Proteomics Exploration of *Helicobacter pylori* to Design an Innovative Multi-Epitope mRNA Vaccine

A Computational Vaccine Design Study



roduction

licobacter pylori?

pylori (*H. pylori*) is a Gram-negative, spiral-shaped
at colonizes the human gastric mucosa. It is associated
gastrointestinal diseases, including:

- gastritis
- lcers
- adenocarcinoma
- -associated lymphoid tissue (MALT) lymphoma

e increasing challenge of antibiotic resistance
ghlights the need for innovative preventive strategies,
cluding vaccine development.

tudy Objective

at Was the Aim of This Research?

study aimed to design a novel multi-epitope mRNA vaccine
nst *H. pylori* using proteomics, reverse vaccinology, and
unoinformatics approaches.

he proposed vaccine was designed to stimulate both
umoral and cellular immune responses.

3. Research Methodology

How Was the Vaccine Designed?

1. Proteome screening of *H. pylori* strain 26695
2. Identification of antigenic and virulence-associated proteins
3. Prediction of B-cell, CTL and HTL epitopes
4. Evaluation of antigenicity, allergenicity, toxicity and human sequence similarity
5. Molecular docking with MHC molecules and TLRs
6. Construction and optimization of mRNA vaccine
7. Prediction of structural stability and immune responses

Key proteins investigated

CagA, FlaA, FlaB, OipA, SabA, UreA, HSP, BabA, FecA, DupA and VacA

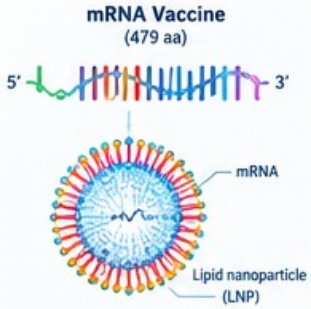

Fig. 3. Schematic representation of the designed mRNA vaccine construct.

4. Key Findings

20 CTL epitopes	**17** HTL epitopes	**19** B-cell epitopes	**96.09%** Population coverage
479 Amino acids	**50.84 kDa** Molecular weight	**0.95** CAI	**66.78%** GC content

5. Vaccine Characteristics

Predicted Biological Properties

Parameter	Result
Antigenicity (VaxiJen)	1.1603
Antigenicity (ANTIGENpro)	0.936101
Instability Index	32.33
Aliphatic Index	65.30
GRAVY	-0.616
Allergenicity	Predicted non-allergenic
Toxicity	Predicted non-toxic

The computational analysis suggested favorable antigenic, physicochemical and structural properties.

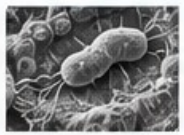

Fig. 1. Scanning electron microscopy of H. pylori (proposed image).

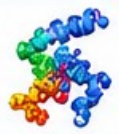

Fig. 4. 3D structure of the vaccine construct (from the article).



Fig. 3. Structure of the mRNA vaccine (from the article).



Fig. 2. Immune response mechanism (from the article).

6. Molecular Docking

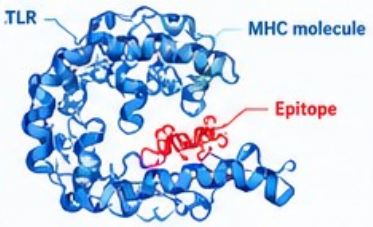

Fig. 1. Molecular docking of the selected epitope with MHC allele (HLA-A*01:01).



Fig. 4. Docking of the e
Toll-like recepto

7. Immune Response Simulation

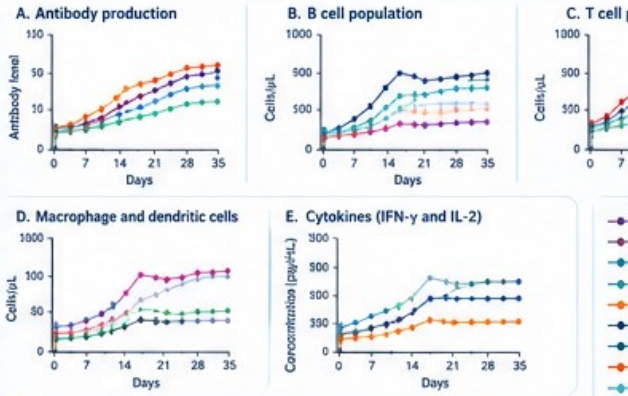

Fig. 2. Predicted immune response profiles using the C-ImmSim model.

8. Conclusion & Future Perspectives

A Promising Computational Vaccine Candidate

This study presents a proteome-based multi-epitope mRNA va
candidate against *H. pylori*. The computational findings sugge
potential to stimulate both humoral and cellular immunity, wit
predicted antigenicity, stability and population coverage.

However, these findings are based on *in silico* analyses.
Further experimental validation is essential, including:

- *In vitro* immunological studies
- *In vivo* animal studies
- Evaluation of vaccine safety and gastric inflammation
- Assessment of protective efficacy and mucosal immune respon
- Future clinical investigations

The proposed vaccine is a research candidate, not an approved or clinically validated vaccine.

9. Article Reference

Maleki MH, Sadeghifard N, Khoshnood S, Omidi N, Yazdanmanesh M, Sadeghi Kalani B.
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