsy specimens. Our findings demonstrate a moderate prevalence of *H. pylori hopQ* types II genotype among Iranian patients with gastric cancer and healthy individuals that are infected to *H. pylori*.

It has been suggested that specific genotyping-based analysis of *H. pylori* isolates can be helpful for predicting post infection disorders (17).

Talebi Bezmin Abadi & Mohabbati Mobarez (2014) reported a high prevalence of *H. pylori hopQ* type II genotype among Iranian patients with gastric cancer that is not according to our finding (18).

In addition, outer membrane proteins of *H. pylori* have shown a strong potential for increasing the severity of related gastroduodenal disorders. Ohno *et al.,* (2009) did not identify any relationship between *hop*Q type II allele and other virulence factors such as *cag*A and vacA in terms of clinical outcomes.

However, the exact relationship between virulence factors of *H. pylori* and *hopQ* alleles needs further investigation especially in genetically different populations.

In contrast to a study from United States (11) which reported a significant association between the carriage of *H. pylori hopQ* type I among the peptic ulcer patients, OHNO *et al.,* (2009) did not identify a relationship between both *hopQ* alleles and clinical outcomes of infection (P > 0.05).

Kazemi et al., (2016) showed that there is not significant relationship between *Hop*QI and gastric cancer in Iranian population (19).

In conclusion, this study showed that *hopQ* II is frequently present in *H. pylori* strains isolated from gastric cancer patients and healthy individuals in Iran. Then *hop*QII can not be a virulence and risk factor in our population.

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