Sequence & Structure Analysis
LBI20503T

HELICOBACTER PYLORI

NOVEL DRUG TARGET IDENTIFICATION FOR ANTIMICROBIAL RESISTANCE BACTERIA IN THE BIOINFORMATICS ANALYSIS

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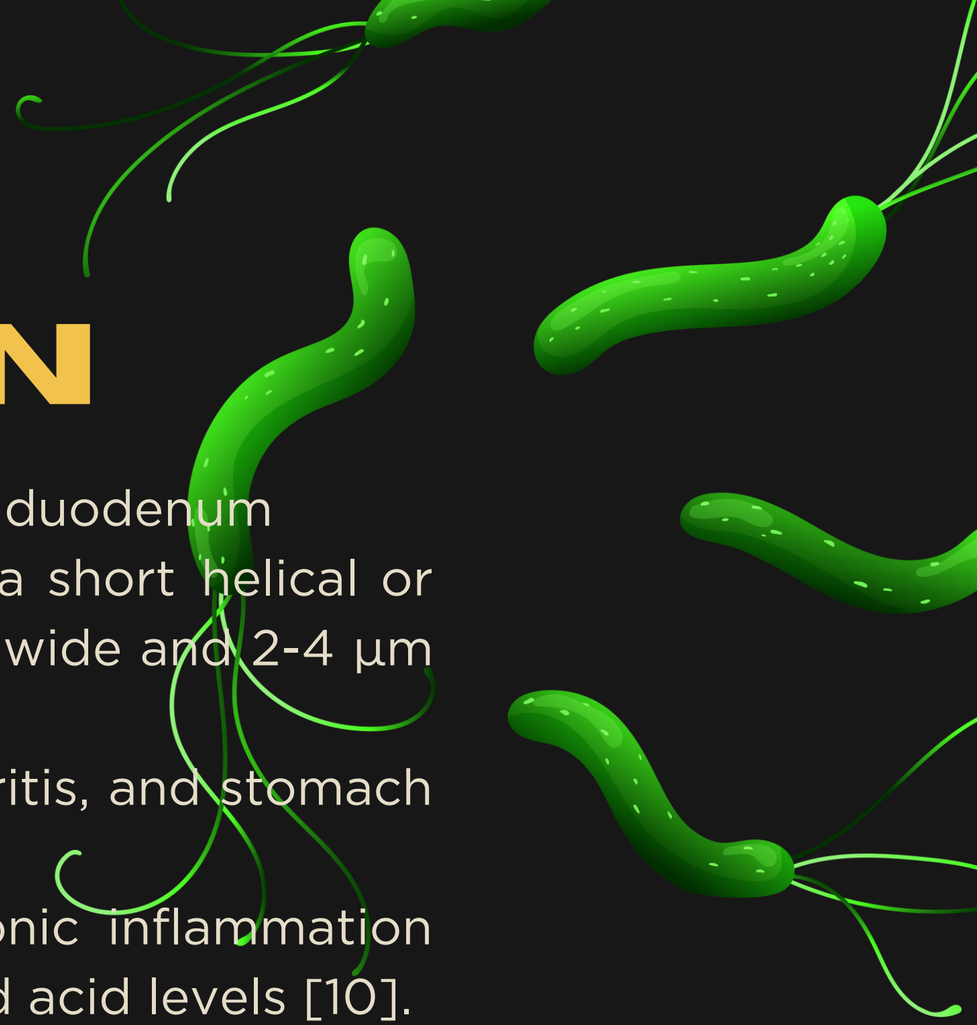
1.0 INTRODUCTION

- is a type of bacteria that can infect the stomach or the duodenum
- Morphology: is a Gram-negative microorganism with a short helical or S-shaped form that measures approximately 0.5-1 µm wide and 2-4 µm long [4]
- Disease: H. pylori can cause peptic ulcer disease, gastritis, and stomach cancer in some cases
- Its ability to survive in the stomach and cause chronic inflammation indicates resistance against both immune response and acid levels [10].
- Various antibiotic treatments are used for treating H. pylori infections; however, studies indicate a rapid increase in strains resistant to these antibiotics
- The emergence of antibiotic resistance in H. pylori necessitates the urgent prioritization of an effective drug target



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2.0 METHODOLOGY

2.1 Sequence Retrieval from NCBI

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2.2 Identification of Paralogous Sequence with Batch Entrez

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2.3 Removal of Paralogous Sequence with CD-Hit

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2.4 Removal of seq with <100 amino acids with Europe Galaxy

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2.5 Subtractive Genomics

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2.6 KASS (KEGG Automatic Annotation Server) Too

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2.7 Prediction of subcellular localization with Psortb

3.0 RESULTS + DISCUSSION

3.1 Preprocessing Steps

Initial Number of Sequence obtained from NCBI	1427
Number of sequences after removal from Batch Entrez	1424
Number of sequences after the removal of gene duplication with CH-Hit Removal	1416
Number of sequences after the removal of the sequence below 100 amino acid	1294

3.0 RESULTS + DISCUSSION

3.2 Subtractive Genomics

Non-homology against human proteome	1228
Essentiality	907
Virulence factor	254
Druggability Analysis	151
Non-homology against gut microbiota proteomes	45
Broad Spectrum Analysis	45
Host-Pathogen Interaction	37
Non-homology against human anti-targets	37

3.0 RESULTS + DISCUSSION

3.3 Automatic annotation genes and subcellular localization

Removal of sequence without KEGG orthology	HSA	6	HPY	25
Removal after the subcellular localization of PsortB	14			

3.0 RESULTS + DISCUSSION

3.4 The genes selected are based on their subcellular localization, specifically those with a final cytoplasmic prediction.

No	ID	Name
1	WP_000133864.1	cag pathogenicity island type IV secretion system ATPase VirB11 [Helicobacter pylori]
2	WP_000688273.1	aminodeoxychorismate/anthranilate synthase component II [Helicobacter pylori]
3	WP_001169746.1	copper response regulator transcription factor CrdR [Helicobacter pylori]
4	WP_001959998.1	polysaccharide deacetylase [Helicobacter pylori]
5	WP_156534302.1	tryptophan synthase subunit alpha [Helicobacter pylori]
6	WP_209611414.1	UDP-4-amino-4,6-dideoxy-N-acetyl-beta-L-altrosamine transaminase [Helicobacter pylori]
7	WP_209611556.1	NADH-quinone oxidoreductase subunit G [Helicobacter pylori]
8	WP_209611663.1	type II/IV secretion system ATPase subunit [Helicobacter pylori]
9	WP_209611808.1	pyridoxine 5'-phosphate synthase [Helicobacter pylori]
10	WP_209612060.1	bifunctional anthranilate synthase component I family protein/aminotransferase class IV [Helicobacter pylori]
11	WP_209612279.1	pyridoxal phosphate-dependent aminotransferase family protein [Helicobacter pylori]
12	WP_209612466.1	flagellar biosynthesis protein FlhF [Helicobacter pylori]
13	WP_209612506.1	anthranilate synthase component I [Helicobacter pylori]
14	WP_209612511.1	HAMP domain-containing sensor histidine kinase [Helicobacter pylori]

5.0 CONCLUSION

- these findings aid in developing targeted antibiotics against H. pylori without affecting human genes.
- Targeting specific proteins minimizes allergic reactions and harm to the host (Homo sapiens).
- Novel drugs based on these proteins could effectively eliminate H. pylori infections.
- Research provides insights into potent drug targets within H. pylori.

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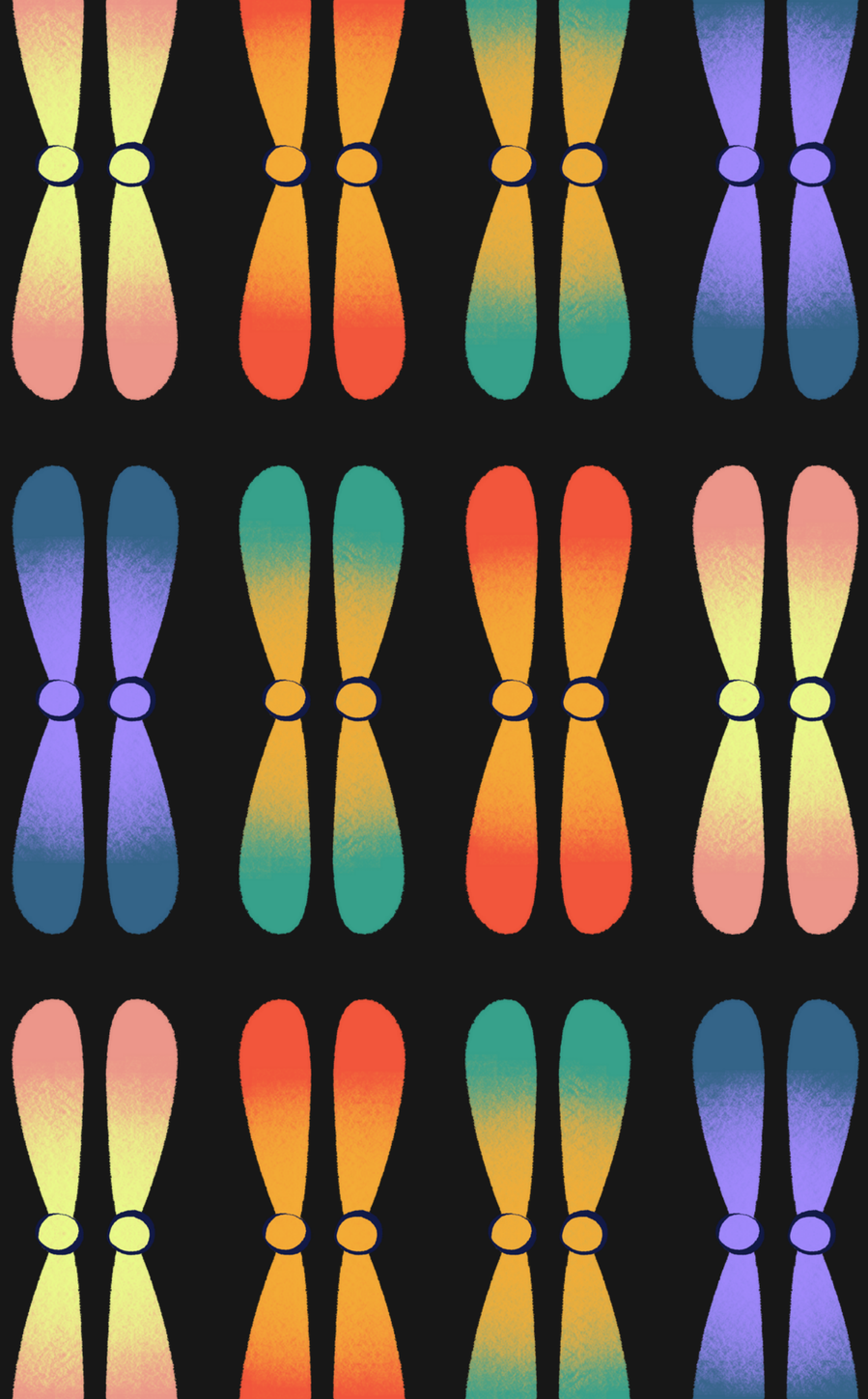

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