

ATG16L1 Single Nucleotide Polymorphism Confers High Cardiac Artery Disease Risk in H. Pylori Chronic Gastritis Patients

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Abstract

Background: Chronic *Helicobacter pylori* (HP) gastritis affects two-thirds of the world's population and is one of the most common chronic inflammatory disorders of humans, the infection clearly results in chronic mucosal inflammation in the stomach and duodenum which in turn might lead to abnormalities in gastroduodenal motility and sensitivity and is the most frequent cause of dyspepsia and peptic disease. The increased inflammatory response related to HP gastrointestinal disease may also lead to damage in non-gastrointestinal tissues. The damage caused by HP is believed to be associated with increased inflammatory markers resulting from immune response and blood cells activation. Autophagy related gene 16 like 1 single nucleotide polymorphism (ATG16L1 SNP) may be associated with impaired autophagy which predisposes to HP persistence and chronicity. Chronic infection is a suspected risk factor for cardiac artery disease.

Aim of Study: The aim of this study is to assess the association between (ATG16L1) SNP and coronary artery disease, pro-inflammatory and atherogenic risk factors in HP patients.

Patients and Methods: This study was carried out on 80 patients suffering from dyspepsia and reflux symptoms. According to the urea breath test results, patients were divided into two groups: group I (45 positive *H. pylori*) patients and group II (35 negative *H. pylori*) patients as control group. All patients were subjected to full medical history taking, clinical examination and laboratory investigations included urea breath testing for *H. pylori* infection, complete blood count (CBC), (ATG16L1) SNP, pro-inflammatory HDL assay and high sensitivity CRP (hs-CRP) assay.

Results: *H. pylori* gastritis patients with AG+GG genotypes had statistically higher levels of hs-CRP, N/L, P/L, pro-oxidant HDL-c index when compared to *H. pylori* gastritis patients with AA genotype and both patient groups had higher levels of these parameters when compared to healthy control subjects

Conclusion: The ATG16L1 SNP impairs autophagy and has a role in persistence of *H. pylori* intracellular infection leading to chronic gastritis and increases the CAD pro-inflammatory pro-atherogenic risk factors; the mutant G allele is accused allele.

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Key Words: Chronic gastritis – *Helicobacter Pylori* – 14C-urea breath test – ATG16L1 SNP – Neutrophil/lymphocyte ratio – Platelet/lymphocyte ratio.

Introduction

HELICOBACTER *pylori* (HP) is a gram-negative, spiral-shaped, flagellar and microaerophilic bacillus found in the gastric mucosa of more than 50% of individuals worldwide [1]. HP has been shown to be a predisposition for chronic gastritis, gastric atrophy and gastric ulcers, as well as certain gastric cancers [2].

Autophagy is a natural cell process that allows the cell to get rid of disorganized or aged organelles [3], to combat intracellular pathogens [4] and to withstand starving conditions [5]. Genetic analysis showed that single nucleotide polymorphisms (SNPs) in autophagy pathway can affect the efficiency of autophagy including impairment of intracellular pathogen killing. One of these SNPs is the polymorphism in autophagy related gene 16 like 1 (ATG16L1) which is associated with higher risk for colonization and chronicity of intracellular infections like *H. pylori* [6] with subsequent increase in T-cell activation that leads to an increase in the secretion of cytokines such as interleukin-1, interleukin-6, interleukin-8 and tumor necrosis factor alpha (TNF- α) with increased C-reactive protein (CRP) levels [7].

The increased inflammatory response related to HP gastrointestinal disease may also lead to damage in non-gastrointestinal tissues [8]. The relationship between HP and vascular disorders has been confirmed in many studies [9]. The damage caused by HP on tissues is believed to be resulting from immune response and platelet activation [10,11]. The impaired chronic infection is a suspect-

ed risk for coronary heart disease through establishment of a chronic inflammatory state [12].

The aim of this study is to assess the association between (ATG 16L 1) SNP and coronary artery disease pro-inflammatory and atherogenic risk factors in *H. pylori* patients.

Patients and Methods

The study was carried out on 45 patients. They were 26 females (57.8%) and 19 males (42.2%) aged between 25-60 years with a mean \pm SD of 41.4 ± 7.97 years. They were suffering from dyspepsia and reflux symptoms. The patients were recruited from the outpatient clinic and the inpatient units of the internal medicine department, Al-Azhar University Hospital, Cairo, Egypt in the period between September 2017 to June 2018. All patients provided their informed consent before being included in the study. Also, an approval of Ethical Committee of Faculty of Medicine, Al-Azhar University was obtained.

Patients were compared to a group of age and gender matched apparently healthy control subjects who were proven to be *H. pylori* negative, they were 35 subjects (24 females (68.6%) and 11 males (31.4%)) aged between 22-65 years with a mean \pm SD of 40.3 ± 11.2 years. The presence or absence of *H. pylori* was diagnosed by ^{14}C -urea breath test for *H. pylori* infection.

All patients were subjected to full medical history taking, clinical examination and laboratory investigations in which few milliliters of peripheral venous blood samples were taken from each patient and placed in two EDTA and one plain vacutainers. Laboratory investigations included urea breath testing for *H. pylori* infection, complete blood count (CBC) including (hemoglobin (Hb), white blood cell (WBC) count, neutrophil count, lymphocyte count, NLR, platelet count and PLR), (ATG 16L 1) SNP, pro-inflammatory HDL assay and high sensitivity CRP (hs-CRP) assay +98/iop4.

Helicobacter pylori infection was diagnosed using the urea breath test testing (UBT) that is based upon the hydrolysis of urea by *H. pylori* to produce CO_2 and ammonia using the non-radioactive ^{14}C test after an overnight fasting and at least two months without antibiotics, proton pump inhibitors (PPIs), histamine H₂ receptor antagonists or NSAIDs therapy. (Helicap) capsules were swallowed with 25ml of water. Breath samples were collected with a special dry cartridge system (Heliprobe Breath Card). At 10 minutes, the

Heliprobe Breath Card was inserted into a Geiger-muller counter (Heliprobe analyzer: Kibion AB, Uppsala, Sweden) and activity counted for 250 seconds. Test results were specified as counts per minute (cpm) and were graded (0: cpm <25: not infected & 1: cpm 25-50: equivocal and; 2: cpm >50 infected).

For the (ATG 16L 1) SNP, genomic DNA was extracted EDTA treated blood sampling Scientific ymobead Genomic DNA kits, MINIPREP (ZYMO RESEARCH) then sequence specific amplification was applied as previously described by Ghazi, 2016 with little modifications [6]. Briefly, for each subject, two primers consisted of a common reverse primer and a different forward specific primer was utilized for amplification of each of A and G alleles (primers supplied from Thermo Fisher Scientific, 168 Third Avenue Waltham, MA USA). The common primer was 5'AGGTGGAAAGGC TTGATATAAG'3. The specific primer for amplification of A allele was 5'CCCCAGGACAA TGTGGATA'3 while the specific primer for amplification of G allele was 5'CCCCAGGACAATGTGGATG'3. Cycling conditions were initial denaturation stage at 95°C for 10 minutes followed by 35 cycles of denaturation at 95°C for 30 seconds, annealing at 59°C for 1 minute and extension at 72°C for 1 minute and a final extension stage 72°C for 5 minutes (thermal cycler: M2000 RT Thermo scientific USA). If the corresponding allele is present, an amplified product of 201 bp is detected by electrophoresis in 2% agarose gel.

CBC was performed by an automated hematology analyzer system (Sysmex, X T2000i, Sysmex, Japan). The total WBC count, neutrophil count, lymphocyte count, platelet count, mean platelet volume (MPV) count and hemoglobin values were recorded. Peripheral blood smears were examined for confirmation of relative differential WBC count and calculating the absolute neutrophil and lymphocyte counts, a minimum of 500 cells were counted. The neutrophil/lymphocyte ratio (NLR) was calculated by dividing the absolute neutrophil count by the absolute lymphocyte count. Similarly, Platelet/lymphocyte ratio (PLR) was calculated by dividing the platelet count by the absolute lymphocyte count.

For determination of pro-inflammatory HDL-c; after elimination of other lipoproteins by precipitation of apo B-containing lipoproteins (Spinreact, Girona, Spain), the supernatant containing HDL-c was separated. Pro-inflammatory HDL-c was measured as described by Navab et al., [13] with

slight modifications. In brief, 25 μ L of standard LDL solution containing 2.5 μ M LDL-c and 2.5 μ M of tested HDL were incubated in a 96-well plate for 30min at 37°C. Then, 25 μ L of 2,2',7,7'-tetrachlorfluorescein (DCFH) (Sigma-Aldrich, Missouri, USA) with a concentration of 0.2mg/ml in methanol were added to each well. The oxidized DCFH turns to a highly fluorescent material (emitted light 530nm). After 60min of incubation at 37°C, fluorescence intensity was measured by Thermo scientific, Multiskan FC, USA. Values for the fluorescence intensity induced by test HDL +standard LDL were divided by the basal values obtained with standard LDLs alone to obtain an index value. Index values \geq 1.0 indicate dysfunctional HDLs (pro-oxidant HDL), while values $<$ 1.0 indicates normal, antioxidant HDLs.

The hs-CRP was measured by immunoturbidimetry using the Cobas C 501, Roche, Japan.

Exclusion criteria included pregnancy, age less than 18 years, diabetes mellitus, hepatic and renal diseases, abnormal thyroid function tests, previous history of local or systemic infection, acute and chronic inflammatory diseases, hematological malignancies, using of medications for eradication of H. pylori, non-steroidal anti-inflammatory drugs (NSAIDs) or corticosteroids in the past three months.

Statistical analysis:

The data collected were tabulated and analyzed by SPSS (statistical package for social science) version 22.0 on IBM compatible computer. Descriptive statistics were expressed as mean (x) and standard deviation (SD). Analytic statistics included Chi-square test (χ^2) for comparison of qualitative data with numerical variables. For comparison between groups having quantitative normally distributed variables, student's t test was used in case of comparing two groups while anova (F) test was used to compare three or more groups and was followed by post hoc to study the pairwise associations. If variables are not normally distributed, Mann-Whitney (U) test was applied to compare two groups and Kruskal Wallis test was applied in case of more than two groups. *p*-value of less than 0.05 was used to indicate a statistically significant difference.

Results

No statistical difference existed between H. pylori patients and healthy control subjects as regard to age and gender. The G containing genotypes and the G allele had a statistically significant

association to H. pylori gastritis in comparison to the AA genotype and A allele respectively (Table 1).

Subjects with G allele containing genotypes (AG+GG) had a 2.92 folds increase in the risk of developing H. pylori gastritis when compared to those with the AA genotype. Similarly, subjects with the A allele had a 2.6 folds increase on the risk of H. pylori gastritis when compared to those with the A allele (Table 2).

H. pylori gastritis patients with AG+GG genotypes had statistically higher levels of hs-CRP, N/L, P/L, pro-oxidant HDL-c index when compared to H. pylori gastritis patients with AA genotype and both patient groups had higher levels of these parameters when compared to healthy control subjects (Table 3).

Table (1): Comparison between H. pylori patients and healthy control subjects as regard to age, gender and ATG16L1 genotype and allele frequency.

	H. pylori patients (n=45)	Normal control subjects (n=35)	Test	
Age (years)	41.4 \pm 7.97	40.3 \pm 11.2	t	0.51 0.6
<i>Gender:</i>				
Male	19	11	χ^2	0.32
Female	26	24		0.97
<i>(ATG16L1) genotype:</i>				
AA	13	19	χ^2	0.052
AG	12	8		5.9
GG	20	8		
AA	13	19	χ^2	0.021
AG+GG	32	16		5.29
GG	20	8	χ^2	0.3
AA+AG	25	27		1.03
<i>Allele frequency:</i>				
A allele	38	46	χ^2	0.003
G allele	52	24		8.7

Table (2): Comparison between the ATG16L1 genotypes as regard to the risk of H. pylori gastritis.

	H. pylori patients (n=45)	Normal control subjects (n=35)	ODD's ratio	<i>p</i> -value
AA	13	19	2.92	0.038
AG+GG	32	16	CI: (1.15-7.38)	
A allele	38	46	2.6	0.005
G allele	52	24	CI: 1.37-5	

Table (3): Comparison between patient and control groups as regard to the pro-inflammatory markers.

	Patients AA (13)	Patients AG+GG (32)	Control AA (19)	Control AG+GG (16)	Test	<i>p</i> - value
N/L	3.51+0.97	4.3 8+2.01	1.96+0.63	2.11+0.37	K:30.31 <i>p</i> <0.001	<i>p</i> 1:0.035 <i>p</i> 2:<0.001 <i>p</i> 3:<0.001 <i>p</i> 4:<0.001 <i>p</i> 5:<0.001 <i>p</i> 6: 0.896
P/L	144+43	186+47	104+30	100+33	F:24.19 <i>p</i> :<0.001	<i>p</i> 1=0.011 <i>p</i> 2=0.035 <i>p</i> 3=0.022 <i>p</i> 4<0.001 <i>p</i> 5<0.001 <i>p</i> 6=0.99
CRP	3.6+1.79	4.86+2.22	1.49+0.8	1.46+0.6	K: 36.09 <i>p</i> <0.001	<i>p</i> 1=0.046 <i>p</i> 2<0.001 <i>p</i> 3<0.001 <i>p</i> 4<0.001 <i>p</i> 5<0.001 <i>p</i> 6= 0.7
HDL index	1.22+0.11	1.46+0.19	0.84+0.27	0.76+0.19	F:59.9 <i>p</i> :<0.001	<i>p</i> 1=0.0031 <i>p</i> 2<0.001 <i>p</i> 3<0.001 <i>p</i> 4<0.001 <i>p</i> 5<0.001 <i>p</i> 6=0.65
HDL						
N	4	5	17	14	χ^2 : 37.8	<i>p</i> 1=0.25
P	9	27	2	2	<i>p</i> :<0.001	<i>p</i> 2<0.001 <i>p</i> 3<0.001 <i>p</i> 4<0.001 <i>p</i> 5<0.001 <i>p</i> 6=0.72

p 1: G1 vs. G2. *p*2: G1 vs. G3. *p*3: G1 vs. G4. *p*4: G2 vs. G3. *p*5: G2 vs. G4. *p*6: G3vs. G4.

Discussion

Autophagy is a cell response by which the cell tries to promote its survival in face of stressful conditions, it enables the cell to decrease its energy needs and recycle its organelles to their basic elements in order to renew itself. In autophagy, cytoplasmic inclusions are sequestered in a double membrane autophagosome which fuses with lysosomes enabling digestions of these inclusions by lysosomal enzymes [14]. These inclusions may be aged cytoplasmic organelles [15] or intracytoplasmic pathogens [16], the latter is termed xenophagy.

H. pylori is one of the common gastric infections, it is essentially an extracellular pathogen. However, it can also replicate in gastric epithelial cells [17] and subsequently is a target for autophagy. Studies have shown that the efficiency of autophagy is determined by bacterial as well as host factors. *H. pylori* virulent strains can inhibit autophagy

and replicate in cytoplasmic niches [18] leading to persistence of infection and resistance to antibiotics which cannot access to the intracellular bacteria [17]. Interestingly, it was described that prolonged exposure to *H. pylori* vacuolating cytotoxin (Vac A) can subvert autophagy by interference with autophagosome maturation [19] while limited exposure to the same toxin increases autophagy leading to degradation of the toxin [20]. Genetic factors also play a role in the effectiveness of autophagy against intracellular pathogens. It was described that the autophagy-related 16-like 1 gene (ATG16L1) T300A polymorphism can disrupt autophagy in *H. pylori* related gastritis [18,19] leading to bacterial localization, persistence of infection and establishment of chronic inflammatory status [6].

Inflammation plays an important role in the pathogenesis of atherosclerosis [21]. It also weakens the atherosclerotic plaque and increases the risk

of embolization [21]. This study aims to inspect the association of ATG16L1 SNP and chronic inflammatory and prothrombotic markers which confer a coronary artery disease (CAD) risk. The study compared hs-CRP, neutrophil/lymphocyte ratio, platelet/lymphocyte ratio and pro-inflammatory HDL-c among different ATG 16L 1 genotypes of age and gender matched *H. pylori* chronic gastritis patients and normal controls.

Hs-CRP, an inflammatory marker, is a known risk predictor of CAD. Many studies proved a higher CAD risk in people having higher hs-CRP levels [22]. It was also shown the response to statins is also more pronounced when hs-CRP levels are reduced [23-27].

Neutrophil/lymphocyte ratio (NLR) and platelet/lymphocyte ratio (PLR) are novel, reliable, inexpensive, simple, safe and non-invasive laboratory markers to determine a systemic inflammation, malignances and it are being measured routinely in peripheral blood [28,29]. Higher platelet/lymphocyte ratio indicates a prothrombotic state [30] and a bad outcome in CAD [31]. Elevated platelet counts are associated with the development and progression of atherosclerosis [32].

The level of high-density lipoprotein (HDL-c), an apolipoprotein A1 containing lipoprotein, is usually monitored for its anti-atherosclerotic function. However, the simple measurement of HDL-c is not reflecting its real anti-atherosclerotic ability. Various disease states change the apo-lipoprotein A1 structure reducing its anti-atherosclerotic properties and even converting it to an inflammatory pro-oxidant pro-atherosclerotic protein [33].

The current study revealed that the G allele containing ATG16L1 genotypes (AG+GG) and the G allele are statistically more prevalent in *H. pylori* patients when compared to normal control subjects. They had 2.92- and 2.6-folds risk of development of chronic *H. pylori* gastritis respectively when compared to the AA genotype and the A allele respectively. According to Raju et al., [19], the GG genotype had a 1.8 folds increased risk of *H. pylori* infection in comparison to the AA genotype. In his study [6], Ghazi compared between *H. pylori* and non-*H. pylori* gastritis patients. He found that the G allele is statistically more associated with *H. pylori* related gastritis with a 1.72 folds increased risk when compared to the A allele. The ATG16L1-G allele polymorphism is considered a loss of function substitution which impairs autophagy against intracytoplasmic invaders [34] while the presence of ATG16L 1 AA genotype helps to over-

come *H. pylori* infection through effective autophagy which combat intracellular invasion and persistence of *H. pylori* infection.

Apart from gastritis, *H. pylori* is accused of other local and distant diseases. *H. pylori* is involved in pathogenesis of mucosa associated lymphoid tissue lymphoma and gastric adenocarcinoma [35]. It was suggested that *H. pylori* may have a role in the pathogenesis of liver cancer [36,37], chronic urticaria [38] and other diseases. The involvement of *H. pylori* infection in the pathogenesis of CAD was previously described. It was attributed to the inflammatory condition which precipitates disturbances in cytokines, fibrinogen, triglycerides, high density lipoprotein, C-reactive protein, heat shock protein, and white blood cell count creating a pro-atherosclerotic prothrombotic state. The *H. pylori* vacuolating cytotoxin A and cytotoxin associated gene A precipitate the formation of cholesterol deposits in arteries [39].

The present study showed that the ATG 16L 1 SNP modulates the systemic inflammatory process in *H. pylori* patients. The presence of (AG+GG) genotype was linked to higher levels of inflammatory markers including hs-CRP, N/L ratio and P/L ratio. Despite that no difference existed between the ATG 16L 1 AA and AG+GG genotype as regard to the number of patients harboring pro-inflammatory HDL-c, the level of impairment of HDL-c function as shown by HDL index was more pronounced in patients with the ATG16L1 AG+GG genotypes. In the presence of chronic inflammation, the HDL-c displays mal-functionality as it loses its LDL-c anti-oxidant ability and acquires an LDL-c pro-oxidant property which induces intracellular reactive oxygen species and promotes atherosclerosis [40].

To summarize, the ATG16L1 SNP impairs autophagy and has a role in persistence of *H. pylori* intracellular infection leading to chronic gastritis and increases the CAD pro-inflammatory pro-atherogenic risk factors; the mutant G allele is accused allele.

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(ATG16L1) متعدد الأشكال النوكليوتيد واحد يعطى مخاطر الإصابة بأمراض الشرايين القلبية عالية في مرضى التهاب جرثومة المعدة المزمن

يؤثر التهاب جرثومة المعدة المزمن على ثلثي سكان العالم وهو أحد أكثر الأمراض الإلتهابية المزمنة شيوعاً بين البشر، حيث تؤدي الإصابة بشكل واضح إلى التهاب مخاطي مزمن في المعدة والأثنى عشر مما قد يؤدي بدوره إلى حدوث تشوهات في المعدة والأمعاء. الحركية والحساسية هي السبب الأكثر شيوعاً لعسر الهضم والأمراض الهضمية. قد تؤدي الاستجابة الإلتهابية إلى تلف الأنسجة غير المعدية المعوية.

يعتقد أن الضرر الناجم عن (HP) يرتبط بزيادة علامات الإلتهابات الناتجة عن الإستجابة المناعية وتفعيل خلايا الدم. قد يرتبط الجين نو الصلة الذاتي ١٦ مثل متعدد الأشكال النوكليوتيد المفردة (ATG16L1 SNP) بضعف البلعمة الذاتية الذي يؤدي إلى استمرار (HP) وخطورته. العدوى المزمنة هي عامل خطر مشتبه به لمرض الشريان القلبي.

الهدف: الهدف من هذه الدراسة هو تقييم الارتباط بين SNP (ATG16L1) ومرض شريان التاجي وعوامل الخطر المؤيدة للإلتهابات وتصلب الشرايين لدى مرضى HP.

المرضى والطرق: أجريت هذه الدراسة على ٨٠ مريضاً يعانون من عسر الهضم وأعراض الجزر. وفقاً لنتائج اختبار التنفس اليوريا، تم تقسيم المرضى إلى مجموعتين: (مجموعة H. pylori إيجابية H. ٣٥ بيوري) والمرضى المجموعة الثانية (H. ٣٥ بيوري سلبية) والمجموعة الضابطة. تعرض جميع المرضى لأخذ التاديع الطبي لكامل، والفحص السريري والفحوصات المخبرية شملت اختبار التنفس باليوريا لعدوى H. pylori. تعداد الدم الكامل (CBC)، SNP (ATG16L1) مقياس HDL الموالية للإلتهابات وحساسية عالية (hs-CRP) الفحص.

النتائج: كان لدى مرضى التهاب المعدة H. بيوري مع الأنماط الوراثية AG+GG مستويات أعلى إحصائياً من hs-CRP، P/L، مؤشر HDL-C الموالي للأكسدة بالمقارنة مع التهاب المعدة H. بيوري مع النمط الوراثي AA وكل من المرضى كان لدى المجموعات مستويات أعلى من هذه المعلمات عند مقارنتها بمواضيع التحكم الصحية.

الخلاصة: أن SNP ATG16L1 يضعف الإلتهاب الذاتي ولها دور في استمرار العدوى بين الخلايا H. بيوري مما يؤدي إلى التهاب المعدة المزمن.