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Helicobacter pylori and gastric cancer: Indian enigma

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studies and from around the globe. This review covers aspects of epidemiology, the various biological strains present in different parts of the country and within individuals, the status of different *H. pylori*-related diseases and the molecular pathogenesis of the bacterium.

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Key words: Gastric cancer; Gastric diseases; *Helicobacter pylori*; p53 mutation; Carcinogen

Core tip: This review highlights the unusual finding of low prevalence of gastric cancer despite high prevalence of *Helicobacter pylori* in India and its probable causes including diet and genetic variations as seen in Indian patients. This finding is attributed to increased genetic resistance in addition to a vegetarian diet rich in antioxidants.

Abstract

Helicobacter pylori (*H. pylori*) is a gram negative micro-aerophilic bacterium which resides in the mucous linings of the stomach. It has been implicated in the causation of various gastric disorders including gastric cancer. The geographical distribution and etiology of gastric cancer differ widely in different geographical regions and *H. pylori*, despite being labeled as a grade I carcinogen, has not been found to be associated with gastric cancer in many areas. Studies in Asian countries such as Thailand, India, Bangladesh, Pakistan, Iran, Saudi Arabian countries, Israel and Malaysia, have reported a high frequency of *H. pylori* infection co-existing with a low incidence of gastric cancer. In India, a difference in the prevalence of *H. pylori* infection and gastric cancer has been noted even in different regions of the country leading to a puzzle when attempting to find the causes of these variations. This puzzle of *H. pylori* distribution and gastric cancer epidemiology is known as the Indian enigma. In this review we have attempted to explain the Indian enigma using evidence from various Indian

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INTRODUCTION

It has been 30 years since the discovery of *Helicobacter pylori* (*H. pylori*) in 1983 by Australian physicians Robert Warren and Barry Marshall^[1] In view of the various epidemiological studies worldwide, the International Agency of Cancer classified *H. pylori* as a Class I carcinogen for gastric cancer in 1994^[2]. Since then the bacterium is thought to be one of the causative factors in the development of gastric cancer.

H. pylori is a gastric pathogen that colonizes approximately 50%-60% of the world's population^[3]. Infection with *H. pylori* causes chronic inflammation and signifi-

cantly increases the risk of developing duodenal and gastric ulcer disease and gastric cancer. *H. pylori* infection is the strongest known risk factor for gastric cancer, which is the second leading cause of cancer-related deaths worldwide^[4].

Studies in Asian countries such as Thailand, India, Bangladesh, Pakistan, Iran, Saudi Arabian countries, Israel and Malaysia, have reported a high frequency of *H. pylori* infection co-existing with a low incidence of gastric cancer^[5-8].

This review aims to explain this Indian enigma through various studies performed in past two decades in different parts of the country.

EPIDEMIOLOGY

Over past few decades there have been many studies related to gastric cancer which showed marked geographical variations with high risk areas in Japan, China, Eastern Europe, and some countries in Latin America. Low risk regions are North America, India, Philippines, Africa, some parts of Western Europe and Australia^[9].

Various epidemiological studies in India have shown a high incidence of gastric cancer in South India as compared with North India^[10]. The prevalence of *H. pylori* infection is high (49.94%-83.30%) in India, but the incidence of gastric cancer is comparatively low indicating mixed results for the association between *H. pylori* and gastric cancer. Human epidemiological studies have shown mixed results with a definite association between *H. pylori* and gastric cancer in approximately 50% patients, and a negative relationship in the remaining patients^[11,12].

In North India the prevalence of *H. pylori* in patients with gastric carcinoma was assessed and correlated with gross appearance and histological types^[13]. The prevalence of *H. pylori* in controls was slightly higher than that in the patient group (80% *vs* 78%). Diffuse type gastric cancer was more common than intestinal type and the prevalence of *H. pylori* was greater in diffuse type gastric cancer than in intestinal type (86% *vs* 68%). A significant association between *H. pylori* and grades of gastritis was noted ($P < 0.01$) in controls as well as in the patient group, but failed to show a significant association with tumor grade, intestinal metaplasia, site of tumor and age of patient. It was inferred that the prevalence of *H. pylori* infection is not directly associated with the pathogenesis of gastric cancer, but may act as a co-carcinogen by damaging the mucosa and thereby making it more susceptible to the effects of a carcinogen.

Quigley *et al.*^[14] in their review stated that human epidemiological studies have produced mixed results with an association between *H. pylori* and gastric cancer in 50% patients, while the remaining patients showed a negative relationship.

Dietary variation in the Indian population

Diet plays an important role in gastric carcinogenesis. In India, southern and eastern parts of the country have a

gastric cancer frequency approximately 4 times higher than that in northern parts of the country^[9,15]. A high incidence of gastric cancer in both males (50.6%) and females (23.3%) has been reported from Mizoram^[16]. Non-vegetarian foods, particularly fish, are very common in the east Indian diet, which is also spicy with more salts. Pickled food, high rice intake, spicy food, excess chili consumption, consumption of high-temperature foods, smoked dried salted meat, use of soda and consumption of dried salted fish have emerged as significant dietary risk factors for gastric cancer^[17-21]. The diet in south India is similar to that in eastern parts with rice, fish, excess spice and salt commonly eaten providing an explanation for the higher incidence of gastric cancer in these regions.

In contrast, the north Indian diet is mainly wheat-based and a greater proportion of people are vegetarian with a high intake of fruits and spices like turmeric^[22,23] and garlic^[24,25] which are known to have anti-cancerous properties. Dietary habits, especially high intake of curcumin and a vegetarian diet, could be one explanation for the Indian enigma^[26,27].

H. PYLORI STRAINS IN INDIA

The study of *H. pylori* genomics began in August 1997 with the publication of the complete genome of *Helicobacter pylori* 26695, which was cultured from a gastritis patient in the United Kingdom^[2,28]. Recent technological advancement has made sequencing of the genome more accessible and less costly resulting in a rapid increase in the number of *H. pylori* isolates sequenced, including some of the important laboratory strains^[29]. Up to March 2013, 43 complete genomes and 198 draft genome sequences had been deposited in GenBank for public access, and the federated genomic databases are still growing.

Based on the country of origin of the source patient: 18 were from North and South America, 14 from Far East Asia (Japan/South Korea/China), 11 from Europe, 10 from Malaysia, six from Africa, four from India, and one from Australia. Based on available data of the complete genomes in GenBank, the average size of an *H. pylori* genome was estimated to be 1.62 Mb (1.51-1.71 Mb) with a gastric cancer (GC) content of 38.92% (38.4%-39.3%). The average *H. pylori* genome was predicted to consist of 1590 (1429-1749) open-reading frames encoding 1532 (1382-1707) proteins^[29].

Between 2012 and 2013, two *H. pylori* strains were isolated from duodenal ulcer patients in Bangalore (NAB47) and Delhi (NAD1) in India^[10]. Based partly on these conventions, Indian *H. pylori* isolates have been shown to have European origins^[11] and are widely held to be mostly innocuous or only mildly pathogenic, unlike their highly virulent Far East Asian counterparts (which may be linked to the high incidence of gastric cancer). It is certain that these genomes representing Indian patients will rekindle our understanding of the genetic makeup

and evolutionary relationships of this pathogen in India.

MULTIPLE STRAINS AT THE SAME SITE

H. pylori exhibits conspicuous genetic diversity as evidenced by an apparently unlimited number of unique strains that differ in genome size, gene order, genetic content, and allelic profiles^[12]. *H. pylori* exhibits more frequent recombination events with heterologous strains than any other known bacterial species^[13]. Microarray and nucleotide sequence analysis of strains isolated longitudinally from the same patient imply that this recombination is a continuous event^[14,30].

Studies from Europe and Western countries showed that almost all strains of *H. pylori* isolated from different sites in the stomach of individual patients show homogeneous DNA profiles. In contrast, Mexican and Chinese populations are infected with genetically heterogeneous strains with high infection rates. In India, the prevalence of *H. pylori* infection is high^[8,24,31] and the chances of infection and re-infection of strains in a single host is relatively high as compared to Western populations. In addition, a similar trend in heterogeneity of strains has been shown in the Indian continent^[32]. Genetic exchanges among mixed bacterial populations may generate a more competitive strain to adapt to a particular host thereby propagating a more virulent strain. In India, the prevalence of *H. pylori* infection is much higher as compared to the most western countries and almost all infected cases were found to carry multiple *H. pylori* strains^[32].

PEPTIC ULCER DISEASE

Researchers have reported the role of *H. pylori* infection in the pathogenesis of peptic ulcer and stomach cancer in India, and some have reported no association between stomach cancer and *H. pylori* infection^[33-39]. In a recent study of 190 peptic ulcer patients, 35 stomach cancer patients, and 125 controls, the author concluded that *H. pylori* infection is associated with peptic ulcer disease. Lower socioeconomic status, consumption of restaurant food, meat, nonfiltered water, and smoking are risk factors for *H. pylori*. Consumption of meat, fish, and a family history of peptic ulcer are risk factors for peptic ulcer. Consumption of chili, peppers and concurrent parasite infestation appears to be protective against *H. pylori*^[38].

The epidemiology of peptic ulcer disease (PUD) in India differs from that in the West. It may have undergone a change with recent improvements in hygiene and availability of potent antisecretory and ulcerogenic drugs. In a time trend study of *H. pylori* infection and PUD, the frequencies of duodenal and gastric ulcer disease in study groups were compared. Of the 30,216 patients (mean age: 41.7 ± 12.7 years, 34% females) during the six study periods, 2360 (7.8%) had PUD. The frequencies of both duodenal ulcer and gastric ulcer declined from 1988 to 2008, *i.e.*, from 12% to 2.9% and from 4.5% to 2.7%, respectively ($P < 0.001$ for each). The decline was more

marked for duodenal ulcer, and the ratio of duodenal to gastric ulcer declined from 2.7 in 1988 to 1.1 in 2008. The epidemiology of PUD in India may have changed in the past two decades with the incidence of duodenal ulcer declining more rapidly than that of gastric ulcer^[40].

In a recent review it was concluded that *H. pylori* is the primary cause of duodenal ulcer supported by strong evidence in the literature linking *H. pylori* etiologically to duodenal ulcer and reports on eradication therapy of *H. pylori* in preventing relapse of uncomplicated and complicated duodenal ulcer^[41].

GC

GC is the third most common cancer in India and the second leading site of cancer occurrence world-wide. The incidence of GC is 4 times higher in South India than in North India^[42]. An understanding of the molecular mechanism of gastric carcinogenesis and its relationship to *H. pylori* improved in the last decade. Most studies showed either no or a negligible effect of *H. pylori* in gastric carcinogenesis in India.

Misra *et al.*^[42] studied the effect of *H. pylori* on the proliferative activity of gastric epithelium by studying Ag-NOR counts, but found no significant difference in normal controls, inflammatory lesions and cancer, concluding that *H. pylori* has no direct effect on the proliferative activity of gastric epithelium. A prospective study reported the association of microsomal epoxide hydrolase exon 3 Tyr113His and exon 4 His139Arg polymorphisms with gastric cancer in India and concluded that 113Tyr-139Arg was associated with GC in the presence of *H. pylori*, in its absence, it appeared to be protective. However, exon 3113His was associated with GC even in the absence of *H. pylori* infection^[43]. The role of cytochrome P450 (CYP), a polymorphic carcinogen-activating enzyme, CYP2E1, CYP1A2 (rs762551), and CYP1A1 (rs4646903) polymorphisms in association with *H. pylori* infection in gastric carcinogenesis was studied and it was found that the presence of CYP2E1 (96-bp insertion) is associated with increased risk of GC even in the absence of *H. pylori*. CYP1A2 CC or CT is associated with a reduced risk of GC^[44]. Another study showed that p53 gene mutation was present in 4.6% of the study population. This mutation was significantly higher in GC when compared with PUD and non-ulcer dyspepsia (NUD), and was independent of *H. pylori* infection indicating a role for p53 gene mutation in gastric carcinogenesis, independent of *H. pylori* infection. K-ras gene mutation was not seen in GC and PUD in Indian patients^[45].

Repression of Runt-related transcription factor 3 (*Runx3*) gene, a tumor suppressor gene, has been shown to be involved in *H. pylori*-associated gastric carcinogenesis and cancer development^[46]. The study was undertaken to investigate *Runx3* intronic T/A polymorphism (rs760805) in *H. pylori*-infected patients and uninfected controls of the Tamil Nadu region, South India. In addition, *Runx3* gene expression, HK alpha (H, K-ATPase)

gene expression and the methylation status of the Runx3 CpG island were determined. Neither significant repression of *Runx3* and HK alpha genes nor methylation were detected in positive patients, suggesting a lack of involvement of this tumor suppressor as a risk factor in *H. pylori*-associated gastric carcinogenesis in the South Indian population studied.

Tobacco-smoking was found to be an important risk factor for the high incidence of stomach cancer in Mizoram. Meiziol (local cigarette) smoking was a more important risk factor than other tobacco related habits. Polymorphisms of *GSTM1* and *GSTT1* genes appeared to be effect modifiers. Persons habituated to tobacco smoking and/or tuibur habit had an increased risk of stomach cancer if they carried the *GSTM1* null genotype and *GSTT1* non-null genotype^[47].

CagL is a pilus protein of *H. pylori* that interacts with host cellular $\alpha 5\beta 1$ integrins through its arginine-glycine-aspartate (RGD) motif, guiding proper positioning of the T4SS and translocation of CagA^[48]. Deletion or sequence variations of CagL significantly diminished the ability of *H. pylori* to induce secretion of interleukin (IL)-8 by the host cell^[49]. In a primary study, prevalence of *H. pylori* infection in the study population was found to be 52.5%. Most of the isolates were CagL genopositive (86.6%), and all had the RGD motif in their amino acid sequences. D58 and K59 polymorphisms in CagL-genopositive strains were significantly higher in GC patients ($P < 0.05$). Combined D58K59 polymorphism was associated with a higher risk of GC (3.8-fold) when compared to NUD. It was concluded that *H. pylori* CagL amino acid polymorphisms, such as D58K59, are correlated with a higher risk of GC in the Indian population^[50].

MOLECULAR PATHOGENESIS OF *H. PYLORI* INFECTION

CD4+ T helper cells (Th) are recognized as a key component of the adaptive immune response to extracellular bacteria and a dominant component of immune responses to *H. pylori*^[51-53]. *H. pylori* evokes a weaker Th17 response, followed by a dominant and more persistent Th1 response that is paralleled by an immunoregulatory CD4+ T cell response characterized by T regulatory cells slowly accumulating at the beginning of the infection, reaching the highest level at 30 d post-infection which is sustained over time^[54].

A close relationship between plasma malondialdehyde (MDA) and nitric oxide (NO) levels was found with gastric histopathology and genotypes of *H. pylori* in South India. Levels of MDA and NO were higher in subjects infected with genotype-1 of *H. pylori* than those with other genotypes suggesting more precise interaction of highly virulent strains of *H. pylori* in eliciting severe tissue damage^[55]. Another study from South India reported that *H. pylori* infection may increase the expression of c-H-ras p21 early in the process of gastric carcinogenesis^[56].

H. pylori infection has a negative effect on the MMR

system, and the activity of various MMR proteins such as hMLH1, PMS1, PMS2, hMSH2 and hMSH6 is significantly reduced in the presence of *H. pylori* infection. An inverse relationship between microsatellite instability (MSI) and CagA protein has also been reported suggesting that other factors are also responsible for MSI in GC in addition to the bacterium CagA protein^[57]. *H. pylori* induces genomic instability of (CA)_n repeats in mice resulting in impairment of MMR machinery and generating a transient mutator phenotype making the gastric epithelia susceptible to aggregation of genetic instability leading to gastric carcinogenesis^[58]. Some researchers contradict the above findings and suggest that both *H. pylori* negative and positive tumors showed the same amount of MSI in GC, and even after eradication of the bacterium there were no changes in chromosomal aberrations^[59]. This suggested that *H. pylori* infection may act as a synergistic factor in GC, but not a direct factor causing carcinogenesis by altering gene expression.

A detailed characterization of a functionally unknown gene (*HP986*) which was detected in isolates from patients with peptic ulcer and gastric carcinoma was performed. Expression and purification of recombinant HP986 (rHP986) revealed a novel, approximately 29 kDa protein in biologically active form that was associated with significant levels of humoral immune response in diseased individuals ($P < 0.001$). In addition, it was reported that rHP986 induced significant levels of tumor necrosis factor (TNF)- α and IL-8 in cultured human macrophages concurrent with the translocation of nuclear transcription factor- κ B (NF- κ B). Furthermore, rHP986 induced apoptosis of cultured macrophages through a Fas mediated pathway. Dissection of the underlying signaling mechanism revealed that rHP986 induces both TNFR1 and Fas expression leading to apoptosis. These authors further demonstrated the interaction of HP986 with TNFR1 through computational and experimental approaches. Independent pro-inflammatory and apoptotic responses triggered by rHP986 may possibly work as a survival strategy to gain a niche through inflammation and to counter the activated macrophages to avoid clearance^[60,61].

Analysis of the p53 codon 72 SNP in 372 biopsy samples from our center revealed that in the North Indian normal population the p53 Arg/Arg (40.59%) and Pro/Arg variant (33.66%) were higher as compared to the p53 Pro/Pro variant (25.75%). Gastritis and gastropathy had a similar distribution, whereas gastric cancer, GU and DU cases showed a decrease in the Arg/Arg variant and an increase in the Arg/Pro and Pro/Pro variant. It was also found that the presence of the p53 Pro allele along with a decrease in the Arg/Arg allele is associated with a small, but non-significant increase in the risk of gastric lesions, suggesting that p53 (Arg), is more effective in protecting stressed cells from neoplastic development than p53 (Pro). These findings are in accordance with Mantovani *et al.*^[62] and Bergamaschi *et al.*^[63]. We also found that the p53 (Arg) (Pro/Arg) variant is higher in normal

subjects. Variation in apoptotic index also correlated with a change in the pattern of the Arg/Arg allele in various diseases showing that this allele may prevent carcinogenic changes by stimulating apoptosis of damaged epithelial cells. This may be the reason for the low incidence of gastric cancer in North India despite a relatively higher incidence of *H. pylori* infection (Under Publication).

CONCLUSION

In conclusion, the Indian enigma is a variation in the prevalence of *H. pylori* infection and gastric cancer in different zones. The incidence of gastric cancer in the Indian continent cannot be attributed to infection by *H. pylori* only, other factors such as diet, tobacco and socio-economic status may also have a role.

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