PEER-REVIEW REPORT

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Title: Identification of Functional TNF-A Promoter Variants Associated with Helicobacter pylori Infection in the Sudanese Population: Computational Approach

Reviewer's code: 02522888

Position: Editorial Board

Academic degree: BSc, MSc, PhD

Professional title: Associate Professor, Director

Reviewer's Country/Territory: United States

Author's Country/Territory: Sudan

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Reviewer chosen by: AI Technique

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Scientific quality	[Y] Grade A: Excellent [ ] Grade B: Very good [ ] Grade C: Good [ ] Grade D: Fair [ ] Grade E: Do not publish
Language quality	[ ] Grade A: Priority publishing [Y] Grade B: Minor language polishing [ ] Grade C: A great deal of language polishing [ ] Grade D: Rejection
Conclusion	[ ] Accept (High priority) [ ] Accept (General priority) [Y] Minor revision [ ] Major revision [ ] Rejection
Re-review	[ ] Yes [Y] No
Peer-reviewer statements	Peer-Review: [Y] Anonymous [ ] Onymous Conflicts-of-Interest: [ ] Yes [Y] No

SPECIFIC COMMENTS TO AUTHORS

In this manuscript the authors evaluate in silico the H pylori TNF-A 5′-region [-584_+107] of Sudanese gastric patients. A total of 122 patients were screened for H Pylori infection. Out of them 61 H Pylori positive were further analysis using sanger sequencing and bioinformatic analysis. The authors also performed in silico prediction of promoter sequences followed by prediction of promoter associated features, prediction of CpG islands, prediction of transcriptional factors and regulatory elements as well we comparative profiling analysis. Five software in order to predict transcription factor binding sites (TFBSs). The study sample size and gender distribution seems reasonable. Among the seven SNPs that were were observed in the TNF-A 5′-region, only one of them (T>A, -76) was located at in silico-predicted promoter region [−146_+10]. This particular SNP was predicted to alter transcription factor binding sites. There was lack of association with the -1030 (T/C; rs1799964) SNP (commonly found in Africans) For a descriptive analysis the studies seem to be optimal The paper switches between 7 SNPs and 8 SNPs in the write up. The authors should carefully check the text for uniformity.

Limitations of the study have not been clearly presented and should be discussed in a paragraph Validation in larger cohort is needed to validate these findings Minor typos were observed throughout the manuscript that should be carefully checked and corrected