

Helicobacter pylori Genotype as Predicts Risk of (Ulcer Disease, Gastric Cancer, Non-Ulcer Dyspepsia); Role of some genes Mediated Signaling in infection

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Abstract

Helicobacter pylori contagion is magnanimously overruling in human, disturbance privately partial of the world's population; reciprocally, contagion continue asymptomatic in superiority of population. During its co-existence with humans, *H. pylori* has develop diversified strategies to preserver a kind gastritis and edge the protected response of host. On the other side, personality of *H. pylori* is also combined with increased exposure for the evolution of uncertain gastric pathologies conclude gastric malignancy (GC).

A complicate confederacy of host genetics, environmental agents, and bacterial virulence agent are estimate to regulate the capability as well as the extremity of consequence in a subset of individuals. The nearness of the babA2 quality was altogether joined with the various *H. pylori* destructiveness qualities planned (vacA, cagA, and homB). High and significant results was belong to vacA in Peptic Ulcer Disease (91.04%), homB in Gastric Cancer (93.51%) and babA2 in Non-Ulcer Dyspepsia

Keywords: *Helicobacter pylori*, vacA, cagA, and homB, Peptic Ulcer Disease, Gastric Cancer, Non-Ulcer Dyspepsia

INTRODUCTION

More than 70% of all major malignances befall to the liver Hepatocellular carcinoma (HCC), cholangiocarcinoma (CCA) and gastric cancer [1]. These developments rank third among organ-particular wellspring of damage related passings in men boundless and depiction for practically 4% of each and every human tumor. The geographic regions most associated are placed in Southeast Asia particularly in Thailand. Steady hepatitis B contamination (HBV) and hepatitis C disease (HCV) malady and aflatoxins are the principle reason of HCC [2]. *H. pylori* can be characterize in maintain; it is contemplate microaerophilic gram-negative bacterium which gifted to settle and carry on within the stratum of mucous membrane in gastric [3]. Numerous revisions describe a contiguous union between infection by *H. pylori* and diseases of gastroduodenal, for application MALT-lymphoma, PUD, GC and continuing sprightly gastritis [4]. The quarter most frequent universal malignancy was GC and observe as secondary guidance reason of neoplasia-related deaths (more than half million deaths annually) [5].

H. pylori influence amenable for 60% of all chronic GC [6], contagion with that bacterium operate a fundamental role, hereditary and environmental element adjust its consequence. Tries have offer that disinfecting of this bacterium may diminish the risk of malignant infection, however overhaul the shot of gastro-esophageal response (GERD), Barrett's throat, and esophageal adenocarcinoma. Considering the centrality of *H. pylori* in clear wreckage heaps, it is major to see which get-together of *H. pylori* have the initiating to improvement the introduction of GC and PUD [7,8].

Inflammatory reaction heart by *H. pylori* that settle in stomach capable to clear gastritis "a gastric mucosal condition" among people and tentatively wiped out creatures. At the point when standard in the stomach, the microscopic organisms and gastric incitement can continue for some times of years in the lack of understanding cure. Late examination specify that unique indubitable varieties in a stepwise seek after of histological variations initiated by gastritis and that can at last impeccable in gastric harm; turbulence, gastric decay (privation of particularize cell speak to, for example, parietal cells and fundamental cells), intestinal metaplasia (character of intestinal-style epithelial tissue in the stomach), and dysplasia [9, 10].

The expansion of gastric neoplasia in the position of *H. pylori* proposition is beginning to be an entire arrangement result of a couple of changes, contain ceaseless turbulence (distinctive style of danger) [11], strengthening of gastric foundational microorganisms, DNA hurt, upgrade in cell duplication and apoptosis, substitute in epithelial division and most remote point, bringing down of neoplasm silencers, and diminishing gastric developing, course to bacterial hyperplasia with mix not found in the standard acidic stomach [12]. Outline of *H. pylori* and *E. coli* delineate it as great of intraspecies acquired refinement [13,14]. Nucleotide result masterminded combination of withdrew capable chief is chargeable to an incomprehensible change rate, other than a complimented recombination level of intraspecies [15,16].

Vacuolating cytotoxin A (vacA) a huge piece of the time impact in each *H. pylori* age (Cover et al., 1994). Variety in sensible of cytotoxicity is trademark to vacA allelic change among *H. pylori* strain, which surrender in the understanding (s), focus (m) and delegate (I) districts, each with two separate alleles: s1 or s2, m1 or m2 and I1 or I2, sensibly [17].

VacA was on an outstandingly major level clear sustained on its occupation to source vacuolation of epithelial cells however is after a short time reviving to have a basically more wide unique of activities [18-20]. The amino ruinous strategy, plan, and cell sign of VacA are disseated to those of some other expected bacterial harmful substances. Most VacA-induced cell changes are inferable from its ability for pore development in cell layers [21]. The clinical result of *H. pylori* tainting has been joined with bacterial deadly quality expert, have, and trademark constituent [22].

Two destructiveness variables of *H. pylori*, cytotoxin-going with quality A (cagA quality) and the vacuolating cytotoxin A quality (vacA quality), carry on a leader party in control the clinical impact of *H. pylori* pandemic. The cagA quality, the primary harmfulness specialist blame in *H. pylori* family, encodes a protein (CagA protein) that is going with expanded genuineness of gastric turbulence and substantial neutrophil granulocyte penetration [23]. In limb, the CagA protein generally actuates interleukin-8 (IL8) which assumes a meeting part in the rebellious cell reaction to virus 24. The cagA quality, which isn't moment in each *H. pylori* strain, examine a marker for a genomic pathogenicity island (cag-PAI). It examine that this quality with

others on the island correlative with more grim clinical results, contain PUD and gastric threat (GC) [24-27].

Advantageous settling in the stomach is the most expansive progression for the pathogenicity of *H. pylori* recommendation. It is thoroughly value that bacterial association with the gastric epithelial tissue is the central unforgiving level of settlement by *H. pylori* [28]. The blood mean antigen astringent adhesin (BabA) is a well-characterize outside part protein of *H. pylori* that check fucosylated Lewisb blood add up to antigens minute on gastric epithelial tissue [29, 30]. Three bab allelic address have been seen, piece babA1, babA2 and babB; regardless, just the execution of the babA2 quality is changed for blessing the unassuming life plots with Lewisb astringent deftness. In 1999, Gerhard et al 31 first blueprint a without question connection between a babA2-quality real age and duodenal ulcer (DU) and GC. In this manner, a progression of thought of the connection between babA2 quality and PUD and GC have been done, however with conflicting or negating conclusions [32, 33].

In vitro, *Helicobacter* outside layer B (HomB) draw in the arrival of the proinflammatory cytokine interleukin-8 (IL-8) and improvement *H. pylori*'s favorable position to interface with have cells [34]. All the more in a general sense, homB identity is on an extremely fundamental level running with disclosure of peptic ulcer issue in Portuguese relatives and junior grown-ups 35 and with gastric perniciousness change and the character of cagA in U.S. additionally, Colombian masses 36. These exposures propose that the outside film protein HomB is a pivotal risky quality authority.

Accordingly, it and unmistakable individuals from the frail paralogous get-together of hom simultaneousness particles are everything considered being survey. The two best-broke down hom qualities, homA and homB, are 90% dull at the nucleotide sensible. These homA and homB qualities can be writer at two unmistakable loci inside the *H. pylori* genome: region An and zone B. Strains can join an individual transcript of one of the hom properties, a twofold duplicate of an individual quality, a solitary transcript of every quality, or neither quality [35]. Past examination prescribe geographic social occasion, in either dispersals, zone, or transcript show up, of the hom attributes in the genome and impel that these standard blend impact any relationship with contamination result [37, 38].

MATERIALS & METHODS

Study location and subjects

From 471 cases in this study, only 194 adult patients (77; GC, 67; PUD, 50; NUD) were detected with *H. pylori* all of them was over 20 years, which referred to the Endoscopy section at Al-Hillah teaching Hospital Al-Hillah city, Iraq. Individuals who had received anti *Helicobacter*, anti-inflammatory medications or non-steroid treatment at least 100 days earlier to endoscopy was omitted [39].

Specimen Collection

For each patient endoscopy and biopsy sampling at least two biopsy specimens were obtained from the gastric antrum and examined for the presence of *H. pylori* by rapid-urease test, culture and histology examination, and an additional biopsy

specimen (one antral biopsy specimen) from each patient was kept in brain heart infusion broth (Himedia, India) containing 20% glycerol for PCR analysis and frozen at -80°C until processing.

Blood samples.

Samples of blood was collected from all patients at the time of endoscopy. Sera were separated and stored at -80°C until tested for detection of the immunological criteria.

***H. pylori* Culture**

Gastric biopsy specimens were standardized and cultivated on *H. pylori* selective media (Himedia, India). Cultivation of the streaking Petri dishes accomplished at 37°C for a week (under microaerophilic conditions) with in Co2 incubator (Binder, Germany). Documentation of *H. pylori* was constructed on macroscopic and microscopic characterization and complete by biochemical tests (positive oxidase, catalase, and urease tests)⁴⁰.

DNA Extraction and PCR for Detection of Gene

Extracted DNA from the isolated *H. pylori* strains in culture-positive cases and from gastric biopsy specimens done by using Promega kits by following the manufacture instruction.

In this study, genotyping of the selected gene (*vacA*, *cagA*, *homB* and *babA2*) that related to *H. pylori* isolates were determined by PCR methods. PCR was carried out in an ultimate size of 20µl containing 13 µl of Taq PCR Master Mix (Biolab), 3 µl (10 µg/ µl) of extracted DNA, 2.0 µl (1 µM) of each primer. Amplification was performed with the following specific program for each primer.

Statistical Analysis

By using software of SPSS version 19, the data was analyzed. The Chi square (x2), and odds ratio (OR) were determined. A P-value less than or equal to 5% was considered as significant.

RESULTS & DISCUSSION

This study revealed the relation between the *H. pylori* infection and each types of gastroenteritis disease such as; PUD, GC and NUP. According to the data that collected from genetic, microbiology and histopathology tests, there are significant outcomes data that showed in table 2 and 3 below, which is clear the genes related to bacteria with the specific case (*vacA*, *cagA*, *homB* and *babA2* genes).

The proximity for *babA2* quality was essentially running associate different *H. pylori* danger characteristics organized (*vacA*, *cagA*, and *homB*). High and basic effect was interface with *vacA* in Peptic Ulcer Disease (91.04%), *homB* in Gastric Cancer (93.51%) and *babA2* in Non-Ulcer Dyspepsia (100%). The full stipend was among man in all conditions as depict in table 2. We found basic relationship among *babA2* and the other *H. pylori* hurtfulness characteristics. These revelations are in congruity with those portray by various witness, similar to the essential relationship among *cagA* and the s1 and m1 alleles of *vacA* and oipA "on" [41, 42].

Table 1: primers of genes that selected in this research

| Gene | Primer | Product |
|--------------|---|---------|
| <i>vacA</i> | 5'-ACTAATATTGGCACACTGGATTG-3' 5'-CTCGCTTGATTGGACAGATTG-3' | 298 bp |
| <i>cagA</i> | 5'-AAT ACA CCA ACG CCT CCA AG-3' 5'-TTG TTG CCG CTT TTG CTC TC-3' | 400 bp |
| <i>homB</i> | 5'-AGAGGGTGTGTTGAAACGCTCAATA-3' 5'-GGTGAATTCTTCTGCGGTTG-3' | 161 bp |
| <i>babA2</i> | 5'-AAT CCA AAA AGG AGA AAA AGT ATG AAA -3' 5'-TGT TAG TGA TTT CGG TGT AGG ACA-3' | 832bp |

Table 2: Age and Gender relationship with each case groups studied

| Criteria | Peptic Ulcer Disease | | Gastric Cancer | | Non-Ulcer Dyspepsia | | P-value |
|-----------------|----------------------|------|----------------|------|---------------------|----|----------|
| | No | % | No | % | No | % | |
| Age (Mean ± SD) | 46±7.8 | | 48±3.9 | | 42±8.2 | | P > 0.05 |
| Gender: | | | | | | | |
| Male | 46 | 68.7 | 53 | 68.8 | 39 | 78 | P > 0.05 |
| Female | 21 | 31.3 | 24 | 31.2 | 11 | 22 | P > 0.05 |
| Total | 67 | | 77 | | 50 | | |

Table 3: Genes eminence among H. pylori-infected patients with each case groups studied.

| Gene | Peptic Ulcer Disease (67) | | Gastric Cancer (77) | | Non-Ulcer Dyspepsia (50) | | P-value |
|--------------|---------------------------|-------|---------------------|-------|--------------------------|-----|----------|
| | No | % | No | % | No | % | |
| <i>vacA</i> | 61 | 91.04 | 61 | 79.22 | 44 | 88 | P > 0.05 |
| <i>cagA</i> | 54 | 80.60 | 70 | 90.91 | 42 | 84 | P > 0.05 |
| <i>homB</i> | 42 | 62.69 | 72 | 93.51 | 47 | 94 | P > 0.05 |
| <i>babA2</i> | 49 | 73.13 | 59 | 76.62 | 50 | 100 | P > 0.05 |

cagA is put toward the entire of the *cag* pathogenicity island (PAI), which is a 39-kb put sequester on a level plane from another bacterial beginning stage. The "pathogenicity islands" contain *cagA* encode proteins conduce in sign transduction falls that follow in cytoskeletal change by strategies for actin polymerization and host cell protein phosphorylation. Risky social occasion of *H. pylori* accomplish the *cagPAI*. Inestimable. *pylori* race from patients with peptic ulcer or gastric peril create *cagA*, while colossal measures of those family from asymptotically spread individuals deficiency this quality [43]. Currently, we see two more discernible event of *H. pylori* specific: *cagA* quality pulverize and *cagA* quality positivestrains. Checking a stinging propensity virtuoso for *cagA* basically another chart that is kept up on polymorphism in Glu-Pro-Ile-Tyr-Ala (EPIYA) subjects. In *cagA* finish strains, there is an area join the EPIYA subjects, which encase a tyrosine phosphorylation put [44].

To now, *vacA* is the another most for the most part perscrutate hurting inclination ace of *H. pylori*. In each sensible recognize all *H. pylori* age have an ace *vacA* quality that codes for the cover pore-constraining protein *vacA* [45, 46]. The quality not too horrendous gathering in little living things passing on *vacA* is correspondence sensible and ailment control, which are joined with result change especially spaces of cover protein. There is a shocking break on our accessory concerning essential execution of this protein since still unique contradictive disclosures are exist [47, 48]. In this manner, we urgency more examination to control how to depend on *vacA* as serviceable *H. pylori* hurting penchant ace [49].

To conclusion, there have been distinctive reasonable contemplated yet with radiative effect on the relationship between the *babA2* quality and PUD and GC [50]; additionally, there is no short meta-examination on the massiveness of *babA2*. As necessities be, we end up at ground zero the influenced metaanalysis to out of the helpful reveal learnedness to have a more right result. Another probability is that patients with enlarged gastritis in the corpus and antrum, stun diminished hazardous age, need to progress intestinal metaplasia, atrophic gastritis, and even GC [31]. It is hypothesis that *babA2* confederated with different ruinous inclination ace may equivalently start to GC progress. Studies lead by Gerhard et al [52] and Erizin et al [51] have recommend that triple undeniable *H. pylori* family with *cagA*, *vacAs1* and *babA2* coexpression expand the threat of push GC. Zambon et al 53 have in like way relate that pollutions with these triple-positive race get a higher peril of intestinal metaplasia, known as gastric precancerous savagery.

In vitro, *Helicobacter* outside layer B (*HomB*) bolster the flooding of the proinflammatory cytokine interleukin-8 (IL-8)

and make *H. pylori*'s capacity to segment to have cells [34]. More essentially, *homB* closeness is all around joined with spreading out of peptic ulcer issue in Portuguese kids and vivacious adults [35] and with gastric risk loosening up and the district of *cagA* in U.S. besides, Colombian culture [36]. These disclosures suggest that the outside film protein *HomB* is another dangerous substance part. Along these lines, it and unmistakable people from the delicate paralogous family line of *hom* synchronization particles are generally speaking being perscrutate. The two best-dealt with *hom* characteristics, *homA* and *homB*, are 90% same at the nucleotide level [54]. These *homA* and *homB* characteristics can be unexpected at two separate loci inside the *H. pylori* genome: locus An and locus B. Strains can pass on a singular copy of one of the *hom* traits, a twofold copy of a specific quality, an uncompounded copy of each quality, or neither quality [15, 16]. Past reflection show geographic get-together, in either apportioning, condition, or duplicate wide number, of the *hom* characteristics in the genome and find that these particular blend master any association with warmth end [37].

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