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Observational Study

Identification of functional tumor necrosis factor-alpha promoter variants associated with *Helicobacter pylori* infection in the Sudanese population: Computational approach

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The data regarding *TNF-A*-1030 T>C genotypes and alleles distributions among participants and the in silico results of the software that used to support the findings of this study are available from the corresponding author at abeer.babiker89@gmail.com on a reasonable request.

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Abstract

BACKGROUND

Helicobacter pylori (*H. pylori*) is a ubiquitous bacterium that affects nearly half of the world's population with a high morbidity and mortality rate. Polymorphisms within the tumor necrosis factor-alpha (*TNF-A*) promoter region are considered a possible genetic basis for this disease.

AIM

To functionally characterize the genetic variations in the *TNF-A* 5'-region (-584 to +107) of Sudanese patients infected with *H. pylori* using in silico tools.

METHODS

An observational study was carried out in major public and private hospitals in Khartoum state. A total of 122 gastric biopsies were taken from patients who had been referred for endoscopy. Genomic DNA was extracted. Genotyping of the *TNF-A*-1030 polymorphism was performed using PCR with confronting two-pair primer to investigate its association with the susceptibility to *H. pylori* infection in the Sudanese population. Furthermore, Sanger sequencing was applied to detect single nucleotide polymorphisms in the 5'-region (-584 to +107) of *TNF-A* in *H. pylori*-infected patients. Bioinformatics analyses were used to predict whether these mutations would alter transcription factor binding sites or composite regulatory elements in this region. A comparative profiling analysis was conducted in 11 species using the ECR browser and multiple-sequence local alignment and visualization search engine to investigate the possible conservation. Also, a multivariate logistic regression model was constructed to estimate odds ratios and their 95% confidence intervals for the association between *TNF-A*-1030, sociodemographic characteristics and *H. pylori* infection. Differences were statistically significant if $P < 0.05$. Statistical analyses were performed using Stata version 11 software.

RESULTS

A total of seven single nucleotide polymorphisms were observed in the *TNF-A* 5'-region of Sudanese patients infected with *H. pylori*. Only one of them (T > A, -76) was located at the in silico-predicted promoter region (-146 to +10), and it was predicted to alter transcription factor binding sites and composite regulatory elements. A novel mutation (A > T, +27) was detected in the 5' untranslated region, and it could affect the post-transcriptional regulatory pathways. Genotyping of *TNF-A*-1030 showed a lack of significant association between -1030T and susceptibility to *H. pylori* and gastric cancer in the studied population ($P = 0.1756$) and ($P = 0.8116$), respectively. However, a significant association was detected between T/C genotype and *H. pylori* infection (39.34% vs 19.67%, odds ratio = 2.69, 95% confidence interval: 1.17-6.17, $P = 0.020$). Mammalian conservation was observed for the (-146 to +10) region in chimpanzee (99.4%), rhesus monkey (95.6%), cow (91.8%), domesticated dog (89.3%), mouse (84.3%), rat (82.4%) and opossum (78%).

CONCLUSION

Computational analysis was a valuable method for understanding *TNF-A* gene expression patterns and guiding further *in vitro* and *in vivo* experimental validation.

Key Words: 5'-region; Promoter; *TNF-A*; *Helicobacter pylori*; In silico analysis; Sudan

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Core Tip: According to the literature, a considerable number of polymorphisms have

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been discovered in the tumor necrosis factor-alpha (*TNF-A*) promoter. A crucial question is whether these polymorphisms have any significant functional impact on disease incidence or severity. Seven single nucleotide polymorphisms were detected in the *TNF-A* 5'-region; only one of them, *TNF-A-76*, was located at the in silico-predicted promoter region (-146 to +10). This single nucleotide polymorphism may lead to the modification of the transcriptional regulation of *TNF-A* in *Helicobacter pylori* infection. Nevertheless, this conclusion cannot substitute for the experimental proofs, but it can provide direction or insight for them.

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INTRODUCTION

Helicobacter pylori (*H. pylori*) is a widespread bacterium that affects nearly half of the world's population with a high morbidity and mortality rate[1]. Generally, the decreasing prevalence of *H. pylori* infection is continuing in many parts of North America and Europe. Still, no such decline has been noted in most developing countries, including Sudan, in which the *H. pylori* infection represents a critical public health challenge[2-4]. Although there is a common consensus that the risk of acquisition and transmission of *H. pylori* can be minimized and prevented to a large extent, this drop in those countries, whether it is a local phenomenon or a national trend, has to be investigated[2].

Infection with *H. pylori* is usually acquired during childhood. However, it may persist if not treated in the host's stomach throughout life due to the synchronized balance between the bacteria and its host[5,6]. The long duration of *H. pylori* in the gastric environment will develop chronic gastritis in *H. pylori*-infected persons. At the same time, a few may be complicated to more severe diseases such as peptic ulcer, atrophic gastritis, mucosa-associated lymphoid tissue lymphoma or gastric adenocarcinoma[7,8]. The variability in *H. pylori* infection outcomes is determined by bacterial factors, genetic characteristics of the host, especially those regarding polymorphisms in specific cytokines, and the environmental factors[7,9,10]. However, the crucial role of cytokine-related polymorphisms in the susceptibility or severity of *H. pylori* infection has been attracting considerable attention after El-Omar *et al*[11] proposed that functional polymorphisms in proinflammatory cytokine genes in *H. pylori*-infected patients are associated with a two- to three-fold increased gastric cancer risk. Because tumor necrosis factor-alpha (TNF-a) production has been implicated as an essential factor in immune regulations and inflammatory responses against *H. pylori* infection[12], polymorphisms within the *TNF-A* promoter are considered a possible genetic basis for this disease[13].

TNF-a is a potent pleiotropic proinflammatory cytokine that mediates diverse biological and pathological processes, in addition to its responsibility for the regulation of two opposite processes: proliferation and apoptosis (reviewed in[14,15]). *TNF* gene transcription is regulated by nucleoprotein complexes known as enhanceosomes that involve distinct sets of transcription factors and coactivators at the proximal *TNF* promoter and in the pattern of chromosomal organization of the *TNF/lymphotoxin* locus that function in synergy to drive transcription[16]. *TNF* enhanceosome assembly is cell type- and stimulus-specific, partially because of differential occupancy of overlapping DNA motifs in the *TNF* promoter. For example, after lipopolysaccharide stimulation of monocytes where no inducible translocation of NFATp can be detected, Sp1 and Ets/Elk proteins can successfully bind to sites that NFATp occupies in T cells[13,14]. Furthermore, many *TNF* activator binding motifs can be recognized by more than one class of transcription factor depending on the ambient concentration of different elements in the nucleus and the stimulus and cell type[16]. These features provide the *TNF* promoter with a remarkable degree of flexibility to respond to multiple stimuli in a specific manner through a short cis-

regulatory region[13].

The *TNF* locus lies within the major histocompatibility complex region on the short arm of human chromosome 6p21.3, a highly polymorphic region[17]. Many bi-allelic polymorphisms and microsatellites are found at or around the *TNF* locus[14,18]. Several have been suggested to be implicated in diseases susceptibility/resistance or severity by modifying the transcriptional regulation of *TNF*[13,18]. There are different transition variants in the *TNF-A* promoter region at the positions of -237, -307, -375, -856, -862 and -1030 in which the positions -307 and -237 have been most frequently evaluated for the association with *H. pylori* infection (susceptibility or progression) [13]. It has been reported that the presence of the adenine allele at -237 or -307 positions causes higher constitutive and inducible transcriptional levels than the guanine allele, which results in enhanced production of TNF- α up to five-fold *in vitro* [19,20]. In addition, the single nucleotide polymorphism (SNP) at the -1030 position, which is frequently observed in African populations[21,22], has been suggested to be related to high TNF- α production[23]. However, the influence of these SNPs on TNF- α production is not fully known and still a contradictory topic of debate, which is explained, in part, by ethnic differences and genetic variations between populations [19,20].

To our knowledge, there are no previous studies in Sudan that have addressed the association between *TNF-A* and *H. pylori* infection or *H. pylori*-associated diseases. Therefore, in this study, we applied DNA Sanger sequencing to detect genetic variations in the *TNF-A* 5'-region (-584 to +107) of Sudanese patients infected with *H. pylori* and predicted if these SNPs could alter transcription factor binding sites (TFBSs) or composite regulatory elements (CEs) using a computational approach. In addition, a comparative profiling analysis was performed to investigate the conservation of these SNPs in 11 species. Regulation mechanisms of TNF- α production may be linked to the difference in responses to *H. pylori* infection. This emphasizes the importance of studying the regulation of *TNF-A* gene expression.

MATERIALS AND METHODS

Research methodology

In the present study, *in silico* analysis was employed for the *TNF-A* 5'-region (-584 to +107) of the Sudanese patients infected with *H. pylori* in two steps: (1) *In silico* prediction of the promoter region; and (2) *In silico* analysis of the predicted promoter region (-146 to +10). To obtain accurate results, we applied various software/servers to predict the promoter region, CpG island and regulatory motifs because promoters have complex and specific architecture and contain multiple transcription factors involved in particular transcription regulation[24]. Therefore, the unique composition of TFBSs and different features of each promoter may lead to different powers and algorithms for promoter identification[25]. In addition, genotyping of the *TNF-A*-1030 T>C polymorphism was performed to assess its association with *H. pylori* infection in the Sudanese population using PCR with confronting two-pair primer method.

However, the initial studies have numbered the positions of SNPs relative to the *TNF* mRNA cap site incorrectly (*e.g.*, -308 instead of -307 and -238 instead of -237)[13]. In contrast, the corrected numbering should have proceeded 5' from the adenine at the +1 position[26] as in the Cytokine Gene Polymorphism In The Human Disease Database[27], and we used it throughout this study. The methodology followed in this study is represented in Figure 1.

Study population and study setting

An observational study was carried out in major public and private hospitals in Khartoum state in 2019-2020. These hospitals included Soba teaching hospital, Ibin Sina specialized hospital, Modern Medical Centre, Al Faisal Specialized Hospital and Police hospital. In addition, the molecular laboratory processes were conducted in the Molecular Biological Research laboratory at the Faculty of Medical Laboratory Sciences at the University of Khartoum.

The matched case-control formula was selected to calculate the sample size using Epi Info software version 7[28,29], assuming 95% confidence interval (CI), 80% power of the study, one ratio of control to the case, 15% of controls exposed, 3.36 odds ratio (OR) and 37.2% of cases exposed. According to the sample size calculation, the present study included 122 patients referred for upper gastrointestinal tract endoscopy, and most of them were because of dyspepsia. Out of that, 61 were *H. pylori*-negative patients and regarded as controls. The demographic characteristics of the study

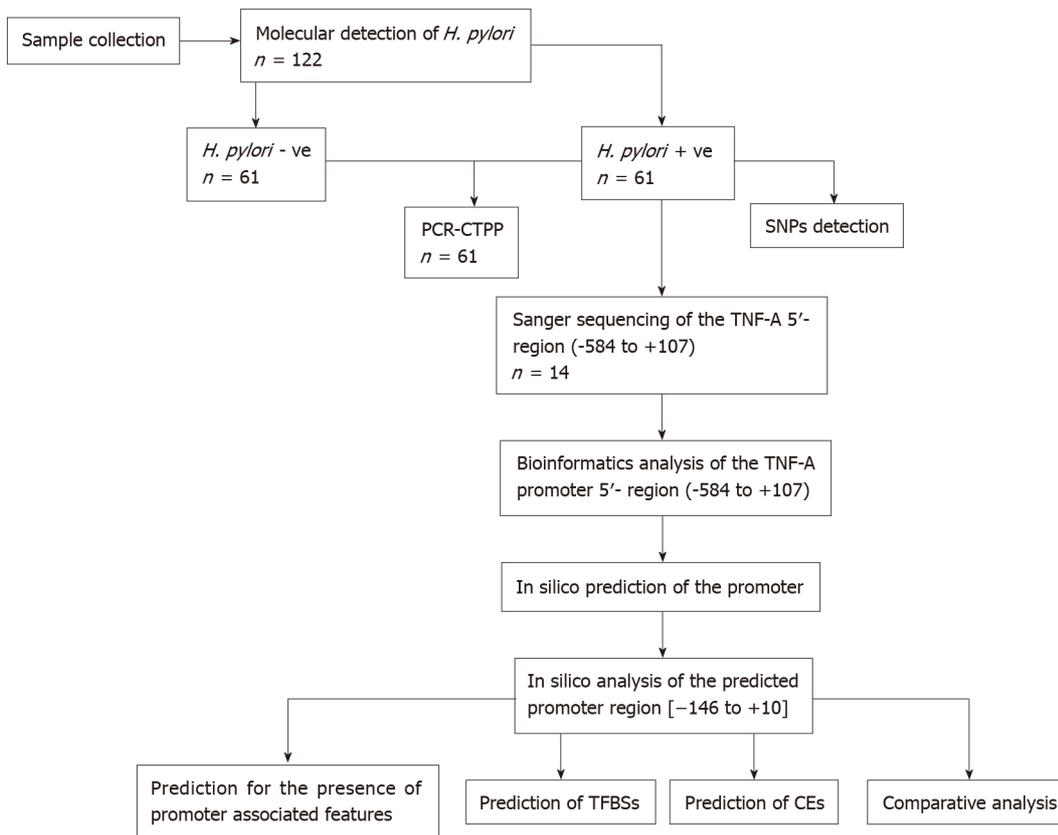


Figure 1 Schematic representation of the study methodology. *H. pylori*: *Helicobacter pylori*; -ve: Negative; +ve: Positive; CTPP: Confronting two-pair primer; SNP: Single nucleotide polymorphism; TNF-A: Tumor necrosis factor-alpha; TFBS: Transcription factor binding site; CE: Composite regulatory elements.

population are shown in [Table 1](#).

The diagnosis of gastroduodenal diseases was based on the assessment of an experienced gastroenterologist, and in cancerous cases, histological examinations were also performed to confirm the diagnosis. The gastric pathologies of the study population are presented in [Table 2](#).

The study population’s demographic and clinical data were obtained by personal interviews, a structured questionnaire and a review of case records. The selection criteria included the Sudanese population from both sexes who were not taking antibiotics or nonsteroidal anti-inflammatory drugs. Written informed consent was granted by the participants after they were informed of the objectives and purposes of the study.

DNA extraction and PCR amplification of specific 16S rRNA gene of *H. pylori*

For DNA extraction purposes, gastric biopsies were collected in 400 µL of phosphate buffered saline. For histological investigation, the biopsies were preserved in 10% formalin. DNA extraction was performed by using innuPREP DNA Mini Kit (analytikjena AG, Germany) and followed the protocol that was given by the manufacturer, as previously described in[30].

Extracted DNA was amplified for the specific 16S rRNA gene to diagnose and confirm the infection of *H. pylori* using the following primers (primers: F: 5'-GCGCAATCAGCGTCAGGTAATG-3'; and R: 5'-GCTAAGAGAGCAGCCTATGTCC-3')[31] and the previously described PCR condition[4]. The amplified product for the 16S rRNA is 522 bp.

Conventional PCR amplification and sequencing of the *TNF-A* promoter region

To amplify the promoter polymorphisms -308 and -238 of the *TNF-A* gene, primers: F: 5'-GCTTGTCCTGCTACCCGC-3' and R: 5'-GTCAGGGGATGTGGCGTCT-3' were used[32]. The following thermal cycling conditions were used: initial denaturation at 95 °C for 5 min, followed by 35 cycles of 94 °C for 60 s, 58 °C for 30 s and 72 °C for 60 s, with a final extension at 72 °C for 10 min. The amplified PCR product is 691 bp located between -585 bp upstream and 107 bp downstream of the *TNF-A* gene.

Table 1 Demographic characteristics of the study population, n (%)

Variable	<i>Helicobacter pylori</i> (+ve)		<i>Helicobacter pylori</i> (-ve)		P value
	n = 61	n = 61	n = 122		
Mean age in yr ± Standard deviation (range)	44.00 ± 16.99 (15-85)		44.74 ± 18.10 (17-89)		0.9184 ¹
Gender	Male	36 (50.00)	36 (50.00)	72 (59.02)	1.0000
	Female	25 (50.00)	25 (50.00)	50 (40.98)	
Residence	Urban	24 (44.44)	30 (55.56)	54 (44.26)	0.3622
	Rural	37 (54.41)	31 (45.59)	68 (55.74)	
Hospital	Public	21 (33.87)	31 (49.21)	52 (41.60)	0.0667
	Private	41 (58.57)	29 (41.43)	70 (57.38)	

¹Mann-Whitney *U*, Gaussian Approximation. +ve: Positive; -ve: Negative.

Table 2 Gastric pathologies of the study population, n (%)

Endoscopy results	n (%)	<i>Helicobacter pylori</i> (+ve)	<i>Helicobacter pylori</i> (-ve)	P value ¹
Normal gastric findings	9 (7.40)	4 (6.45)	5 (7.94)	0.2686
Esophagitis	4 (3.30)	3 (4.80)	1 (1.59)	
Esophageal varices	6 (4.90)	1 (1.61)	5 (7.94)	
Gastritis	55 (45.10)	28 (45.16)	27 (42.86)	
Duodenitis	6 (4.90)	3 (4.84)	3 (4.76)	
Peptic ulcer	27 (22.13)	17 (27.42)	10 (15.87)	
Cancer	15 (12.30)	5 (8.20)	10 (16.4)	
Total	122 (100)	61 (50.00)	61 (50.00)	

¹ χ^2 test, df: 7.603, 6. +ve: Positive; -ve: Negative.

Fourteen PCR products of *H. pylori*-infected patients, which had the clearest bands, were sent for commercial DNA purification and Sanger dideoxy sequencing by MacroGen Inc., Korea.

Sequence analysis and SNPs detection

Two chromatograms (forward and reverse) for each sequence were visualized, checked for their quality and analyzed with the Finch TV program version 1.4.0[33]. In addition, the Basic Local Alignment Search Tool nucleotide (<https://blast.ncbi.nlm.nih.gov/>) was used to look for and assess nucleotide sequence similarities[34].

For SNP detection in the *TNF-A* promoter region, multiple alignment sequences were performed for the tested sequences with a reference sequence (*TNF-A*; NG_007462) using Clustal W[35].

Bioinformatics analysis of the *TNF-A* promoter region in *H. pylori*-infected patients

In silico prediction of the promoter: In this study, we employed five programs for human promoter prediction and recognition of human PolII promoter region and start of transcription (TSS) which include: Berkeley Drosophila Genome Project (<http://www.fruitfly.org/>)[36], Promoter 2.0 Prediction Server (<http://www.cbs.dtu.dk/>)[37], FPROM, TSSG and TSSW (<http://softberry.com/>) which are based on neutral network and linear discriminant approach[25,38,39].

In silico analysis of the predicted promoter region: Assessment for the presence of promoter-associated features: The computationally predicted promoter regions were additionally assessed for the presence of promoter-associated features using the ENCODE data (<https://www.encodeproject.org/>)[40-42]. These features include promoter-associated histone marks, DNase I hypersensitivity clusters, broad

chromatin state segmentation, transcription factor ChIP-seq and CpG islands.

Prediction of CpG islands: A CpG island is a DNA segment with high GC and CpG dinucleotide content and often regarded as a marker for the initiation of gene expression. In this study, we applied MethPrimer and GpC finder software (<http://www.softberry.com/berry.phtml?topic=cpfinder&group=programs&subgroup=promoter>) to predict CpG islands using default search parameter values for the software: CpG island length >200 bp, CG% > 50%, and Obs/Exp > 0.6[43,44].

Prediction of TFBSs: Prediction of the potentially functional TFBSs is a crucial step in the chain of promoter analytical events. Therefore, we applied five prediction software programs to analyze the predicted promoter region for possible TFBSs: (1) AliBaBa2 (<http://www.gene-regulation.com/>)[45]; (2) Algen Promo (http://algen.lsi.upc.es/cgi-bin/promo_v3/)[46,47]; (3) TF-Bind (<http://tfbind.hgc.jp/>)[48]; (4) Tfsitescan (<http://www.ifti.org/>)[49]; and (5) Gene Promoter Miner (GPMiner) (<http://GPMiner.mbc.nctu.edu.tw/>), which is an integrated system. For predicting TFBSs, MATCH tool was utilized to scan TFBSs in an input sequence[50].

Prediction of CEs: CE is the minimal functional unit composed of two closely located DNA binding sites for distinct transcription factors, but its regulatory function is qualitatively different from the regulation effects of either individual DNA binding site. Thus, the MatrixCatch algorithm (<http://gnaweb.helmholtz-hzi.de/cgi-bin/MCatch/MatrixCatch.pl>) was used to identify the CEs in our region (-146 to +10) [51].

Comparative profiling analysis: ECR Browser (<http://ecrbrowser.dcode.org/>)[52], NCBI Basic Local Alignment Search Tool nucleotide (<http://blast.ncbi.nlm.nih.gov/Blast.cgi>) and Clustal W (<https://www.genome.jp/tools-bin/clustalw/>)[35] were utilized to analyze the possible conservation of the predicted promoter region. The conservation was assessed in 11 species which include: Cow (*Bos taurus*), chimpanzee (*Pan troglodytes*), rhesus monkey (*Macaca mulatta*), dog (*Canis lupus familiaris*), mouse (*Mus musculus*), rat (*Rattus norvegicus*), chicken (*Gallus gallus*), zebrafish (*Danio rerio*), frog (*Xenopus laevis*), opossum (*Monodelphis domestica*), fugu pufferfish (*Takifugu rubripes*) and spotted green pufferfish (*Tetraodon nigroviridis*). Furthermore, multiple-sequence local alignment and visualization search engine (<https://mulan.dcode.org/>) was used to evaluate the conservation of the promoter's SNPs and to screen the possible conservation of TFBSs at these SNP locations[53].

Molecular detection of the *TNF-A-1030 C/T* polymorphism using PCR with confronting two-pair primer method

Two sets of primers were used in PCR with confronting two-pair primer to detect the *TNF-A-1030 C/T* polymorphism as follow: for allele T, the sequences of the primers were F: 5'-AAGGCTCTGAAAGCCAGCTG-3' and R: 5'-CCAGACCCT-GACTTTTCCTTCA-3'; and for allele C, F: 5'-GAAGCAAAGGAGAAGCT-GAGAAGAC-3' and R: 5'-CTCCATAGCCCTGGACATTCT-3'[54]. The PCR mixture components were the same as in[30]. The amplification conditions were initial denaturation at 95 °C for 10 min, followed by 30 cycles of denaturation at 95 °C for 1 min, annealing at 66 °C for 1 min, extension at 72 °C for 1 min and final extension at 72 °C for 5 min. The resulting PCR products were visualized by electrophoresis on a 1% agarose gel containing ethidium bromide. The predicted size was confirmed using a 50 bp DNA molecular weight marker. Genotyping was distinguished as follows; 444 bp and 316 bp for TT genotype, 444 bp, 316 bp and 174 bp for TC genotype and 444 bp and 174 bp for CC genotype.

Statistical analysis

Fisher's test or χ^2 test investigated Hardy-Weinberg equilibrium of allele and genotype distributions. Descriptive statistical analysis was applied to calculate percentages, proportions and means \pm standard deviation. Regarding the incidence of *H. pylori* infection, differences in frequency distribution by age were examined by the Mann-Whitney test, while differences in the frequency distribution of the categorical demographic and clinical variables of the study population were assessed by Fisher's test or χ^2 test. A multivariate logistic regression model was constructed to estimate OR and their 95% CIs for the association between *TNF-A-1030*, sociodemographic characteristics and *H. pylori* infection. Differences were considered to be statistically significant if $P < 0.05$. The statistical analyses were performed using Stata version11 (StataCorp, College Station, Texas) software.

RESULTS

Nucleotide variations in the 5'-regulatory region (-585 to +107) of the *TNF-A* gene

In the Sudanese *H. pylori*-infected patients, a total of seven nucleotide variations were detected in the 5'-regulatory region (six substitution mutations and one insertion mutation of C at +70). Among which, five were bimodally mutated heterozygous SNPs, and two are homozygous SNPs, as illustrated in Table 3 and Figure 2. The results of the multiple sequence alignment were visualized in Jalview[55]. The nucleotide sequences of the *TNF-A* 5'-region (-584 to +107) were deposited in the GenBank database under the following accession numbers: from MW251712 to MW251725.

In silico prediction of the *TNF-A* promoter regions

Five types of promoter prediction programs were applied to predict the promoter regions of the *TNF* 5'-region (-584 to +107), and the results are overviewed in Table 4. Neural Network Promoter Prediction (NNPP version 2.2) predicted one promoter region, located at +1 bp relative to the *TNF- α* mRNA cap site[26]. In addition, FPROM and TSSG programs predicted two promoter regions -146 bp and +5 bp, respectively. The TSSW program also expected these two regions. In comparison, no promoter region was predicted by Promoter 2.0 Prediction Server.

In silico analysis of predicted *TNF-A* promoter region

Presence of promoter-associated features: ENCODE data revealed a high level of transcription factor occupancy patterns, promoter-associated histone modifications and DNase I hypersensitivity at the in silico predicted promoter region, from -146 to +10 nt relative to the *TNF- α* mRNA cap site[26]. Furthermore, CpGfinder and MethPrimer software were employed to predict the presence of CpG islands. However, both software predicted no CpG islands present in the predicted promoter region, and ENCODE data confirmed no presence of the CpG island in the predicted promoter (see Figure 3).

Conservancy of the predicted promoter: As illustrated in Figure 4, the ECR Browser showed mammalian conservation for the (-146 to +10) region in chimpanzee (*Pan troglodytes* - pan-Tro2) (99.4%), rhesus monkey (*Macaca mulatta* - rheMac2) (95.6%), cow (*Bos taurus* - bosTau3) (91.8%), domesticated dog (*Canis lupus familiaris* - canFam2) (89.3%), rat (*Rattus norvegicus* - rn4) (82.4%), mouse (*Mus musculus* - mm9) (84.3%) and opossum (*Monodelphis domestica* - monDom5) (78.0%). But the region was not conserved in chicken (*Gallus gallus*), frog (*Xenopus laevis*), zebrafish (*Danio rerio*), fugu pufferfish (*Takifugu rubripes*) and spotted green pufferfish (*Tetraodon nigroviridis*). An overview of the mammalian conservation of the in silico-predicted promoter of *TNF* is shown in Figure 5.

Prediction of TFBSs: In the present study, we used five software programs to predict TFBSs. To ensure accurate analysis, only factors predicted by three out of the five programs or predicted by two programs but verified in the literature were selected. The five prediction programs reported multiple putative TFBSs within the (-146 to +10) region, as illustrated in Table 5. Moreover, screening of this region using the NCBI SNP databases showed four SNPs, as shown in Table 5. The ECR Browser and NCBI Basic Local Alignment Search Tool nucleotide revealed the conservation of these SNPs in chimpanzees, rhesus monkey, cow and dog. Multiple-sequence local alignment and visualization presented multiple TFBSs to be located at rs765073823 and rs537401710. The overview from the multiple-sequence local alignment and visualization software for conserved TFBSs predicted to be conserved (100%) between humans, chimpanzees, rhesus monkeys, cows, and domesticated dogs is summarized in Table 6.

Prediction of CEs: In the present study, CEs were predicted using MatrixCatch, which can find experimentally known regulatory elements (both single sites and pairs) and novel regulatory elements by computational comparison to the known ones in a library of CE models[51]. An overview of predicted CEs by MatrixCatch is presented in Table 7.

Allele and genotype frequencies of *TNF-A*-1030 and susceptibility to *H. pylori* infection

Sixty-one participants from each group (*H. pylori*-infected and uninfected) were successfully genotyped for *TNF-A*-1030 polymorphism; a representative gel is shown

Table 3 Nucleotide variations in the 5'-regulatory (-584 to +107) region of tumor necrosis alpha in Sudanese *Helicobacter pylori*-infected patients

SNP	Event	SNP locus ¹	Chromosomeposition	Serialnumber (rs)
C>G (homozygous)	Transversion	-567	NG_007462.1:g.4422 C>G	rs2857711
G>A (heterozygous)	Transition	-375	NG_007462.1:g.4614 G>A	rs1800750
G>A (heterozygous and homozygous)	Transition	-307	NG_007462.1:g.4682 G>A	rs1800629
G>A (heterozygous)	Transition	-237	NG_007462.1:g.4752 G>A	rs361525
T>A (heterozygous)	Transversion	-76	NG_007462.1:g.4913 T>A	rs41297589
A>T (heterozygous)	Transversion	+27	NG_007462.1:g.5016 A>T ²	-
Insertion of C	-	+70	NG_007462.1:g.5058-5059 InsC	-

¹Position of the single nucleotide polymorphism is relative to the tumor necrosis factor-alpha mRNA cap site[26].

²Novel mutation at the 5' untranslated region detected in this study. SNP: Single nucleotide polymorphism.

Table 4 Overview of the in silico predicted tumor necrosis factor-alpha promoter regions for the respective prediction programs. The most predicted region is indicated in bold

Prediction program	Predicted promoter regions ¹
BDGP (NNPP version 2.2) ²	-40 to +10
Promoter 2.0 Prediction Server	no promoter
FPROM	+5
TSSG ³	-146
TSSW ⁴	-140
	+6

¹All positions are relative to the tumor necrosis factor-alpha mRNA cap site[26].

²NNPP: Neural network promoter prediction; Threshold 0.80.

³Threshold for LDF- 4.00.

⁴Thresholds for TATA+ promoters - 0.45, for TATA-/enhancers - 3.70.

in **Figure 6**. Allele and genotype frequencies of *TNF-A*-1030 polymorphism in patients infected with *H. pylori* and uninfected controls are presented in **Table 8**. Although the *TNF-A*-1030-C allele was more prevalent in patients infected with *H. pylori* compared to uninfected controls, no significant association was found between the allele frequencies of *TNF-A*-1030 and *H. pylori* infection (27.87% vs 19.67%, OR = 0.6339, 95%CI: 0.3490-1.151, *P* = 0.176). However, a significant association was detected between T/C genotype and *H. pylori* infection (39.34% vs 19.67%, OR = 2.69, 95%CI: 1.17-6.17, *P* = 0.020) (**Tables 8 and 9**). In contrast, no significant association was observed between allele and genotype frequencies of *TNF-A*-1030 and gastric cancer (*P* = 0.8116 and *P* = 0.3900, respectively) (**Table 10**). The allelic and genotype distributions at -1030 of *TNF-A* were in Hardy-Weinberg equilibrium, with non-significant χ^2 values (for uninfected subjects *P* = 0.1520; and subjects with benign disorders *P* = 0.2089).

DISCUSSION

Many SNPs have been observed in the vicinity of the *TNF* locus, particularly in the distal *TNF* promoter. Some of these have been implicated in the disease susceptibility, resistance or severity by modifying the transcriptional regulation of *TNF*[13,56-58]. In this study, we functionally analyzed SNPs in the *TNF-A* 5'-region (-584 to +107) of the Sudanese patients infected with *H. pylori* and had divergent clinical outcomes that ranged from simple asymptomatic gastritis to more serious conditions, *i.e.* peptic ulcer disease and gastric cancer. The exploratory sequencing of *TNF-A* 5'-region (-584 to +107) of the Sudanese patients infected with *H. pylori* revealed six previously reported

Table 5 Summary of the in silico predicted transcription factor binding sites for tumor necrosis factor-alpha (-146 to +10) region

TranscriptionFactor	Position ¹		SNP in binding site	Software				
	Start	End		AliBaba2.1	Aliggen Promo	Tfsitescan	TF-Binding	GPMiner
Elk-1	-145	-130			X ²		X	
Sp1	-138	-126		X		X		
AP-2	-129	-118			X		X	
Ets-1	-118	-111				X		
PEA3/ Ets-1	-118	-110				X		
T3R_TRE1	-115	-108			X	X	X	
TNF-alpha-CRE	-112	92				X	X	
C/EBP-beta	-100	-74	rs41297589 [-76] ³			X	X	
NF-kappaB	-99	-86				X	X	
AP-1	-67	-57				X		
NF-kappaB	-55	-46	rs765073823 [-48]rs537401710 [-47]	X				
Sp1	-54	-41	rs765073823 [-48]rs537401710 [-47]	X	X	X		
Sp1	-48	-39	rs765073823 [-48]rs537401710 [-47]	X	X	X		
GATA	-40	-30	rs539666421 [-38]	X	X		X	
AP-2	-38	-27	rs539666421 [-38]	X		X	X	
TBP	-29	-20		X			X	X

¹Position is relative to the tumor necrosis factor-alpha transcription start site.
²X means the transcription factor is predicted by the software that is marked with X.
³Observed in this study. SNP: Single nucleotide polymorphism.

Table 6 Overview of conserved transcription factor binding sites predicted by multiple-sequence local alignment and visualization

Transcription Factor	Binding sequence	Position ¹		Conserved SNPs
		Start	End	
V\$CEIS168_Q6	gCTTCCTC	-115	-108	
V\$ETS_Q6	gcTTCCtc	-115	-108	
V\$SP1_Q4_01	ttccCCGCCctcc	-51	-39	rs765073823 [-48]rs537401710 [-47]
V\$SP1_Q6_01	tcCCCGCCct	-50	-41	rs765073823 [-48]rs537401710 [-47]
V\$SP1_Q2_01	cCCCGCCctc	-49	-40	rs765073823 [-48]rs537401710 [-47]

¹All positions are relative to the tumor necrosis factor-alpha mRNA cap site. Multiple-sequence local alignment and visualization (<https://mulan.dcode.org/>) to be conserved (100%) between human, chimpanzee, rhesus monkey, cow, and domesticated dog at the (-146 to +10) region. The crucial transcription factor for tumor necrosis factor transcription, nuclear factor, was not included.

SNPs located at -567, -375, -307, -237, -76 and +70 and one novel SNP at +27 relative to the *TNF-A* transcription start site. A C to G homozygous transversion at -567 nt was found in all our studied populations. At the same time, the novel A to T heterozygous transversion at +27 nt was observed in five patients who had normal upper gastroendoscopy or gastritis. This SNP is located in the 5' untranslated region. Therefore, it could affect the post-transcriptional regulatory pathways that control mRNA localization, stability and translation efficiency[59]. Further studies are encouraged to investigate this SNP in terms of the frequency of the minor allele (T) in the Sudanese population and its functional significance using computational and experimental

Table 7 Summary of the in silico predicted composite regulatory elements for the -146 to +10 region of tumor necrosis factor-alpha

Composite element	MatrixName for a 1 st element	Score, strand	Distance in between	MatrixName for a 2 nd element	Score, strand	Position of CE, orientation	orientation	Composite score	P value	Sequence
CE00266	V\$ETS_Q6	0.991+	12	V\$AP1_Q2_01	0.831+	-118	+	0	1.08e-03	GCTTCCTCCagaTGAGTCATGGG
CE00109	V\$AP1_C	0.853-	8	V\$NFAT_Q6	0.943-	-66	-	0.007	3.42e-03	TTGAATGATTCTTTCCCCGC
CE00150	V\$AP1_C	0.853-	8	V\$NFAT_Q6	0.943-	-66	-	-0.237	3.42e-03	TTGAATGATTCTTTCCCCGC
CE00058	V\$HMGYIY_Q6	0.955-	-5	V\$NFKB_Q6_01	0.759-	-78	-	-0.09	6.89e-03	GTTTTCCGCTG
CE00058	V\$HMGYIY_Q6	0.955-	-4	V\$NFKB_Q6_01	0.662-	-78	-	0.005	9.20e-03	GTTTTCCGCTGG
CE00064	V\$HNF3_Q6	0.780+	15	V\$NF1_Q6	0.956+	-28	+	-0.254	4.83e-02	ACATATAAAGGCAGtGTTGGCACACC

CE: Composite regulatory elements.

Table 8 Allele and genotype frequencies of tumor necrosis factor-alpha-1030 polymorphism among *Helicobacter pylori*-infected and uninfected subjects and their contributions to *Helicobacter pylori* infection, n (%)

	<i>H. pylori</i> (+ve), n = 61	<i>H. pylori</i> (-ve), n = 61	P value	OR (95%CI)
Allele frequency				
<i>TNF-A</i> -1030-T	88 (72.13)	98 (80.33)	0.176	0.63 (0.349-1.151)
<i>TNF-A</i> -1030-C	34 (27.87)	24 (19.67)		
Genotype frequency				
T/T	32 (52.46)	43 (70.49)	-	1 (reference)
T/C	24 (39.34)	12 (19.67)	0.020 ^a	2.69 (1.17-6.17)
C/C	5 (8.20)	6 (9.84)	0.862	1.12 (0.31-3.99)

^aP value < 0.05 statistically significant difference. OR: Odds ratio; 95%CI: 95% confidence interval; *H. pylori*: *Helicobacter pylori*; +ve: Positive; -ve: Negative; *TNF-A*: Tumor necrosis factor-alpha.

approaches.

Intriguingly, the heterozygous SNP T>A at -76 was located at the in silico-predicted promoter region. However, in this study, the in silico analysis predicted promoter region was located from -146 to +10 nt relative to the *TNF-α* mRNA cap site using different algorithms[26]. This finding is in agreement with previous studies conducted on 411 *TNF* promoters from individuals of distinct ethnic backgrounds that concluded that the human *TNF* promoter sequences up to 200 bp relative to the transcription start site involved in enhanceosome formation and the regulation of the gene are completely conserved in humans[21,26,60,61]. Also, the ENCODE data showed a high level of the hallmarks of cis-regulatory regions at the in silico predicted promoter region (-146_+10), which include nuclease hypersensitivity and histone modifications [40-42].

Functional elements in the mammalian gene promoters can be detected by high conservation between species distantly related on the evolutionary scale[62,63]. In this study, the computational comparative analysis revealed mammalian conservation for the -146 to +10 region in chimpanzee (*Pan troglodytes* - pan-Tro2) (99.9%), rhesus monkey (*Macaca mulatta* - rheMac2) (93.7%), cow (*Bos taurus* - bosTau3) (78.2%), domesticated dog (*Canis lupus familiaris* - canFam2) (77.8%), rat (*Rattus norvegicus* - rn4) (76.3%), mouse (*Mus musculus* - mm9) (78.7%) and opossum (*Monodelphis domestica* - monDom5) (72.2%). In an earlier study conducted by Leung *et al*[64], the region from positions -131 to -63 and -53 and -45 relative to the start site of *TNF* gene transcription showed high sequence conservation among primates, with complete conservation

Table 9 Multivariate analysis of genotype frequencies of tumor necrosis factor-alpha-1030 polymorphism and sociodemographic characteristics in *Helicobacter pylori* infection

Variables		P value	OR (95%CI)
Age		0.946	0.99 (0.98-1.02)
Gender	Male		1 (reference)
	Female	0.845	0.93 (0.42-2.02)
Residence	Urban		1 (reference)
	Rural	0.341	1.46 (0.67-3.18)
Hospital	Private		1 (reference)
	Public	0.045 ¹	0.45 (0.21-0.98)
Genotype frequency	T/T		1 (reference)
	T/C	0.016 ^a	2.87 (1.22-6.78)
	C/C	0.982	1.02 (0.27-3.88)

¹Weak evidence of significant different.

^aP value < 0.05 statistically significant different. OR: Odds ratio; 95%CI: 95% confidence interval.

Table 10 Tumor necrosis factor-alpha-1030 polymorphism and gastric cancer association risk in gastric cancerous patients and subjects with benign gastric disorders, n (%)

	Gastric pathologies		OR (95%CI)
	Benign disorders ¹ , n = 108	Cancer, n = 14	
Allele frequency			
<i>TNF-A</i> -1030-T	176 (90.28)	21 (75.00)	1.150 (0.4627 - 2.8600)
<i>TNF-A</i> -1030-C	51 (9.72)	7 (25.00)	
P value	0.8116		
Genotype frequency			
T/T	68 (62.96)	7 (50.00)	1.700 (0.5556 - 5.2020)
C carrier	40 (37.04)	7 (50.00)	
P value	0.3900		

¹Benign disorders, *i.e.* gastritis, duodenitis or ulcer.

OR: Odds ratio; 95%CI: 95% confidence interval; *TNF-A*: Tumor necrosis factor-alpha.

within phylogenetic footprints across seven primate species, including Old World monkeys and New World monkeys[64].

However, the *TNF-A* gene is located within the major histocompatibility complex region of chromosome 6, the highly polymorphic region of the human genome, which includes the human leukocyte antigen (HLA) genes[65]. In fact, all of the common ten detected SNPs (-1030, -862, -856, -574, -375, -307, -243, -237, and +70 nt relative to the start site of transcription) fall outside of the identified *TNF* primate phylogenetic footprints[66-70]. This feature is consistent with the accrual of mutations under neutral evolution[64,72]. Furthermore, several of these SNPs (-1030, -862, -856, -307, -243, -237) have been shown to be in non-random association with extended HLA haplotypes[21, 26,71-73], which are HLA regions that exhibit fixity of the genomic interval between HLA-B and HLA-DR, that includes *TNF-A* and complement (complotype) regions[21, 74,75].

Intiguently, we detected one mutation (T>A, -76) located at the identified *TNF* primate phylogenetic footprints[64] in a patient with reinfection with *H. pylori* multiple times. The presence of this SNP in the conserved region that is involved in regulating the *TNF* gene could affect the expression and create a condition of hypoacidity that favors the survival and colonization of *H. pylori*[76,77]. The -76 SNP

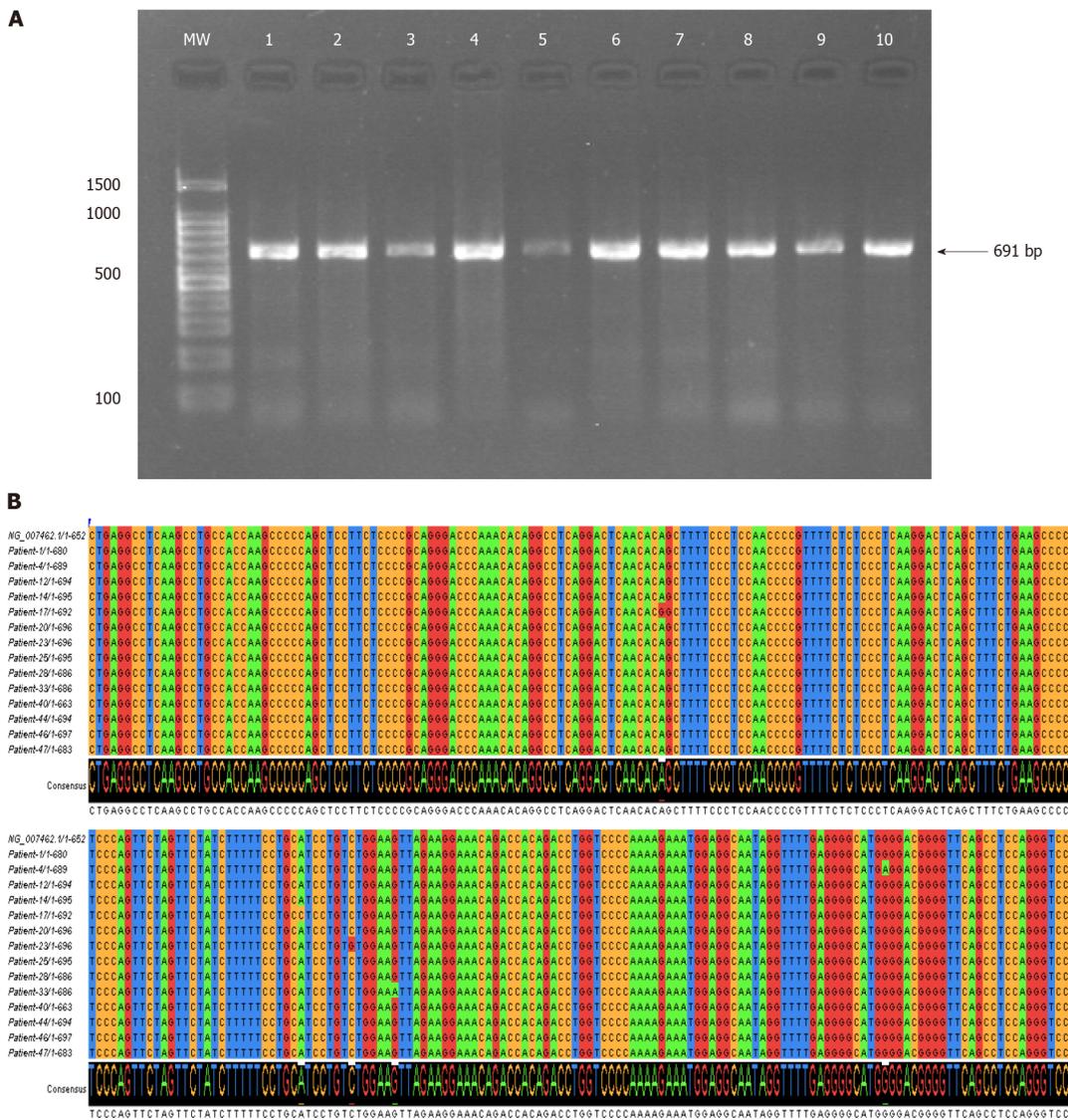


Figure 2 Nucleotide variations of the tumor necrosis factor-alpha 5'-region (-584 to +107) in the Sudanese *Helicobacter pylori*-infected patients. A: PCR amplification results of the tumor necrosis factor-alpha 5'-region (-584 to +107) examined on 1% agarose gel electrophoresis; B: Multiple sequence alignment of the nucleotide sequences of the tumor necrosis factor-alpha 5'-region performed in Clustal W and visualized in Jalview[55]. The levels of identity are visible as histograms at the bottom.

was first discovered with an overall minor allele frequency of 0.031 in the Indian population while studying polymorphisms of *TNF*-enhancer and the gene for *FcγRIIIa* correlated with the severity of *Falciparum malaria* in the ethnically diverse Indian population[78]. It is present at the low-affinity transcription factor Ets-1 binding site in macrophages and the high affinity NFATp binding site in T and B cells[79]. Also, it is located at an in silico-predicted C/EBP-beta (also known as NF-IL6) binding site (in this study, see Table 5), which was experimentally proven in myelomonocytic cells[80-82].

Sequence analysis of the *TNF-A* 5'-region (-584 to +107) of the Sudanese patients revealed relative variability of *TNF-A* SNPs (Figure 2 and Table 3). This finding is in agreement with a study conducted by Baena *et al*[21] that found that the highest relative diversity of *TNF-A* SNPs was revealed among the three African studied populations (Malawian, Southern Nigerian, African-American and African-Caribbean). Also, it is consistent with the “out of Africa” hypothesis based upon human mitochondrial DNA analyses[83]. Despite this high level of variation, here in this study, the sequences involved in enhanceosome formation and gene regulation are highly conserved[64]. Remarkably, we detected only a single SNP (-76) in this region. By contrast, the novel +27 variant and other *TNF-A* SNPs described in this study occur within or immediately adjacent to promoter regions with high diversity in the primate lineage. Unexpectedly, the -243 variant, the first *TNF-A* SNP linked to an African-derived extended HLA haplotype[70], was not detected in our studied population.

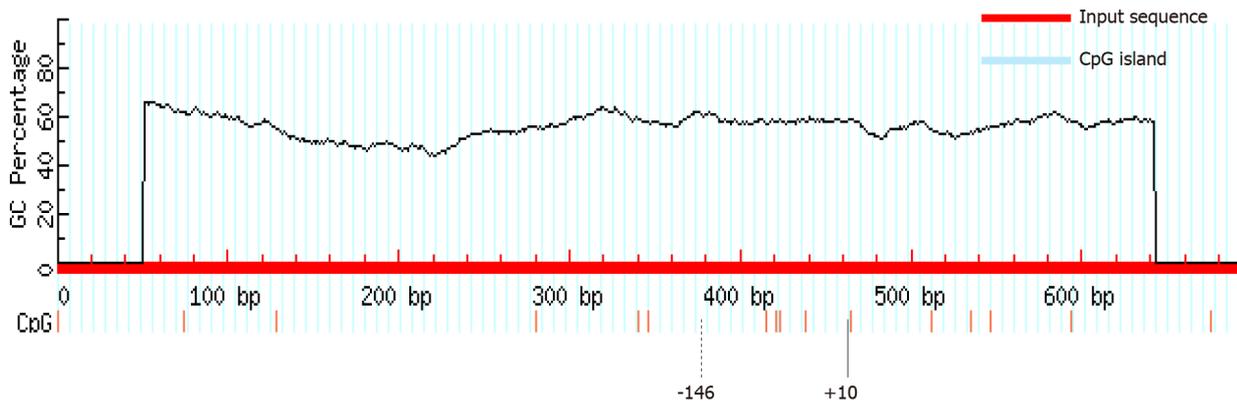


Figure 3 MethPrimer software prediction of no CpG islands in the in silico predicted promoter region.

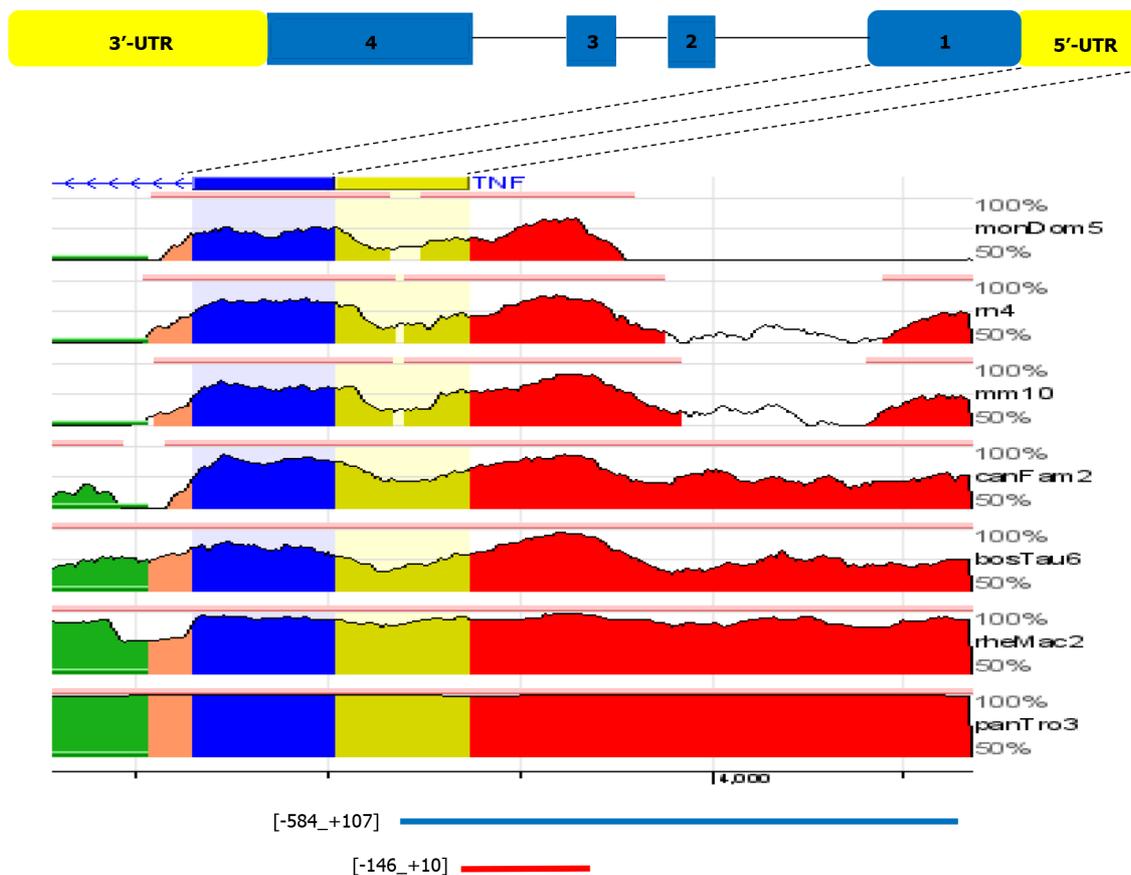


Figure 4 Overview from the ECR Browser shows mammalian conservation of the tumor necrosis factor 5'-upstream region compared to the human sequence in the region (-584 to +107) (hg19 chr6:31542751-31543444). Blue boxes represent the first tumor necrosis factor exon, while yellow indicates the tumor necrosis factor 5' untranslated region. Intragenic positions are highlighted in red or in green when corresponding to transposable elements and simple repeats. UTR: Untranslated region.

Other previously identified SNPs in this region (-584 to +107), which include -567, 375, -307, -237, -76 and +70 nt relative to the start site of transcription, were observed[66-68, 84].

The -1030 (T/C; rs1799964) SNP is frequently observed in African populations (17%-25% Malawian, 7% Nigerian, 29% African-American/Caribbean and 14% Gambia)[21, 22]. In this study, the -1030 SNP was detected in 47 Sudanese (38% of our studied population). Many studies have been published that examine the association between the -1030 SNP and multiple diseases[60,85,86] and diseases related to *H. pylori* such as gastroesophageal reflux disease, gastritis, peptic ulceration and gastric cancer[87-90]. In this study, we found a lack of association between -1030T and susceptibility to *H.*

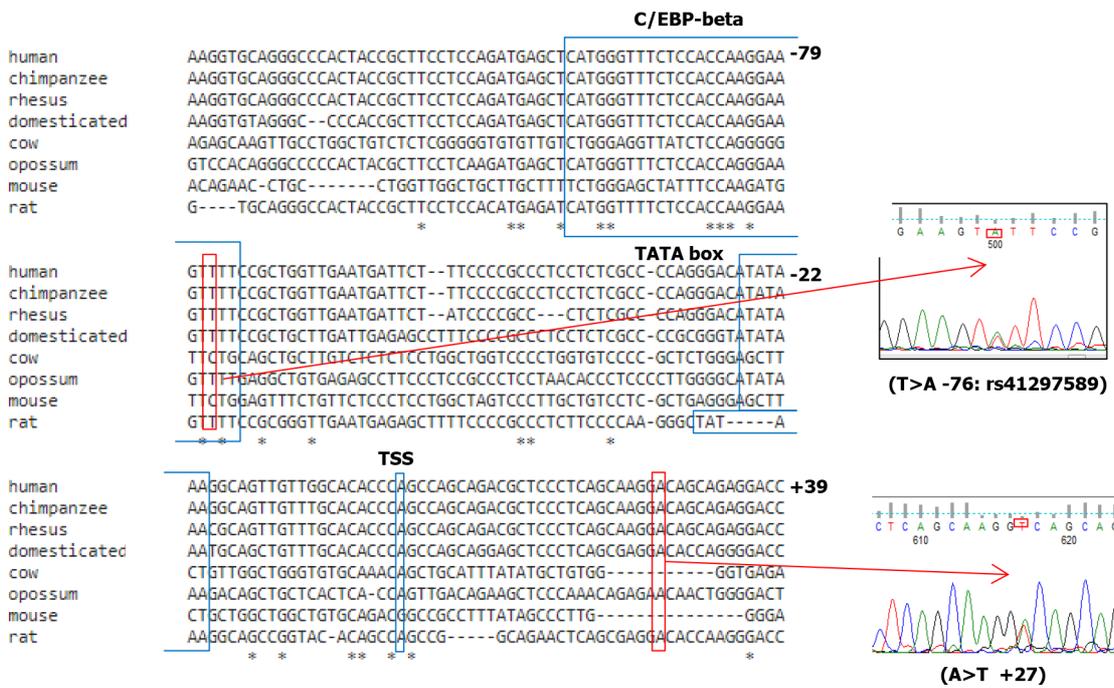


Figure 5 Mammalian conservation of (AT; single nucleotide polymorphism databases dbSNP: rs41297589) at position -76 and the novel mutation (A>T at +27) in the 5' untranslated region among various species. The nucleotides are enumerated at each line on the right side, and the in silico predicted TATA-, C/EBP-beta and transcription start site have marked inboxes. The chromatogram results of the polymorphisms are visualized using Finch TV software. TSS: Transcription start site.

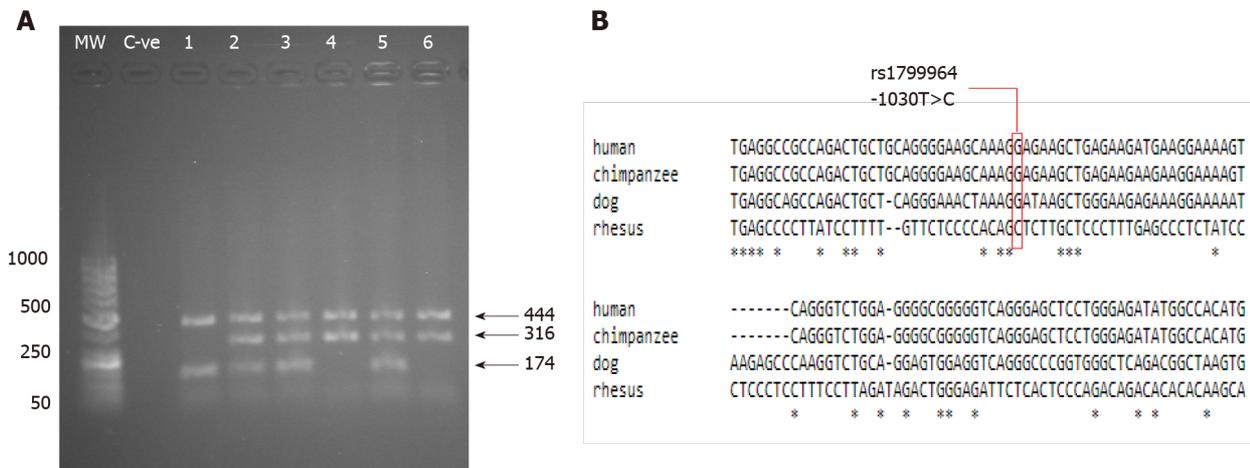


Figure 6 Molecular detection of the tumor necrosis factor-alpha-1030 C/T polymorphism. A: PCR with confronting two-pair primer products analyzed on a 1% agarose gel stained with ethidium bromide. Three genotypes can be seen. Lanes 2, 3 and 5 showed 444 bp, 316 bp and 174 bp, indicating a heterozygous genotype. Lanes 4 and 6 showed 444 bp and 316 bp, which indicated a homozygous T genotype. Lane 1 showed 444 bp and 174 bp, which indicated a homozygous C genotype; B: Mammalian conservation of (TC; dbSNP: rs1799964) position -1030 among different species. MW: Molecular weight marker; C-ve: Negative control.

pylori and gastric cancer in the studied population ($P = 0.1756$ and $P = 0.8116$, respectively). This finding is in agreement with previous studies[87,88,91]. In contrast to a study conducted in Japan that observed a significant association between -1030T and gastric cancer[91]. This variation could be attributed mainly to differences in genetic backgrounds of the studied population, the method of genotyping and sample size[76,92].

The study's limitations include the relatively small number of the enrolled subjects and depending on the in silico tools for studying the influence of the detected promoter variants on the *TNF-A* gene expression and *H. pylori* infection (susceptibility and progression). Further large cohort studies are needed to validate the study findings. However, the computational analysis provides a basis for identifying

promoter regions, recognizing regulatory motifs and understanding gene expression patterns[25].

According to the literature, a considerable number of polymorphisms have been discovered in the *TNF-A* promoter. However, a crucial question that remains to be answered is whether these polymorphisms have any functional effect that may significantly impact disease incidence or severity. Identifying which of these many variants are functional is of great significance for discovering new preventive, diagnostic and therapeutic strategies against the incidence and/or progression of multifactorial diseases such as *H. pylori* infection. This study detected seven SNPs in the *TNF-A* 5'-region; only one of them (T>A, -76) was located at the in silico-predicted promoter region (-146 to +10). This SNP could lead to the modification of the transcriptional regulation of *TNF-A* in *H. pylori* infection. However, this conclusion cannot substitute for the experimental proofs (*in vitro* or *in vivo*), but it can provide a direction or insight for such experiments to validate the in silico predictions.

CONCLUSION

In the Sudanese *H. pylori*-infected patients, seven SNPs were observed in the *TNF-A* 5'-region; only one of them (T>A, -76) was located at the in silico-predicted promoter region (-146 to +10). In addition, it was predicted to alter TFBSs and CEs. Furthermore, a novel mutation (A>T, +27) was detected in the 5' untranslated region, and it could affect the post-transcriptional regulatory pathways. In addition, computational analysis was a valuable method for understanding gene expression patterns and providing guidance for further *in vitro* and *in vivo* experimental validation.

ARTICLE HIGHLIGHTS

Research background

Helicobacter pylori (*H. pylori*) infection represents a major public health challenge in Sudan. However, functional polymorphisms within the tumor necrosis factor-alpha (*TNF-A*) promoter are associated with the incidence and progression of *H. pylori* infection by increasing *TNF-α* production.

Research motivation

TNF lies within the major histocompatibility complex region of chromosome 6, which is a highly polymorphic region. Therefore, many polymorphisms have been detected in the *TNF-A* promoter and studying which variants could affect *TNF-A* gene expression is relevant. However, the influence of these single nucleotide polymorphisms (SNPs) on *TNF-α* production is not fully known and still a contradictory topic of debate due to the ethnic differences between populations. Furthermore, to our knowledge, there are no previous studies in Sudan that have addressed the association between *TNF-A* and *H. pylori* infection or *H. pylori*-associated diseases.

Research objectives

To functionally characterize the genetic variations in the *TNF-A* 5'-region (-584 to +107) of Sudanese patients infected with *H. pylori* and predict if these SNPs could alter the regulatory motifs using bioinformatics analyses. Also, to investigate the mammalian conservation of these SNPs using comparative profiling analysis in 11 species.

Research methods

An observational study was conducted in the major hospitals in Khartoum state. Genomic DNA was extracted from 122 gastric biopsies of patients who had been referred for endoscopy. Genotyping of the *TNF-A*-1030 polymorphism was performed using PCR with confronting two-pair primer to investigate its association with *H. pylori* infection in the Sudanese population. Sanger sequencing was applied to detect SNPs in the 5'-region (-584 to +107) of *TNF-A* in *H. pylori*-infected patients; in silico tools were used to predict whether these mutations would alter transcription factor binding sites or composite regulatory elements in this region. In addition, the ECR browser and multiple-sequence local alignment and visualization search engine were

used to study the conservation of the detected SNPs among 11 mammalian species.

Research results

A total of seven SNPs were observed in the *TNF-A* 5'-region of Sudanese patients infected with *H. pylori*. Among them, the SNP (T>A, -76) was located at the in silico-predicted promoter region (-146 to +10), and it was predicted to alter transcription factor binding sites and composite regulatory elements, while the novel mutation (A>T, +27) was detected in the 5' untranslated region. It could affect the post-transcriptional regulatory pathways. Mammalian conservation was detected for the (-146 to +10) region in chimpanzee (99.4%), rhesus monkey (95.6%), cow (91.8%), domesticated dog (89.3%), mouse (84.3%), rat (82.4%) and opossum (78.0%). Furthermore, genotyping of *TNF-A*-1030 revealed a lack of significant association between -1030T and susceptibility to *H. pylori* and gastric cancer in the studied population ($P = 0.1756$ and $P = 0.8116$, respectively).

Research conclusions

Despite the high level of genetic variation in the *TNF-A* 5'-region (-584 to +107) of the Sudanese patients, the sequences involved in enhanceosome formation and gene regulation are highly conserved. Remarkably, only a single SNP (-76) was detected in this region. In addition, computational analysis was a valuable method for studying gene expression patterns and insights for further *in vitro* and *in vivo* experimental proofs.

Research perspectives

Further large cohort studies are needed to assess the association between (T>A, -76) mutation and *H. pylori* infection (susceptibility and progression). Also, further studies are encouraged to investigate the novel mutation (A>T, +27) in terms of the frequency of the minor allele (T) in the Sudanese population and its functional significance using computational and experimental approaches. Identifying which of these detected variants are functional is of great relevance for discovering new preventive, diagnostic and therapeutic strategies against the incidence and/or progression of multifactorial diseases such as *H. pylori* infection.

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