**Name of Journal:** *World Journal of Gastroenterology*

**Manuscript NO:** 54808

**Manuscript Type:** MINIREVIEWS

**Novel virulence factor *dupA* of *Helicobacter pylori* as an important risk determinant for disease manifestation: An overview**

Alam J *et al*. Novel virulence factor *dupA* of *Helicobacter pylori*

Jawed Alam, Avijit Sarkar, Bipul Chandra Karmakar, Mou Ganguly, Sangita Paul, Asish K Mukhopadhyay

**Jawed Alam,** Division of Infectious Diseases, Institute of Life Science, Bhubaneswar 751023, India

**Avijit Sarkar, Bipul Chandra Karmakar, Mou Ganguly, Sangita Paul, Asish K Mukhopadhyay,** Division of Bacteriology, ICMR-National Institute of Cholera and Enteric Diseases, Kolkata 700010, India

**Author contributions:** Alam J and Mukhopadhyay AK was involved in the conceptualization; Alam J, Karmakar BC and Sarkar A were involved in the writing the original draft; Sarkar A and Paul S performed the methodology; Karmakar BC was involved in collecting research; Ganguly M took part in the visualization; Ganguly M and Paul S wrote and edited the review; Paul S performed the validation; Mukhopadhyay AK supervised, critically revised and edited the manuscript; All authors have read and approve the final manuscript.

**Supported by** Council of Scientific and Industrial Research, Government of India, No. 12458; Department of Science and Technology, India, No. IF140909; and the Council of Scientific and Industrial Research, India, No. 09/482(0065)/2017-EMR-1.

**Corresponding author: Asish K Mukhopadhyay, PhD, Senior Scientist,** Division of Bacteriology, ICMR-National Institute of Cholera and Enteric Diseases, P 33, CIT Road, Scheme XM, Beliaghata, Kolkata 700010, India. asish1967@gmail.com

**Received:** February 20, 2020

**Revised:** June 23, 2020

**Accepted:**

**Published online:**

**Abstract**

*Helicobacter pylori* (*H. pylori*) is a microaerophilic, Gram-negative, human gastric pathogen found usually in the mucous lining of stomach. It infects more than 50% of the world’s population and leads to gastroduodenal diseases. The outcome of disease depends on mainly three factors: host genetics, environment and bacterial factors. Among these, bacterial virulence factors such as *cagA*, *vacA* are well known for their role in disease outcomes. However, based on the global epidemiological results, none of the bacterial virulence (gene) factors was found to be associated with particular diseases like duodenal ulcer (DU) in all populations. Hence, substantial importance has been provided for research in strain-specific genes outside the *cag* pathogenicity island, especially genes located within the plasticity regions. *dupA* found within the plasticity regions was first demonstrated in 2005 and was proposed for duodenal ulcer development and reduced risk of gastric cancer in certain geographical regions. Due to the discrepancies in report from different parts of the world in DU development related to *H. pylori* virulence factor, *dupA* became an interesting area of research in elucidating the role of this gene in the disease progression. In this review, we shed light on the detailed information available on the polymorphisms in *dupA* and their clinical relevance. We have critically appraised several pertinent studies on *dupA* and discussed their merits and shortcomings. This review also highlights *dupA* gene as an important biomarker for DU in certain populations.

**Key words:** *Helicobacter pylori*; Plasticity region;Duodenal ulcer; Gastric cancer; *dupA* gene

Alam J, Sarkar A, Karmakar BC, Ganguly M, Paul S, Mukhopadhyay AK. Novel virulence factor *dupA* of *Helicobacter pylori* as an important risk determinant for disease manifestation: An overview. *World J Gastroenterol* 2020; In press

**Core tip:** A novel virulence factor *dupA* located in the plasticity region of *Helicobacter pylori* genome was found to be associated with duodenal ulcer development in certain geographical regions. Well-known bacterial virulence factors in this pathogen like *cagA*, *vacA* are not found to be associated with duodenal ulcer in Asia. Studies focused on the epidemiology and clinical relevance of *dupA* around the world exhibit significant variations. Hence, we focused on the variations in *dupA* and the plausible role of such variation in disease etiology with the goal of bringing attention to this topic to the scientific community and eventually opening up avenues for further research*.*

**INTRODUCTION**

*Helicobacter pylori* (*H. pylori*) is a curved rod-shaped, Gram-negative, microaerophilic bacterium found usually in the mucous lining of the stomach. *H. pylori* infects more than 50% of the world’s population and 70%-80% of the Indian population[1,[2](applewebdata://067B6769-274E-4B7B-A129-E27D096DD09C#_ENREF_2)]. *H. pylori* is acquired during childhood and remains in the stomach throughout the life if not treated effectively[[3](applewebdata://067B6769-274E-4B7B-A129-E27D096DD09C#_ENREF_3)]. Infection with *H. pylori* causes duodenal ulcer (DU), gastric ulcer (GU), gastric cancer (GC) and gastric mucosa-associated lymphoid tissue lymphoma[[4-7](applewebdata://067B6769-274E-4B7B-A129-E27D096DD09C#_ENREF_4)]. Considering its clinical importance, the World Health Organization has declared *H. pylori* as a class I carcinogen and enlisted GC as the fifth most common cancer and the third most common cause of cancer-related death[[8](applewebdata://067B6769-274E-4B7B-A129-E27D096DD09C#_ENREF_8),[9](applewebdata://067B6769-274E-4B7B-A129-E27D096DD09C#_ENREF_9)]. Infection of *H. pylori* is comparatively more prevalent in developing countries than Western countries due to socioeconomic and sanitary conditions[[10](applewebdata://067B6769-274E-4B7B-A129-E27D096DD09C#_ENREF_10)]. The mode of transmission of *H. pylori* is not clearly understood. However, most of the studies suggest that *H. pylori* is transmitted from person to person *via* oral-oral and fecal-oral route and also through contaminated food and water[[11](applewebdata://067B6769-274E-4B7B-A129-E27D096DD09C#_ENREF_11)-14].

The enigma of *H. pylori* research is that the majority of infected patients remain asymptomatic, whereas around 15%-20% of infected individuals develop symptoms of peptic ulcer (duodenal or gastric) as a long-term consequence of infection. It is not clear what governs the manifestation of *H. pylori* infection in some people. This apparent puzzle prompted the proposal that the sheer presence of *H. pylori* in the stomach is inadequate to develop acute gastric disease and that other conditions are required. However, it is assumed that the responsible factors in *H. pylori*-associated diseases are due to its virulence factors, host genetics, immunity and environmental influences. Host factors like polymorphism in the genes (pro-inflammatory cytokine genes) increase the risk of the specific clinical outcome[[15](applewebdata://067B6769-274E-4B7B-A129-E27D096DD09C#_ENREF_15)]. None of the *H. pylori* virulence factors such as *cagA*, *vacA*, the blood group antigen *babA* and *oipA* have been linked with specific diseases like DU or GC uniformly in all populations[[16-20](applewebdata://067B6769-274E-4B7B-A129-E27D096DD09C#_ENREF_16)].

Analysis of the full genome sequences of different *H. pylori* strains reported specific genetic locus whose G+C content was lower than that of the rest of the *H. pylori* genome. This indicates the possibility of horizontal deoxyribonucleic acid (DNA) transfer from other species. *H. pylori* carry an open pan-genome, which maintain a discrete group of strain-specific genes. These strain-specific genes mostly reside in genomic regions that had earlier been coined as plasticity zones. This term was previously used to describe a specific genetic segment with high variation between the *H. pylori* genome sequences[21,22]. The complete genome sequence of *H. pylori* reveals that part of the plasticity zone is normally arranged as genomic islands that may be integrated in the genetic loci. About 50% of the strain-specific genes of *H. pylori* are located in the plasticity region. Here, our focus is on the gene *dupA*, which is located within the plasticity region. This gene was first reported in 2005 as an important biomarker for DU[23]. During subsequent years, several investigations were carried out on *dupA*, and this has become an interesting area of research, as shown in Table 1.

**METHODOLOGY**

To review the importance of *dupA*, we have searched the “NCBI-PubMed” using the keywords: “*dupA*”, “*H. pylori*” and a total of 80 articles were found, of which 76 were published in English till January 2020. Out of 76, 13 are published as review articles and two as meta-analysis of previous data. The remaining 61 documented as research articles. The research on *dupA* has spanned 15 years with contradictory findings. In this review, we summarize the result of relevant studies and discuss the pathogenesis of *dupA* since its early stage to recent advancements. Finally, this review highlights the significance of *dupA* gene of *H. pylori* as a virulence factor (virulence marker) and its role in pathogenesis including the progression of DU.

**DISCREPANCIES OF *DUPA* WITH CLINICAL OUTCOMES**

Studies conducted with *H. pylori* strains from East Asia and South America identified a novel *H. pylori* virulence factor encoded in the *dupA* that was associated with increased risk of DU and decreased risk of GC. However, this perception seems to be region specific. This *dupA* was homologous to *virB*4 gene, located in the plasticity zone of *H. pylori.* *dupA* contained two open reading frames (ORFs), *jhp0917* and *jhp0918*, with an overlap of twelve bases and an insertion of either base thymine (T) or cytosine (C) after the position 1385 of the *jhp0917* that leads to continuous gene of 1839 bp. Since 2005, several studies have been conducted from different geographical areas to check the association of *dupA* with disease outcome considering the *dupA* has two ORFs (*jhp0917/jhp0918*) with the insertion of one base (T/C) at position 1385 of *jhp0917*. Studies performed in North India during 2007 support the finding of Lu *et al*[24]. However, studies conducted in different countries (Belgium, South Africa, China, North America and Brazil) found that *dupA* is not associated with DU in the respective population[25-27].

Investigations made in Sao Paulo, Brazil showed that *dupA* was detected in *H. pylori* strains of 41.5% patients, which was less from a previous study made by Gomes *et al*[26] (2008), in which *dupA* was present in 89.5% patients[28]. This study showed an association of *dupA* with *cagA* and *vacA s1m1* genotypes but without any link to disease outcome. The difference in the results of these two studies from Brazil could be explained by variation in geographic regions, a re-arrangement in the plasticity zone distribution in *H. pylori* and various methods used for the analysis.

The distribution of *dupA* in *H. pylori* was similar in Iraqi and Iranian population, but there was an association between peptic ulcer and *dupA* only in the Iraqi population[29]. An independent study by Douraghi *et al*[30](2008) reported a non-significant higher distribution of *dupA* in DU than non-cardia GC patients in the Iranian population[30]. Another study by Talebi Bezmin Abadi *et al*[31] (2012) found a positive association between the presence of *dupA* and DU along with an inverse association between *dupA* and GU in Iranian population[31]. The discrepancy in the finding of Douraghi *et al*[30] (2008) and Talebi Bezmin Abadi *et al*[31](2012) may be due to differences in the study populations. Douraghi *et al*[30] (2008) focused mainly in Tehran (the densely populated capital of Iran), whereas Talebi Bezmin Abadi *et al*[31](2012) collected samples from the extremely rural northern areas of Iran. Recently, Fatahi *et al*[32](2019) tested a highly conserved region of *dupA* and showed a significant relationship between the occurrence of DU and the presence of an 112 bp segment of *dupA* in the Iranian population[32]. Another group from Iran studied the relationship between antibiotic resistance pattern and virulence genotype among 68 *H. pylori* strains and found that metronidazole resistance was significantly associated with the strains harboring *cagA, sabA* and *dupA*[33]. One study from Kurdistan region of Northern Iraq reported that *cagA* gene was significantly associated with peptic ulcer disease rather than *dupA,* which contradict the result of Hussein *et al*[29](2008). This might be due to the differences in sample size and also in the geographical location of Iraq[34]. In the Shiraz area of Iran, a significant relationship was found between strains with *dupA*, CagA motif (ABC types) and DU disease, which supports the previous finding in this region[35]. Another study from Western Iran indicated that presence of *dupA* gene could be considered as a marker for the onset of severe gastroduodenal diseases[36]. However, there was no association of *dupA* with DU in the results obtained from the Turkish population[37].

In China and South Korea, presence of *dupA* in clinical *H. pylori* isolates is significantly associated with DU and peptic ulcer (DU, benign GU, dysplasia), respectively[38,39]. In the Taiwanese female population, the host factor matrix metalloproteinase-3/tissue inhibitor matrix metalloproteinase-1 genotypes rather than *dupA* was found to increase the risk of DU in *H. pylori* infected cases[40]. A case control study conducted in Sweden, Australia, Malaysia and Singapore showed that there was significant variation in the prevalence of *dupA* in different locations and among different ethnic groups (Chinese, Indian and Malaya) within a country[41]. Another study in ethnic groups (Indian, Chinese and Malaya) of Malaysia reported that the prevalence of *dupA* was 22.9% in patients, which was in line with previous data (21.3%) conducted in Malaysia by Schmidt *et al*[41] (2009). In the later study, there was no association between *dupA* and clinical outcome[42].

Two independent systematic review and meta-analyses showed that *dupA* is more associated with DU in some Asian populations than in Western populations[43,44]. Between 2005 and 2009, almost all the studies used polymerase chain reaction (PCR) of two ORFs *jhp0917, jhp0918* and sequencing to identify the *dupA*. Functional analysis of *dupA* in the Japanese population showed no association with DU but another study from different parts of Japan showed that *dupA* is inversely related to GC[45,46].

Results from a study using different molecular methods [PCR, dot-blot hybridization, sequencing and reverse transcription PCR (RT-PCR)] indicated that *dupA* gene was prevalent more than six times in DU than in non-ulcer dyspepsia patients, indicating its significant association in India[47]. This result also corroborated the finding of Arachchi *et al*[24] (2007) from North India. The RT-PCR analysis of South and East Indian population revealed that all PCR positive strains were not able to produce *dupA* transcripts, which was inconsistent with the finding of Nguyen *et al*[45] (2009) where all the *dupA* positive strains showed the expression of the gene[47]. Further, the real-time PCR analysis revealed that the expression level of the *dupA* transcripts varied from strain to strain in this study.

Studies conducted in Chile supported a significant association of *dupA* gene with non-severe clinical outcome like DU and also played a role in protecting severe diseases like GC[[48](applewebdata://F99D4E33-EA9B-4348-8B27-D6A77F633E40#_ENREF_35)]. The Costa Rica study with 151 dyspeptic patients showed that presence of *dupA* was significantly associated with decreased risk of DU[[49](applewebdata://F99D4E33-EA9B-4348-8B27-D6A77F633E40#_ENREF_36)].

Some of the above-mentioned studies verified the finding of Lu *et al*[[23](applewebdata://F99D4E33-EA9B-4348-8B27-D6A77F633E40#_ENREF_36)] (2005), but others could not find an association between *dupA* and disease outcome in their study populations. The differences in the results could be explained due to variation in the distribution of plasticity region genes and differences in the study population and techniques chosen for detection of *dupA* gene. Several studies on *dupA* were restricted to PCR of *jhp0917* and *jhp0918* along with sequencing of only the 3' region of *jhp0917* to find the insertion of T/C at 1385 position of *jhp0917.* Numerous studies have shown the presence of frame shift mutation within *dupA* gene leading to the formation of truncated non-functional DupA. These findings provide evidence that only PCR based analysis of *dupA* may yield erroneous interpretation. Studies conducted by Queiroz *et al*[50] (2011) and Moura *et al*[51] (2012) from Brazil showed the presence of a mutation in *dupA* that results in a stop codon, making the gene truncated or non-functional. In addition, these studies revealed the importance of sequence analysis of *dupA* amplicons[50,51]. Truncated *dupA* might not be involved in thepathogenesis of *H. pylori.*

Hussein *et al*[52] (2010) coined the term “*dupA*1”. The *dupA* positive *H. pylori* strains were categorized into two alleles based on the sequence; *dupA1* (intact 1884 bp) and *dupA2* (truncated). It was shown that the intact *dupA1* positive strains induced the production of interleukin (IL)-12 subunit p40 (IL-12p40) and IL-12p70 from CD14 (+) mononuclear cells and IL-8 expression in the human stomach, respectively[52].Takahashi *et al*[53] (2012) first reported the presence of an additional 615 bp in the 5' region of ORF *jhp0917* (absent in strain J99) and 45 bp in the 3' of *jhp0918* (consist of 37 bp of intergenic region of *jhp0918-jhp0919* and 8 bp of 5' region of *jhp0919* inJ99*)* to make 2499 bp of *dupA* in the Japanese population (Figure 1). This variation formed the basis for classification of *dupA* into two types; “long and short types”. The long type of intact 2499 bp (with an additional 615 bp at 5' region of *jhp0917*) has been considered as an actual virulence factor, and the absence of the additional segment should be interpreted with caution[53].

None of the *H. pylori* strains from Iraq carried the complete *dupA* cluster containing *virB8*, *virB9*, *virB10*, *virB11*, *virD4* and *virD2*, but there was a significant association between *dupA*1 and DU. Moreover, higher levels of gastric mucosa IL-8 production were documented in *dupA1* than in *dupA2* or *dupA* negative strains[54]. Further studies with *H. pylori* infected patients showed that *cagA*, complete *dupA* cluster and smoking habit were associated with increased levels of IL-8 production from gastric mucosa[[55](applewebdata://F99D4E33-EA9B-4348-8B27-D6A77F633E40#_ENREF_30)]. It was also shown in another study that the high IL-8 level in gastric mucosa was neither significantly associated with *dupA1* positive strains nor with *dupA* negative strains[56]. A significant association has also been found between *dupA1* and A2147G clarithromycin resistance mutation. However, the result of *dupA1* and IL-8 association in the Iraqi population was not well elucidated. In Brazilian *H. pylori* strains, it was found that *H. pylori* strains had the 45 base at the 3' end of *dupA,* similar to that of *dupA1*[57].

*dupA* gene of Indian *H. pylori* strains has been classified into two forms based on the presence of additional 615 bp at the 5' region of *dupA* followed *by* astop codon.This includes *dupA*1 without any frameshift mutation (either long type or short type) and *dupA*2 with the truncated version having frameshift mutation[58]. Among these, *dupA*1 (intact *dupA*) was significantly associated with DU. Phylogenetic analysis of complete *dupA* gene sequencing revealed that Indian *H. pylori* strains intermingled with the East Asian strains, but differed from European strains[58]. *dupA* is the first known genetic element of Indian *H. pylori* strains, which phylogenetically formed the same cluster with the East Asian strains. *In vitro* study showed that IL-8 production was significantly associated with DU in intact *dupA*1 rather than truncated *dupA*2 or *dupA* negative strains[58]. In Chinese strains, the prevalence of long type *dupA* (2499 bp) was significantly higher in patients with GU, GC and DU than in those with gastritis[59].

In the Japanese population, prevalence of *dupA* was higher in the group where *H. pylori* cannot be eradicated, indicating that *dupA* may be an associated risk factor in the eradication failure[60]. A study from Pakistan on the influence of *dupA* in the eradication failure showed that *H. pylori* strains harboring *dupA* and *cagA* were multidrug (metronidazole, clarithromycin and amoxicillin) resistant as compared to strains having other virulence factors*.* This finding was similar to the observation made in the Japanese population[61]. In the northern part of Spain, *dupA* was more prevalent in mild diseases (peptic ulcer) than severe diseases (GC)[62]. In Switzerland and South Africa, *dupA* of *H. pylori* was not associated with severe gastritis or DU[63,64].

**DUPA CLUSTER: THIRD TYPE IV SECRETION SYSTEM (T4SS) OF *H. PYLORI***

The T4SS is an important bacterial transport system, and it is involved in the transport of large molecules (*e.g*., DNA, protein, *etc*) across the bacterial cell envelope[65,6[6](applewebdata://A3838050-2032-4BBD-910E-EDF5B9753E9F#_ENREF_38)]. Till now, three types of T4SS have been identified in *H. pylori,* of which much work has been done for the first two categories (*cag*PAI and ComB) and little is known about the third T4SS termed *dupA* cluster or *tfs3* (Figure 2)[[67,6](applewebdata://A3838050-2032-4BBD-910E-EDF5B9753E9F#_ENREF_39)8]. The third putative type IV secretion system (*tfs3)* is a 16 kb gene fragment present in the plasticity zone of *H. pylori*, whose seven ORFs (*viB4*, *virB8, virB9, virB10, virB11, virD4* and *virD2*) were homologous to virB4/D of *Agrobacterium tumefecians* (*A. tumefecians*)*.* The function of the *tfs3* elements is not yet clear as there is no direct evidence to show its role in transformation, conjugation or mouse colonization[69,[70](applewebdata://A3838050-2032-4BBD-910E-EDF5B9753E9F#_ENREF_42)]. Some researchers divided the *tfs3* into *tfs3a* (all six *virB* homologues with *dupA*) and *tfs3*b (all six *virB* homologues with *virB4*), whereas others named all six *virB* homologues with virB4as *tfs3* and all six *vir*B homologues with *dupA* as *tfs*4[71-73]. In order to avoid confusion, we will use the term *tfs3a* or *dupA* cluster (all six *virB* homologues with *dupA*). VirB8, VirB9 and VirB10 are expected to form the core complex that bridges cytoplasm and the outer membrane. The VirB4, VirB11, VirD4 may be localized to the inner bacterial membrane and recognize the substrate and energize translocation and assembly of T4SS[[74](applewebdata://A3838050-2032-4BBD-910E-EDF5B9753E9F#_ENREF_46)]. Further, the novel putative T4SS (*tfs3a*) or *dupA* cluster has been divided into three groups: Viz, a complete *dupA* cluster (*dupA*-positive and all six *virB* genes-positive), an incomplete *dupA* cluster (*dupA*-positive but one/more than one *virB* genes negative) and *dupA*-negative group (*dupA* negative and *virB* gene positive/negative).

The study of *dupA* cluster from the United States population showed that the complete *dupA* cluster (*dupA* with six *virB* homologues) was associated with DU rather than *dupA* gene only[75]. Another report from the northeast part of China showed a significant association of complete *dupA* cluster with IL-8 production (*P* < 0.01), but it did not show any correlation between *dupA* cluster and disease outcome[[76](applewebdata://A3838050-2032-4BBD-910E-EDF5B9753E9F#_ENREF_47)]. The studies from United States and China were conducted to check the prevalence of *tfs3a* or *dupA* cluster in their population by PCR only. However, the mere presence of the gene does not express functional protein and there is no direct evidence that shows *tfs3a* or *dupA* cluster forming a functional T4SS. The earlier studies on *tfs3a*did not find a direct pathogenic role of *tfs3a* in *H. pylori,* but found increased colonization fitness and up-regulation of pro-inflammatory signaling from cultured cells. A novel pathogenicity island (PAI) called *tfs3*-PAI was identified in China that had 17 ORFs, of which six are functionally homologues of T4SS and coordinate with the well-studied *cag*-PAI[[77](applewebdata://A3838050-2032-4BBD-910E-EDF5B9753E9F#_ENREF_48)]. The complete *tfs* plasticity cluster was associated with IL-8 induction. The expression of some of the genes of *tfs3a/tf*s4 (*virB2*, *virB4*, *virB6*, *virB8*, *virB10*) in*H. pylori* is up-regulated in low pH and enhances bacterial adhesion that support the role of *tfs3a/tfs4* in the colonization and virulence[[78](applewebdata://A3838050-2032-4BBD-910E-EDF5B9753E9F#_ENREF_49)]. It is not known whether the *virB* genes of *dupA* cluster work independently or in a coordinated manner by interacting among themselves or complementing each other’s function. We checked the interaction of *dupA* with six *virB* genes of *tfs3a* to identify the assembly and function of complete *tfs3* using *in vivo* studies (yeast two-hybrid system) and found that *dupA* gene did not interact directly with any *virB* gene. It seems that *dupA* may interact with some intermediates or work independently (unpublished data). This interpretation supports our earlier finding that *tfs3* is not significantly associated with DU in Indian population**.** More studies are required to know the structure, assembly and functions of the VirB proteins in *H. pylori*.

**THE PROSPECTIVE FUNCTIONS OF DUPA**

The bioinformatics analysis (PDB search tool, UniProt database) showed that the *dupA* gene is homologous to VirB4 adenosine triphosphate (ATP)ase of virB/virD of *A. tumefecians* and is predicted to be involved in DNA/protein transfer. The N-terminal of long type DupA has no homologous motif. Only the middle portion (*jhp0917*) and C-terminal (part of *jhp0918*) showed homologous motifs suggesting that the N-terminal region might act as signal sequence. The amino acid sequence (210-406 AA) of *jhp0917* gene proteinwas homologous to CagE\_TrbE\_VirB family, a component of type IV transporter secretion system.The first middle region of the DupA protein (430-500 AA) is homologous to FtsK/SpoIIIE family, which contains ATP binding P-loop motif. This was found in the Ftsk protein of *Escherichia coli* involved in peptidoglycan synthesis and spoIIIE of *Bacillus subtilis*, facilitating in the intercellular chromosomal DNA transfer.

The second middle region (464-503aa) is homologous to TrwB, which has an ATP binding domain, and a part of T4SS may be responsible for the DNA binding and horizontal DNA transfer. The C-terminal region (668-738aa) is homologous to TraG\_C\_D, which is involved in the interaction of DNA-processing (Dtr) and mating pair formation (Mpf) system, leading to DNA transfer in bacterial conjugation. Many reports have shown that the growth rate of *dupA* positive strains is higher in low pH as compared to *dupA* deleted/negative strains. This phenomenon indicates that DupA protein acts as an interactive protein and hence regulates urease secretion in *H. pylori*[[79](applewebdata://565F63D9-49D4-4755-A5B9-EED1D9E6CEE6#_ENREF_50)].

The *in vitro* and *in vivo* studies showed the role of *dupA* gene in the activation of transcription factors nuclear factor kappa light chain enhancer of activated B cells and activator protein-1, which leads to IL-8 production. DupA protein act as an ATPase associated efflux pump, which probably confers its virulence. Evidence suggests that *DupA* is involved in the pathogenesis of *H. pylori* by activating the mitochondria dependent apoptotic pathway of the host’s cell, which ultimately inhibits gastric cell growth.

Studies to understand the apoptotic effect of *dupA* on human gastric adenocarcinoma epithelial cell line (commonly known as AGS) by propidium iodide staining and fragmentation assay determined that *dupA* gene can induce apoptosis in AGS cells during an early stage of infection (unpublished data). This finding supports the results of Wang *et al*[79] (2015) and finds that *dupA* may act as a pathogenic factor of *H. pylori* to cause gastroduodenal diseases. Further studies are required to confirm the pathogenic effect of *dupA* in an *in vivo* model.

The growth kinetics between wild type *dupA*positivestrains and its isogenic mutant strain showed that exponential phase was retarded in *dupA* mutant cells as compared to the wild type strain. Our growth curve results, supported by the microarray data, showed that cell division gene in the mutant *H. pylori* was downregulated (unpublished data). It has also been suggested that motility is an essential feature in the colonization and therefore the pathogenicity of *H. pylori*. The decrease in motility in *dupA* mutant strain as compared to wild type inferred the role of *dupA* gene in the motility. This motility result was further confirmed by the gene expression profile of *dupA* mutant strain whose flagella proteins (FlgE, FliD and FliG) were found to be down-regulated (unpublished data). It might be possible that *dupA* gene is directly or indirectly involved in negatively affecting the expression of cell division and flagellar genes of *H. pylori*.

As predicted from the bioinformatics analysis, our experimental data (unpublished data) have shown that natural transformation ability in *dupA* mutant strains has been totally inhibited in comparison to their wild type counterparts. There is a need for more studies on the heat-shock transformation efficiency, which will confirm the natural transformation assay, if any. Resistance to antimicrobials is of serious concern in *H. pylori* infection, as this may be the basis for eradication failure. It is important to use therapeutic regimens based on the results of antibiotic susceptibility testing. Metronidazole is considered a key drug in several therapies against *H. pylori* infection. The results of the metronidazole susceptibility test showed that inactivation of *dupA* gene transforms the *H. pylori* strains to resistance phenotype. This phenomenon has not been explained very well. It is possible that the *dupA* gene might help in the DNA/protein/drug import (unpublished data).

The *dupA* or *dupA* cluster may have an intermediate function to link *cag*PAI and *comB* system, as *dupA* gene shows homology with *cagE* of *cag*PAI and *comB4* of *comB* system. So, there is a need of an *in vivo* study to establish the precise function of *dupA*. It is assumed that the *dupA* in combination with other six *vir* genes form a novel third T4SS called *tfs3a* or *dupA* cluster that might play a pathogenic role in gastroduodenal diseases.

**CONCLUSION**

*H. pylori* is one of the most diverse bacterial species. *H. pylori* demonstrate panmictic population structure. DNA-fingerprint of two strains isolated from two different persons generally displays a non-identical pattern, which suggests genetic exchange along with co-evolution of this gastric pathogen with its host. One study from the Indian population demonstrated that all the tested patients carried multiple *H. pylori* strains in their gastric mucosa[80]**.** Analyses of certain genetic loci showed the micro diversity among the colonies from a single patient, which may be due to the recombination events during long-term carriage of the pathogen. From the results of this study, researchers predicted that many patients from the developing world acquired infections of *H. pylori* due to repeated exposure to this pathogen with different genetic make-up[80]. This may enhance the probability of super infections, which favor genetic exchanges among these unrelated *H. pylori* strains. As a result, this led to the genesis of certain *H. pylori* variants with different genetic makeup than the parental strain, which in turn increases the chance of the severe infection. Therefore, the exploration of appropriate biomarker(s) that envisage the clinical condition in *H. pylori*-infected patient is a challenging area of research.

There is a lack of relevant biomarker(s) capable of predicting important digestive diseases in clinical settings. Even though there is ample information regarding the *dupA* of *H. pylori,* many unanswered questions still exist, especially regarding the specificity of the *dupA* proposed for clinical manifestation. *dupA* was categorized as long and short types in one study, but in another study, this gene was typed as *dupA*1 (intact *dupA1* may be long type or short type) and *dupA*2 (truncated version). This gene classification should be resolved for international use to avoid any misperception. We propose the long *dupA* as *dupA*1 and short type *dupA* as *dupA*2, and the truncated version of *dupA* has to be disregarded, as it has no role in pathogenesis. *dupA* should be screened by PCR, sequencing of the full-length gene (1884 and 2499 nt) and western blotting. Nevertheless, the discrepancy prevails between the association of *dupA* (short type or long type) or *dupA* cluster and the disease outcome. Currently, the prevalence of intact *dupA* in East Asian countries is lower than Western countries. DupA with another six Vir proteins (VirB8, VirB9, VirB10, VirB11, VirD4 and VirD2) predicted to form novel third type-IV secretion system (*tfs3a*), which may be involved in transformation/conjugation or injection of DNA/new effector molecules in gastric epithelial cells. However, the function of specific Vir protein of complete *dupA* cluster (*tfs3a*) is not well characterized. Recent reports and other unpublished data showed that DupA has multifunctional biological activities, and it can be considered as an important biomarker for DU. It is also not clear whether the DupA works alone or in combination with other VirB proteins. There is an urgent need for reliable *in vitro* and animal models from diverse geographical areas of the world to elucidate further the pathogenic role of *dupA* and *dupA* cluster in gastroduodenal diseases, particularly the DU and GC.

**REFERENCES**

1 **Buzás GM**. Benign and malignant gastroduodenal diseases associated with Helicobacter pylori: a narrative review and personal remarks in 2018. *Minerva Gastroenterol Dietol* 2018; **64**: 280-296 [PMID: 29458240 DOI: 10.23736/S1121-421X.18.02481-9]

2 **Misra V**, Pandey R, Misra SP, Dwivedi M. Helicobacter pylori and gastric cancer: Indian enigma. *World J Gastroenterol* 2014; **20**: 1503-1509 [PMID: 24587625 DOI: 10.3748/wjg.v20.i6.1503]

3 **Abadi AT**, Kusters JG. Management of Helicobacter pylori infections. *BMC Gastroenterol* 2016; **16**: 94 [PMID: 27520775 DOI: 10.1186/s12876-016-0496-2]

4 **Wotherspoon AC**, Ortiz-Hidalgo C, Falzon MR, Isaacson PG. Helicobacter pylori-associated gastritis and primary B-cell gastric lymphoma. *Lancet* 1991; **338**: 1175-1176 [PMID: 1682595 DOI: 10.1016/0140-6736(91)92035-z]

5 **Parsonnet J**, Friedman GD, Vandersteen DP, Chang Y, Vogelman JH, Orentreich N, Sibley RK. Helicobacter pylori infection and the risk of gastric carcinoma. *N Engl J Med* 1991; **325**: 1127-1131 [PMID: 1891020 DOI: 10.1056/NEJM199110173251603]

6 **Suerbaum S**, Michetti P. Helicobacter pylori infection. *N Engl J Med* 2002; **347**: 1175-1186 [PMID: 12374879 DOI: 10.1056/NEJMra020542]

7 **Pellicano R**, Ribaldone DG, Fagoonee S, Astegiano M, Saracco GM, Mégraud F. A 2016 panorama of Helicobacter pylori infection: key messages for clinicians. *Panminerva Med* 2016; **58**: 304-317 [PMID: 27716738]

8 Schistosomes, liver flukes and Helicobacter pylori. IARC Working Group on the Evaluation of Carcinogenic Risks to Humans. *IARC Monogr Eval Carcinog Risks Hum* 1994; **61**: 1-241 [PMID: 7715068]

9 **McGuire S**. World Cancer Report 2014. Geneva, Switzerland: World Health Organization, International Agency for Research on Cancer, WHO Press, 2015. *Adv Nutr* 2016; **7**: 418-419 [PMID: 26980827 DOI: 10.3945/an.116.012211]

10 **Smith S**, Fowora M, Pellicano R. Infections with *Helicobacter pylori* and challenges encountered in Africa. *World J Gastroenterol* 2019; **25**: 3183-3195 [PMID: 31333310 DOI: 10.3748/wjg.v25.i25.3183]

11 **Mamishi S**, Eshaghi H, Mahmoudi S, Bahador A, Hosseinpour Sadeghi R, Najafi M, Farahmand F, Khodadad A, Pourakbari B. Intrafamilial transmission of Helicobacter pylori: genotyping of faecal samples. *Br J Biomed Sci* 2016; **73**: 38-43 [PMID: 27182676 DOI: 10.1080/09674845.2016.1150666]

12 **Bui D**, Brown HE, Harris RB, Oren E. Serologic Evidence for Fecal-Oral Transmission of Helicobacter pylori. *Am J Trop Med Hyg* 2016; **94**: 82-88 [PMID: 26598563 DOI: 10.4269/ajtmh.15-0297]

13 **Ranjbar R**, Khamesipour F, Jonaidi-Jafari N, Rahimi E. Helicobacter pylori isolated from Iranian drinking water: vacA, cagA, iceA, oipA and babA2 genotype status and antimicrobial resistance properties. *FEBS Open Bio* 2016; **6**: 433-441 [PMID: 27419049 DOI: 10.1002/2211-5463.12054]

14 **Talaei R**, Souod N, Momtaz H, Dabiri H. Milk of livestock as a possible transmission route of Helicobacter pylori infection. *Gastroenterol Hepatol Bed Bench* 2015; **8**: S30-S36 [PMID: 26171135]

15 **Amieva MR**, El-Omar EM. Host-bacterial interactions in Helicobacter pylori infection. *Gastroenterology* 2008; **134**: 306-323 [PMID: 18166359 DOI: 10.1053/j.gastro.2007.11.009]

16 **Yamaoka Y**, Kwon DH, Graham DY. A M(r) 34,000 proinflammatory outer membrane protein (oipA) of Helicobacter pylori. *Proc Natl Acad Sci U S A* 2000; **97**: 7533-7538 [PMID: 10852959 DOI: 10.1073/pnas.130079797]

17 **Covacci A**, Censini S, Bugnoli M, Petracca R, Burroni D, Macchia G, Massone A, Papini E, Xiang Z, Figura N. Molecular characterization of the 128-kDa immunodominant antigen of Helicobacter pylori associated with cytotoxicity and duodenal ulcer. *Proc Natl Acad Sci U S A* 1993; **90**: 5791-5795 [PMID: 8516329 DOI: 10.1073/pnas.90.12.5791]

18 **Censini S**, Lange C, Xiang Z, Crabtree JE, Ghiara P, Borodovsky M, Rappuoli R, Covacci A. cag, a pathogenicity island of Helicobacter pylori, encodes type I-specific and disease-associated virulence factors. *Proc Natl Acad Sci U S A* 1996; **93**: 14648-14653 [PMID: 8962108 DOI: 10.1073/pnas.93.25.14648]

19 **Atherton JC**, Cao P, Peek RM Jr, Tummuru MK, Blaser MJ, Cover TL. Mosaicism in vacuolating cytotoxin alleles of Helicobacter pylori. Association of specific vacA types with cytotoxin production and peptic ulceration. *J Biol Chem* 1995; **270**: 17771-17777 [PMID: 7629077 DOI: 10.1074/jbc.270.30.17771]

20 **Ghosh P**, Sarkar A, Ganguly M, Raghwan, Alam J, De R, Mukhopadhyay AK. Helicobacter pylori strains harboring babA2 from Indian sub population are associated with increased virulence in ex vivo study. *Gut Pathog* 2016; **8**: 1 [PMID: 26759607 DOI: 10.1186/s13099-015-0083-z]

21 **Fischer W**, Breithaupt U, Kern B, Smith SI, Spicher C, Haas R. A comprehensive analysis of Helicobacter pylori plasticity zones reveals that they are integrating conjugative elements with intermediate integration specificity. *BMC Genomics* 2014; **15**: 310 [PMID: 24767410 DOI: 10.1186/1471-2164-15-310]

22 **Ganguly M**, Sarkar S, Ghosh P, Sarkar A, Alam J, Karmakar BC, De R, Saha DR, Mukhopadhyay AK. Helicobacter pylori plasticity region genes are associated with the gastroduodenal diseases manifestation in India. *Gut Pathog* 2016; **8**: 10 [PMID: 27006705 DOI: 10.1186/s13099-016-0093-5]

23 **Lu H**, Hsu PI, Graham DY, Yamaoka Y. Duodenal ulcer promoting gene of Helicobacter pylori. *Gastroenterology* 2005; **128**: 833-848 [PMID: 15825067 DOI: 10.1053/j.gastro.2005.01.009]

24 **Arachchi HS**, Kalra V, Lal B, Bhatia V, Baba CS, Chakravarthy S, Rohatgi S, Sarma PM, Mishra V, Das B, Ahuja V. Prevalence of duodenal ulcer-promoting gene (dupA) of Helicobacter pylori in patients with duodenal ulcer in North Indian population. *Helicobacter* 2007; **12**: 591-597 [PMID: 18001398 DOI: 10.1111/j.1523-5378.2007.00557.x]

25 **Argent RH**, Burette A, Miendje Deyi VY, Atherton JC. The presence of dupA in Helicobacter pylori is not significantly associated with duodenal ulceration in Belgium, South Africa, China, or North America. *Clin Infect Dis* 2007; **45**: 1204-1206 [PMID: 17918084 DOI: 10.1086/522177]

26 **Gomes LI**, Rocha GA, Rocha AM, Soares TF, Oliveira CA, Bittencourt PF, Queiroz DM. Lack of association between Helicobacter pylori infection with dupA-positive strains and gastroduodenal diseases in Brazilian patients. *Int J Med Microbiol* 2008; **298**: 223-230 [PMID: 17897881 DOI: 10.1016/j.ijmm.2007.05.006]

27 **Pacheco AR**, Proença-Módena JL, Sales AI, Fukuhara Y, da Silveira WD, Pimenta-Módena JL, de Oliveira RB, Brocchi M. Involvement of the Helicobacter pylori plasticity region and cag pathogenicity island genes in the development of gastroduodenal diseases. *Eur J Clin Microbiol Infect Dis* 2008; **27**: 1053-1059 [PMID: 18560912 DOI: 10.1007/s10096-008-0549-8]

28 **Pereira WN**, Ferraz MA, Zabaglia LM, de Labio RW, Orcini WA, Bianchi Ximenez JP, Neto AC, Payão SL, Rasmussen LT. Association among H. pylori virulence markers dupA, cagA and vacA in Brazilian patients. *J Venom Anim Toxins Incl Trop Dis* 2014; **20**: 1 [PMID: 24456629 DOI: 10.1186/1678-9199-20-1]

29 **Hussein NR**, Mohammadi M, Talebkhan Y, Doraghi M, Letley DP, Muhammad MK, Argent RH, Atherton JC. Differences in virulence markers between Helicobacter pylori strains from Iraq and those from Iran: potential importance of regional differences in H. pylori-associated disease. *J Clin Microbiol* 2008; **46**: 1774-1779 [PMID: 18353934 DOI: 10.1128/JCM.01737-07]

30 **Douraghi M**, Mohammadi M, Oghalaie A, Abdirad A, Mohagheghi MA, Hosseini ME, Zeraati H, Ghasemi A, Esmaieli M, Mohajerani N. dupA as a risk determinant in Helicobacter pylori infection. *J Med Microbiol* 2008; **57**: 554-562 [PMID: 18436587 DOI: 10.1099/jmm.0.47776-0]

31 **Talebi Bezmin Abadi A**, Taghvaei T, Wolfram L, Kusters JG. Infection with Helicobacter pylori strains lacking dupA is associated with an increased risk of gastric ulcer and gastric cancer development. *J Med Microbiol* 2012; **61**: 23-30 [PMID: 21903829 DOI: 10.1099/jmm.0.027052-0]

32 **Fatahi G**, Talebi Bezmin Abadi A, Peerayeh SN, Forootan M. Carrying a 112 bp-segment in Helicobacter pylori dupA may associate with increased risk of duodenal ulcer. *Infect Genet Evol* 2019; **73**: 21-25 [PMID: 30981881 DOI: 10.1016/j.meegid.2019.04.009]

33 **Farzi N**, Yadegar A, Sadeghi A, Asadzadeh Aghdaei H, Marian Smith S, Raymond J, Suzuki H, Zali MR. High Prevalence of Antibiotic Resistance in Iranian *Helicobacter pylori* Isolates: Importance of Functional and Mutational Analysis of Resistance Genes and Virulence Genotyping. *J Clin Med* 2019; **8**: 2004 [PMID: 31744181 DOI: 10.3390/jcm8112004]

34 **Salih AM**, Goreal A, Hussein NR, Abdullah SM, Hawrami K, Assafi M. The distribution of cagA and dupA genes in Helicobacter pylori strains in Kurdistan region, northern Iraq. *Ann Saudi Med* 2013; **33**: 290-293 [PMID: 23793434 DOI: 10.5144/0256-4947.2013.290]

35 **Haddadi MH**, Bazargani A, Khashei R, Fattahi MR, Bagheri Lankarani K, Moini M, Rokni Hosseini SM. Different distribution of Helicobacter pylori EPIYA- cagA motifs and dupA genes in the upper gastrointestinal diseases and correlation with clinical outcomes in iranian patients. *Gastroenterol Hepatol Bed Bench* 2015; **8**: S37-S46 [PMID: 26171136 DOI: 10.1016/j.ccep.2012.02.001]

36 **Souod N**, Sarshar M, Dabiri H, Momtaz H, Kargar M, Mohammadzadeh A, Abdi S. The study of the oipA and dupA genes in Helicobacter pylori strains and their relationship with different gastroduodenal diseases. *Gastroenterol Hepatol Bed Bench* 2015; **8**: S47-S53 [PMID: 26171137]

37 **Tuncel IE**, Hussein NR, Bolek BK, Arikan S, Salih BA. Helicobacter pylori virulence factors and their role in peptic ulcer diseases in Turkey. *Acta Gastroenterol Belg* 2010; **73**: 235-238 [PMID: 20690562 DOI: 10.1007/s00261-009-9502-2]

38 **Zhang Z**, Zheng Q, Chen X, Xiao S, Liu W, Lu H. The Helicobacter pylori duodenal ulcer promoting gene, dupA in China. *BMC Gastroenterol* 2008; **8**: 49 [PMID: 18950522 DOI: 10.1186/1471-230X-8-49]

39 **Kim JY**, Kim N, Nam RH, Suh JH, Chang H, Lee JW, Kim YS, Kim JM, Choi JW, Park JG, Lee YS, Lee DH, Jung HC. Association of polymorphisms in virulence factor of Helicobacter pylori and gastroduodenal diseases in South Korea. *J Gastroenterol Hepatol* 2014; **29**: 984-991 [PMID: 24372834 DOI: 10.1111/jgh.12509]

40 **Yeh YC**, Cheng HC, Chang WL, Yang HB, Sheu BS. Matrix metalloproteinase-3 promoter polymorphisms but not dupA-H. pylori correlate to duodenal ulcers in H. pylori-infected females. *BMC Microbiol* 2010; **10**: 218 [PMID: 20707923 DOI: 10.1186/1471-2180-10-218]

41 **Schmidt HM**, Andres S, Kaakoush NO, Engstrand L, Eriksson L, Goh KL, Fock KM, Hilmi I, Dhamodaran S, Forman D, Mitchell H. The prevalence of the duodenal ulcer promoting gene (dupA) in Helicobacter pylori isolates varies by ethnic group and is not universally associated with disease development: a case-control study. *Gut Pathog* 2009; **1**: 5 [PMID: 19338650 DOI: 10.1186/1757-4749-1-5]

42 **Osman HA**, Hasan H, Suppian R, Hassan S, Andee DZ, Abdul Majid N, Zilfalil BA. Prevalence of Helicobacter pylori cagA, babA2, and dupA genotypes and correlation with clinical outcome in Malaysian patients with dyspepsia. *Turk J Med Sci* 2015; **45**: 940-946 [PMID: 26422871 DOI: 10.3906/sag-1409-77]

43 **Hussein NR**. The association of dupA and Helicobacter pylori-related gastroduodenal diseases. *Eur J Clin Microbiol Infect Dis* 2010; **29**: 817-821 [PMID: 20419465 DOI: 10.1007/s10096-010-0933-z]

44 **Shiota S**, Matsunari O, Watada M, Hanada K, Yamaoka Y. Systematic review and meta-analysis: the relationship between the Helicobacter pylori dupA gene and clinical outcomes. *Gut Pathog* 2010; **2**: 13 [PMID: 21040520 DOI: 10.1186/1757-4749-2-13]

45 **Nguyen LT**, Uchida T, Tsukamoto Y, Kuroda A, Okimoto T, Kodama M, Murakami K, Fujioka T, Moriyama M. Helicobacter pylori dupA gene is not associated with clinical outcomes in the Japanese population. *Clin Microbiol Infect* 2010; **16**: 1264-1269 [PMID: 19832706 DOI: 10.1111/j.1469-0691.2009.03081.x]

46 **Imagawa S**, Ito M, Yoshihara M, Eguchi H, Tanaka S, Chayama K. Helicobacter pylori dupA and gastric acid secretion are negatively associated with gastric cancer development. *J Med Microbiol* 2010; **59**: 1484-1489 [PMID: 20829397 DOI: 10.1099/jmm.0.021816-0]

47 **Alam J**, Maiti S, Ghosh P, De R, Chowdhury A, Das S, Macaden R, Devarbhavi H, Ramamurthy T, Mukhopadhyay AK. Significant association of the dupA gene of Helicobacter pylori with duodenal ulcer development in a South-east Indian population. *J Med Microbiol* 2012; **61**: 1295-1302 [PMID: 22653921 DOI: 10.1099/jmm.0.038398-0]

48 **Paredes-Osses E**, Sáez K, Sanhueza E, Hebel S, González C, Briceño C, García Cancino A. Association between cagA, vacAi, and dupA genes of Helicobacter pylori and gastroduodenal pathologies in Chilean patients. *Folia Microbiol (Praha)* 2017; **62**: 437-444 [PMID: 28283946 DOI: 10.1007/s12223-017-0514-y]

49 **Molina-Castro S**, Garita-Cambronero J, Malespín-Bendaña W, Une C, Ramírez V. Virulence factor genotyping of Helicobacter pylori isolated from Costa Rican dyspeptic patients. *Microb Pathog* 2019; **128**: 276-280 [PMID: 30654009 DOI: 10.1016/j.micpath.2019.01.018]

50 **Queiroz DM**, Rocha GA, Rocha AM, Moura SB, Saraiva IE, Gomes LI, Soares TF, Melo FF, Cabral MM, Oliveira CA. dupA polymorphisms and risk of Helicobacter pylori-associated diseases. *Int J Med Microbiol* 2011; **301**: 225-228 [PMID: 21050811 DOI: 10.1016/j.ijmm.2010.08.019]

51 **Moura SB**, Costa RF, Anacleto C, Rocha GA, Rocha AM, Queiroz DM. Single nucleotide polymorphisms of Helicobacter pylori dupA that lead to premature stop codons. *Helicobacter* 2012; **17**: 176-180 [PMID: 22515354 DOI: 10.1111/j.1523-5378.2011.00933.x]

52 **Hussein NR**, Argent RH, Marx CK, Patel SR, Robinson K, Atherton JC. Helicobacter pylori dupA is polymorphic, and its active form induces proinflammatory cytokine secretion by mononuclear cells. *J Infect Dis* 2010; **202**: 261-269 [PMID: 20533870 DOI: 10.1086/653587]

53 **Takahashi A**, Shiota S, Matsunari O, Watada M, Suzuki R, Nakachi S, Kinjo N, Kinjo F, Yamaoka Y. Intact long-type dupA as a marker for gastroduodenal diseases in Okinawan subpopulation, Japan. *Helicobacter* 2013; **18**: 66-72 [PMID: 23067336 DOI: 10.1111/j.1523-5378.2012.00994.x]

54 **Hussein NR**, Abdullah SM, Salih AM, Assafi MA. dupA1 is associated with duodenal ulcer and high interleukin-8 secretion from the gastric mucosa. *Infect Immun* 2012; **80**: 2971-2; author reply 2973 [PMID: 22811495 DOI: 10.1128/IAI.00076-12]

55 **Hussein NR**, Tuncel IE. Helicobacter pylori dupA and smoking are associated with increased levels of interleukin-8 in gastric mucosa in Iraq. *Hum Pathol* 2015; **46**: 929-930 [PMID: 25791584 DOI: 10.1016/j.humpath.2015.01.021]

56 **Hussein NR**, Tunjel I, Majed HS, Yousif ST, Aswad SI, Assafi MS. Duodenal ulcer promoting gene 1 (dupA1) is associated with A2147G clarithromycin-resistance mutation but not interleukin-8 secretion from gastric mucosa in Iraqi patients. *New Microbes New Infect* 2015; **6**: 5-10 [PMID: 26042186 DOI: 10.1016/j.nmni.2015.02.005]

57 **Queiroz DM**, Moura SB, Rocha AM, Costa RF, Anacleto C, Rocha GA. The genotype of the Brazilian dupA-positive Helicobacter pylori strains is dupA1. *J Infect Dis* 2011; **203**: 1033-1034 [PMID: 21402555 DOI: 10.1093/infdis/jiq147]

58 **Alam J**, Ghosh P, Ganguly M, Sarkar A, De R, Mukhopadhyay AK. Association of Intact dupA (dupA1) rather than dupA1 cluster with duodenal ulcer in Indian population. *Gut Pathog* 2015; **7**: 9 [PMID: 25829953 DOI: 10.1186/s13099-015-0056-2]

59 **Wang MY**, Chen C, Gao XZ, Li J, Yue J, Ling F, Wang XC, Shao SH. Distribution of Helicobacter pylori virulence markers in patients with gastroduodenal diseases in a region at high risk of gastric cancer. *Microb Pathog* 2013; **59-60**: 13-18 [PMID: 23583809 DOI: 10.1016/j.micpath.2013.04.001]

60 **Shiota S**, Nguyen LT, Murakami K, Kuroda A, Mizukami K, Okimoto T, Kodama M, Fujioka T, Yamaoka Y. Association of helicobacter pylori dupA with the failure of primary eradication. *J Clin Gastroenterol* 2012; **46**: 297-301 [PMID: 22298090 DOI: 10.1097/MCG.0b013e318243201c]

61 **Rasheed F**, Campbell BJ, Alfizah H, Varro A, Zahra R, Yamaoka Y, Pritchard DM. Analysis of clinical isolates of Helicobacter pylori in Pakistan reveals high degrees of pathogenicity and high frequencies of antibiotic resistance. *Helicobacter* 2014; **19**: 387-399 [PMID: 24827414 DOI: 10.1111/hel.12142]

62 **Fernández-Reyes M**, Tamayo E, Rojas-Rengifo D, Fischer W, Carrasco-García E, Alonso M, Lizasoain J, Bujanda L, Cosme Á, Montes M. Helicobacter pylori pathogenicity and primary antimicrobial resistance in Northern Spain. *Eur J Clin Invest* 2019; **49**: e13150 [PMID: 31192451 DOI: 10.1111/eci.13150]

63 **Imkamp F**, Lauener FN, Pohl D, Lehours P, Vale FF, Jehanne Q, Zbinden R, Keller PM, Wagner K. Rapid Characterization of Virulence Determinants in *Helicobacter pylori* Isolated from Non-Atrophic Gastritis Patients by Next-Generation Sequencing. *J Clin Med* 2019; **8**: 1030 [PMID: 31336977 DOI: 10.3390/jcm8071030]

64 **Idowu A**, Mzukwa A, Harrison U, Palamides P, Haas R, Mbao M, Mamdoo R, Bolon J, Jolaiya T, Smith S, Ally R, Clarke A, Njom H. Detection of Helicobacter pylori and its virulence genes (cagA, dupA, and vacA) among patients with gastroduodenal diseases in Chris Hani Baragwanath Academic Hospital, South Africa. *BMC Gastroenterol* 2019; **19**: 73 [PMID: 31088381 DOI: 10.1186/s12876-019-0986-0]

65 **Christie PJ**. Type IV secretion: intercellular transfer of macromolecules by systems ancestrally related to conjugation machines. *Mol Microbiol* 2001; **40**: 294-305 [PMID: 11309113 DOI: 10.1046/j.1365-2958.2001.02302.x]

66 **Fischer W**, Püls J, Buhrdorf R, Gebert B, Odenbreit S, Haas R. Systematic mutagenesis of the Helicobacter pylori cag pathogenicity island: essential genes for CagA translocation in host cells and induction of interleukin-8. *Mol Microbiol* 2001; **42**: 1337-1348 [PMID: 11886563 DOI: 10.1046/j.1365-2958.2003.03406.x]

67 **Backert S**, Ziska E, Brinkmann V, Zimny-Arndt U, Fauconnier A, Jungblut PR, Naumann M, Meyer TF. Translocation of the Helicobacter pylori CagA protein in gastric epithelial cells by a type IV secretion apparatus. *Cell Microbiol* 2000; **2**: 155-164 [PMID: 11207572 DOI: 10.1046/j.1462-5822.2000.00043.x]

68 **Karnholz A**, Hoefler C, Odenbreit S, Fischer W, Hofreuter D, Haas R. Functional and topological characterization of novel components of the comB DNA transformation competence system in Helicobacter pylori. *J Bacteriol* 2006; **188**: 882-893 [PMID: 16428391 DOI: 10.1128/JB.188.3.882-893.2006]

69 **Kersulyte D**, Velapatiño B, Mukhopadhyay AK, Cahuayme L, Bussalleu A, Combe J, Gilman RH, Berg DE. Cluster of type IV secretion genes in Helicobacter pylori's plasticity zone. *J Bacteriol* 2003; **185**: 3764-3772 [PMID: 12813069 DOI: 10.1128/jb.185.13.3764-3772.2003]

70 **Kersulyte D**, Lee W, Subramaniam D, Anant S, Herrera P, Cabrera L, Balqui J, Barabas O, Kalia A, Gilman RH, Berg DE. Helicobacter Pylori's plasticity zones are novel transposable elements. *PLoS One* 2009; **4**: e6859 [PMID: 19727398 DOI: 10.1371/journal.pone.0006859]

71 **Delahay RM**, Croxall NJ, Stephens AD. Phylogeographic diversity and mosaicism of the *Helicobacter pylori tfs* integrative and conjugative elements. *Mob DNA* 2018; **9**: 5 [PMID: 29416569 DOI: 10.1186/s13100-018-0109-4]

72 **Fernandez-Gonzalez E**, Backert S. DNA transfer in the gastric pathogen Helicobacter pylori. *J Gastroenterol* 2014; **49**: 594-604 [PMID: 24515309 DOI: 10.1007/s00535-014-0938-y]

73 **Grove JI**, Alandiyjany MN, Delahay RM. Site-specific relaxase activity of a VirD2-like protein encoded within the tfs4 genomic island of Helicobacter pylori. *J Biol Chem* 2013; **288**: 26385-26396 [PMID: 23900838 DOI: 10.1074/jbc.M113.496430]

74 **Vergunst AC**, Schrammeijer B, den Dulk-Ras A, de Vlaam CM, Regensburg-Tuïnk TJ, Hooykaas PJ. VirB/D4-dependent protein translocation from Agrobacterium into plant cells. *Science* 2000; **290**: 979-982 [PMID: 11062129 DOI: 10.1126/science.290.5493.979]

75 **Jung SW**, Sugimoto M, Shiota S, Graham DY, Yamaoka Y. The intact dupA cluster is a more reliable Helicobacter pylori virulence marker than dupA alone. *Infect Immun* 2012; **80**: 381-387 [PMID: 22038914 DOI: 10.1128/IAI.05472-11]

76 **Wang MY**, Shao C, Li J, Yang YC, Wang SB, Hao JL, Wu CM, Gao XZ, Shao SH. Helicobacter pylori with the Intact dupA Cluster is more Virulent than the Strains with the Incomplete dupA Cluster. *Curr Microbiol* 2015; **71**: 16-23 [PMID: 25847580 DOI: 10.1007/s00284-015-0812-z]

77 **Wang GQ**, Xu JT, Xu GY, Zhang Y, Li F, Suo J. Predicting a novel pathogenicity island in Helicobacter pylori by genomic barcoding. *World J Gastroenterol* 2013; **19**: 5006-5010 [PMID: 23946608 DOI: 10.3748/wjg.v19.i30.5006]

78 **Silva B**, Nunes A, Vale FF, Rocha R, Gomes JP, Dias R, Oleastro M. The expression of Helicobacter pylori tfs plasticity zone cluster is regulated by pH and adherence, and its composition is associated with differential gastric IL-8 secretion. *Helicobacter* 2017; **22** [PMID: 28436598 DOI: 10.1111/hel.12390]

79 **Wang MY**, Chen C, Shao C, Wang SB, Wang AC, Yang YC, Yuan XY, Shao SH. Intact long-type DupA protein in Helicobacter pylori is an ATPase involved in multifunctional biological activities. *Microb Pathog* 2015; **81**: 53-59 [PMID: 25745877 DOI: 10.1016/j.micpath.2015.03.002]

80 **Patra R**, Chattopadhyay S, De R, Ghosh P, Ganguly M, Chowdhury A, Ramamurthy T, Nair GB, Mukhopadhyay AK. Multiple infection and microdiversity among Helicobacter pylori isolates in a single host in India. *PLoS One* 2012; **7**: e43370 [PMID: 22952670 DOI: 10.1371/journal.pone.0043370]

**Footnotes**

**Conflict-of-interest statement:** All authors declare no conflicts of interest.

**Open-Access:** This article is an open-access article that was selected by an in-house editor and fully peer-reviewed by external reviewers. It is distributed in accordance with the Creative Commons Attribution NonCommercial (CC BY-NC 4.0) license, which permits others to distribute, remix, adapt, build upon this work non-commercially, and license their derivative works on different terms, provided the original work is properly cited and the use is non-commercial. See: http://creativecommons.org/licenses/by-nc/4.0/

**Manuscript source:** Invited manuscript

**Peer-review started:** February 20, 2020

**First decision:** February 29, 2020

**Article in press:**

**Specialty type:** Gastroenterology and hepatology

**Country/Territory of origin:** India

**Peer-review report’s scientific quality classification**

Grade A (Excellent): 0

Grade B (Very good): B

Grade C (Good): C, C

Grade D (Fair): 0

Grade E (Poor): 0

**P-Reviewer:** Fagoonee S,Huang YQ, Ulaşoğlu C **S-Editor:** Yan JP **L-Editor:** Filipodia **E-Editor:**

**Figure Legends**

**![图片包含 游戏机, 截图

描述已自动生成]()**

**Figure 1 Schematic representation of the *jhp0917*, *jhp0918* and *jhp0919* gene in strain J99 and that of the *dupA* alleles in the clinical isolates.** The long type *dupA* (2499 nt) in some clinical isolates contained an additional 615 nt in 5' region before *jhp0917* gene and ended 5 bp after the start codon of *jph0919* gene. The short type *dupA* (1884 nt) in some clinical isolates starts from the 5' region of *jhp0917* gene and ended 5 bp after the start codon of *jph0919* gene.

图片包含 游戏机

描述已自动生成

**Figure 2 Organization of three types of** **type IV secretion system in the** ***Helicobacter pylori* compared to** ***Agrobacterium tumefaciens* prototype type IV secretion system.** Genes are not drawn to scale. *H. pylori*:*Helicobacter pylori*; *A. tumefaciens*: *Agrobacterium tumefaciens*; T4SS: Type IV secretion system.

Table 1 Important finding on dupA of Helicobacter pylori in chronological order

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Year** | **Observation and conclusion** | **Sample location** | **Sample size** | **Techniques used in the study** | **Proposed name** | **Ref.** |
| 2005 | *dupA* was novel marker associated with increased risk for DU and reduced risk for gastric cancer in East Asia and South America | Japan, Korea, Colombia | 500 | PCR, southern blot | *dupA* | Lu *et al*[23] |
| 2007 | Significant association of *dupA* gene with DU | North India | 166 | PCR, Dot-blot hybridization, partial sequencing | *dupA* | Arachchi *et al*[24] |
| 2007 | Presence of *dupA* significantly associated with GC than DU | Belgium, South Africa, china, North America | 258 | PCR | *dupA* | Argent *et al*[25] |
| 2008 | *dupA* gene was not associated with any diseases outcome | Iran | 157 | PCR, partial sequencing | *dupA* | Douraghi *et al*[30] |
| 2008 | *dupA* was not associated with *H. pylori* associated diseases in children and adults | Brazil | 482 | PCR, partial sequencing | *dupA* | Gomes *et al*[26] |
| 2008 | *dupA* was associated with peptic ulcer in Iraqi population but not with Iranian population | Iraq and Iran | 108 | PCR | *dupA* | Hussein *et al*[29] |
| 2008 | There was no association between the occurrence of *dupA* and DU | Brazil (Sao Paulo) | 79 | PCR | *dupA* | Pacheco *et al*[27] |
| 2008 | The prevalence of *dupA* was significantly higher in DU patients than in gastric cancer | china | 360 | PCR | *dupA* | Zhang *et al*[38] |
| 2009 | There was no consistent association between *dupA* and DU or GC development | Sweden, Australia, Malaysia (ethnic groups Indian, Malaya) | 243 | PCR, partial sequencing | *dupA* | Schmidt *et al*[41] |
| 2010 | *dupA* was not associated with gastroduodenal diseases or IL-8 production | Japan | 244 | PCR, partial sequencing RT-PCR, IL-8 assay | *dupA* | Nguyen *et al*[45] |
| 2010 | *dupA* is not association with DU in patients from Turkey | Turkey | 91 | PCR | *dupA* | Tuncel *et al*[37] |
| 2010 | Meta-analysis of case control studies confirmed the presence of *dupA* gene for DU | Asian and western countries | 2466 | - | *dupA* | Shiota *et al*[44] |
| 2010 | Meta-analysis of previous report showed *dupA* gene promotes DU formation some population and GU and GC in others | Around the world | 2358 |  | *dupA* | Hussein *et al*[43] |
| 2010 | In Taiwanese female population, MMP-3 promoter polymorphism is correlated with DU rather than *dupA* gene | Taiwan female | 181 | PCR | *dupA* | Yeh *et al*[40] |
| 2010 | *dupA* and gastric cancer is negatively associated with GC in Japanese population | Japan | 136 | PCR | *dupA* | Imagawa *et al*[46] |
| 2010 | Proposed two alleles of *dupA* [*dupA*1 (intact), *dupA*2 (truncated)]. *dupA*1 (not *dupA*2) increased IL-12p40 and IL-12p70 production from CD14+ mononuclear cell | United Kingdom, United States, Belgium, South Africa, China | 34 | PCR, full Sequencing, Cytokine ELISA, real tome PCR, flow cytometry | *dupA1* | Hussein *et al*[52] |
| 2011 | Presence of mutation on *dupA* at 1311 and 1426 leads to stop codon called truncated *dupA* | Brazil | 252 | PCR, full sequencing | *dupA* | Queiroz *et al*[50] |
| 2011 | Intact *dupA* (*dupA1*) without stop codon was associated with decreases rate of gastric carcinoma in Brazilian population | Brazil | 6 | Full sequencing | *dupA1* | Queiroz *et al*[57] |
| 2012 | Found a positive association between presence of *dupA* and DU [OR 24.2; 95%CI: 10.6-54.8] and inverse association between presence of *dupA* and GU [OR 0.34; 95%CI: 0.16-0.68] and GC [OR 0.16; 95%CI: 0.05-0.47] | Iran | 216 | PCR | *dupA* | Abadi *et al*[31] |
| 2012 | Prevalence of *dupA* was higher in the eradication failure group than in the success group (36.3% *vs* 21.9%) | Japan | 142 | PCR, Drug sensitivity test | *dupA* | Shiota *et al*[60] |
| 2012 | The logistic analysis report in Brazilian population showed the presence of intact *dupA* independently associated with duodenal ulcer (OR = 5.06; 95%CI: 1.22-20.96, *P* = 0.02) | Brazil | 75 | Sequencing | Intact *dupA* | Moura *et al*[51] |
| 2012 | *dupA* gene was found to be significantly associated with DU than in NUD in south east Indian population | India | 140 | PCR, partial sequencing, real time PCR, | *dupA* | Alam *et al*[47] |
| 2012 | Found a significant association between *dupA*1 and DU (*P* < 0.01) along with a significant higher level of gastric mucosa IL-8 in *dupA1* than in *dupA2* or *dupA* negative Iraqi strain | Iran | 68 | PCR, full sequencing, IL-8 ELISA | *dupA1* | Hussein *et al*[54] |
| 2012 | classified *dupA* into two types (long types and short types) depend on the presence of 615 bp at the N-terminal of *dupA*. Found high prevalence of intact long type *dupA* (24.5%) than short type *dupA* (6.6%) and significantly associated with GU and GC than gastritis (*P* = 0.001 and *P* = 0.019) in Japanese population | Japan | 319 | PCR, full sequencing | Long type and short type | Takahashi *et al*[53] |
| 2012 | Complete *dupA* cluster (*dupA* with six *virB* homologues) was associated with DU rather than *dupA* gene only in United States population | United States | 245 | PCR and cytokine ELISA | *dupA* cluster | Jung *et al*[75] |
| 2013 | Prevalence of long type *dupA* (2499 bp) was significantly higher in GU, GC and DU (40.3%) than from gastritis (20.4%) (*P* = 0.02) in China | China | 116 | PCR, Full sequencing | *dupA* cluster | Wang *et al*[59] |
| 2013 | PUD was significantly associated with *cagA* (*P* ≤ 0.017; OR 0.4; 95%CI: 0.18-0.85) rather than *dupA* | Iraq | 154 | PCR | *dupA* | Salih *et al*[34] |
| 2014 | *dupA* was found to play an important role in the development of DU, BGU and dysplasia in South Korean population | South Korea | 401 | PCR | *dupA* | Kim *et al*[39] |
| 2014 | *dupA* was associated with *cagA* and *vacAs1m1* genotypes | Brazil | 205 | PCR | *dupA* | Pereira *et al*[28] |
| 2014 | The prevalence of *dupA* and *cagA* were more in MTZ, CLR and AML resistance strain as compared to other virulence factor in Pakistan | Pakistan | 46 | PCR | *dupA* | Rasheed *et al*[61] |
| 2015 | *cagA*, complete *dupA* cluster and smoking were significantly associated with increased level of IL-8 production from gastric mucosa of Iraqi population | Iraq | 81 | PCR, IL-8 ELISA | *dupA* | Hussein *et al*[55] |
| 2015 | Prevalence of *dupA*1 was significantly higher in DU than NUD (*P* = 0.02) in Indian strains and *dupA1* positive strains were similar to East Asian strains and distinct from western strains. | India | 170 | PCR, sequencing, IL-8 ELISA | *dupA1* | Alam *et al*[58] |
| 2015 | Significant association of complete *dupA* cluster with IL-8 production (*P* < 0.01) in north East of China | China | 262 | PCR, western blotting, IL-8 ELISA | *dupA* cluster | Wang *et al*[76] |
| 2015 | DupA protein have ATPase activity and play a role in apoptosis of gastric cancerous cells through mitochondrial pathway but neither adhere nor translocate to host cell | China | 1 (WH21) | PCR, western blotting, ATPase, Adhesion, translocation and cytotoxic assay | Long type *dupA* | Wang *et al*[79] |
| 2015 | *dupA1* have a significant association with A2147G clarithromycin resistance strain but not with Il-8 production from gastric mucosa | Iraq | 74 | PCR, IL-8 ELISA, antibiotic susceptibility teat | *dupA1* | Hussein *et al*[56] |
| 2015 | Significant association between the presence of *dupA* and DU diseases (*P* = 0.03 OR 3.14, 95%CI: 1.47-7.8). | Iran | 128 | PCR | *dupA* | Haddadi *et al*[35] |
| 2015 | There was no significant relationship between *dupA* status  and duodenal ulcer disease (*P* = 0.25) but, there was a converse relationship between *dupA* negative strains and gastric cancer disease (*P* = 0.02) | Iran | 123 | PCR | *dupA* | Souod *et al*[36] |
| 2015 | There was no association of *dupA* gene with the ethnic group (Indian, Chinese, Malaya) of Malaysia | Malaysia | 105 | PCR | *dupA* | Osman *et al*[42] |
| 2017 | Significant association of *dupA* gene with non-severe clinical outcome (*P* = 0.0032, OR 0.25, 95%CI: 0.09-0.65) and play a role in protecting against gastric cancer in Chile | Chile | 132 | PCR | *dupA* | Paredes *et al*[48] |
| 2017 | A complete *tfs* plasticity zone cluster including *dupA* is a virulence factor that may be important for the colonization of *H. pylori* and to the development of severe outcomes of the infection with *cagA*-positive strains | Portugal | 18 | PCR, whole genome sequencing, cytokine assay | *dupA* | Silva *et al*[78] |
| 2019 | *dupA* was significantly associated with decreased risk of duodenal ulcer (*P* = 0.024) | Costa Rica | 151 | PCR | *dupA* | Molina Castro *et al*[49] |
| 2019 | Significant relationship was observed between the occurrence of DU and the presence of the 112 bp segment (*P* = 0.002; OR 6.98; 95%CI: 1.94-25.00) | Iran | 143 | PCR | *dupA* | Fatahi *et al*[32] |
| 2019 | The prevalence of *dupA* was 53.4% in South African population, but it was not associated with duodenal ulcer | South Africa | 234 | PCR | *dupA* | Idowu *et al*[64] |
| 2019 | The prevalence of *dupA* was higher (30.4%) in peptic ulcer (mild diseases) than gastric cancer (severe diseases) 18.2% | Northern Spain | 102 | PCR | *dupA* | Fernandez-Reyes *et al*[72] |
| 2019 | *dupA* was present in 10/41 (24.4%) of population, and it was not associated with severe gastritis | Switzerland | 41 | Whole genome sequence | *dupA* | Imkamp *et al*[63] |
| 2019 | Significant association was found between metronidazole resistance and *dupA* genotypes (*P* = 0.0001) | Iran | 68 | PCR | *dupA* | Farzi *et al*[33] |

CI: Confidence interval; DU: Duodenal ulcer; GC: Gastric cancer; GU: Gastric ulcer; IL-8: Interleukin-8; MMP-3: Matrix metalloproteinase -3; NUD: Non-ulcer dyspepsia; OR: Odds ratio; PCR: Polymerase chain reaction.