Annotation of *Helicobacter pylori* at Locus Tags HP1198, HP1241, HP1319, and HP1450

Deanna Meyer, Elizabeth Newell, Natalie Perl, Mary Weber, and Laura O'Donnell Attica High School-Attica, NY and The Western New York Genetics in Research

and Health Care Partnership

Abstract

A group of genes from the microorganism Helicobacter pylori were annotated using the collaborative genome annotation website GENI-ACT. The GenBank proposed gene product name for each gene was assessed in terms of the general genomic information, amino acid sequence-based similarity data, structure-based evidence from the amino acid sequence, and cellular localization data. The GenBank proposed gene product name did not differ significantly from the proposed gene annotation for each of the genes in the group and as such, the genes appear to be correctly annotated by the computer database.

Introduction

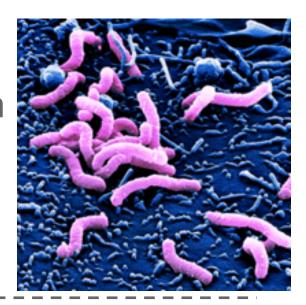
Helicobacter pylori was first discovered in the biopsies of patients suffering from chronic gastritis and stomach ulcers. The bacteria is fairly common with about two-thirds of the population having the bacteria in their body already. Although the bacteria is in the body for years, a person may never experience symptoms of stomach ulcers or any other issues H. pylori can cause. Scientists suspect that the bacteria is contagious through unclean food or water and it seems to be more common in people that live in unsanitary conditions.

Once *H. pylori* enters the stomach, it goes through four steps to establish a successful settlement. First, it has to survive the acidity of the stomach by releasing an enzyme that changes urea into ammonia which neutralizes the acid and creates a more hospitable environment. After H. pylori remains in the stomach, it moves toward epithelium cells using its flagella. As soon as it reaches the cells, the bacteria attaches itself to the host where it releases toxins which harm the stomach tissue and cause damage to the stomach and intestinal walls.

The World Health Organization classified *H. pylori* as a group

one carcinogen, meaning that it has a high chance of giving a person cancer. Doctors treat *H. pylori* antibiotics but resistance is on the rise.

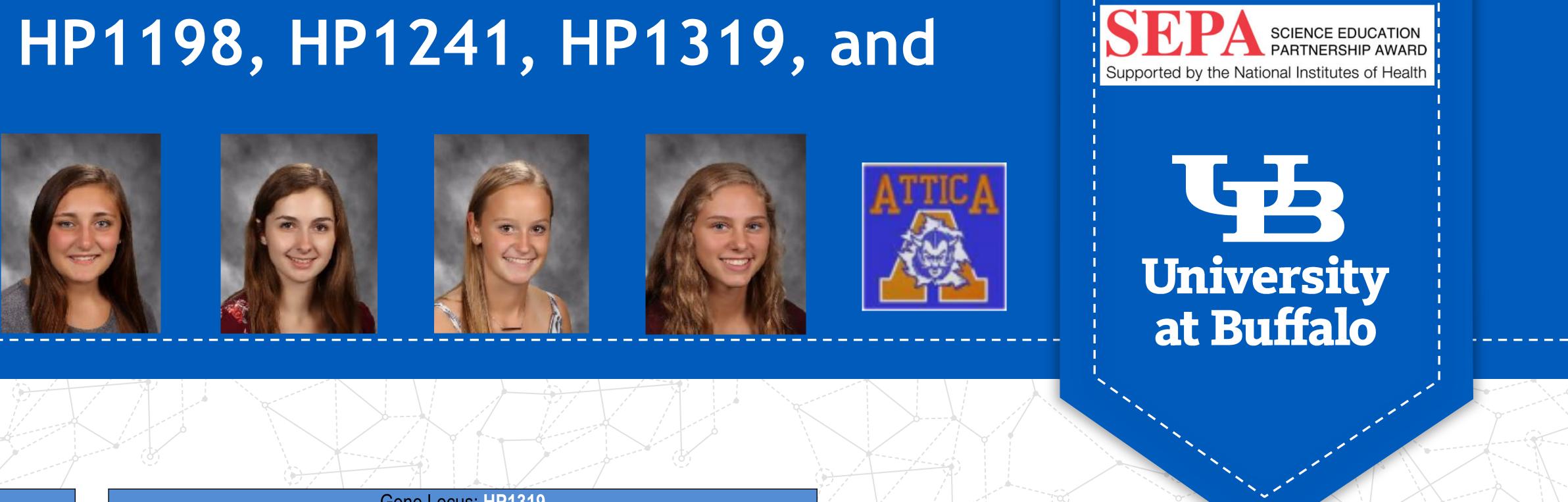
Colored scanning electron micrograph of *H pylori* on surface of gastric cells web.stanford.edu



Methods

Modules of the GENI-ACT (http://www.geni-act.org/) were used to complete Helicobacter pylori genome annotation. The modules are described below:

Modules	Activities	Questions Investigated
Module 1- Basic Information Module	DNA Coordinates and Sequence, Protein Sequence	What is the sequence of my gene and protein? Where is it located in the genome?
Module 2- Sequence-Based Similarity Data	Blast, CDD, T-Coffee, WebLogo	Is my sequence similar to other sequences in Genbank?
Module 3- Structure-Based Evidence	TIGRfam, Pfam, PDB	Are there functional domains in my protein?
Module 4- Cellular Localization Data	Gram Stain, TMHMM, SignalP, PSORT, Phobius	Is my protein in the cytoplasm, secreted or embedded in the membrane?



Gene Locus: HP1198			Gene Locus: HP1319		
Basic Information	DNA Coordinates	complement(12683771277049)		DNA Coordinates	complement(13802901380865)
	DNA Length	8673 nt	Basic Information	DNA Length	576 nt
	Amino Acid Sequence Length	2890 aa		Amino Acid Sequence Length	191 aa
Sequence-based Similarity	COGS T-Coffee	no significant hits no orthologs present		COGS	COG0087: RpIC:Ribosomal protein L3 [Translation, ribosomal structure]
	Web-Logo	no orthologs present	Sequence-based		and biogenesis];
Structure-based Evidence	TIGRFAMs PFAMs	no significant hits pfam00562 RNA polymerase	Similarity	T-Coffee	Well conserved until the very end
		Rpb2		Web-Logo	Not well conserved
	HMM Logo Key Residues	D95, G243, D244, G254, P284, R286		TIGRFAMs	TIGR03625:L3_bact; ribosomal protein L3
	PDB	RNA polymerase	Structure-based	PFAMs	pfam00297; Ribosomal_L3
Cellular Localization	Transmembrane Helices	none	Evidence	HMM Logo Key Residues	W236
	Signal Peptide PSORTb Final Prediction	none cytoplasmic		PDB	complex containing domain 3 bound to the 70S ribosome.
Helicobacter pylori HP1198:				Transmembrane Helices	none
			Cellular Localization	Signal Peptide	none
PFAM, and PD	B data supports			PSORTb Final Prediction	cytoplasmic

HP1198 to be an RNA polymerase protein which synthesizes RNA from DNA during transcription in the process of protein synthesis. No orthologs were shown in the BLAST database. Cellular localization predicts that this protein functions in the cytoplasm.

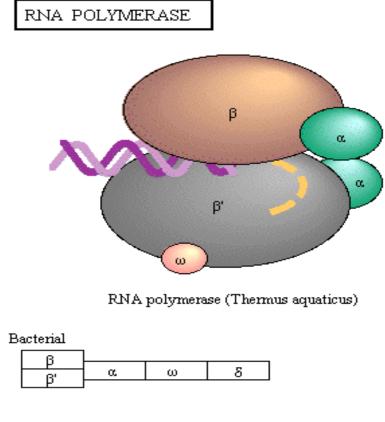
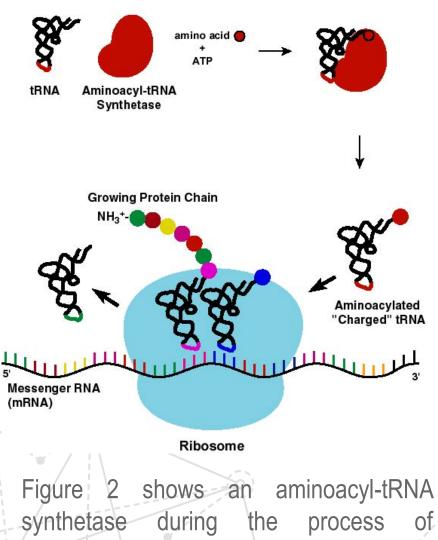


Figure 1 shows RNA polymerase and its subunits in the bacteria Thermus aquaticus- www.genome.jp/kegg/

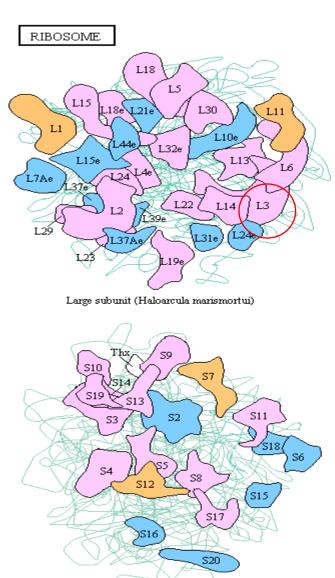
Gene Locus: HP1241		
	DNA Coordinates	complement(13141881316731)
Basic Information	DNA Length	2544 nt
	Amino Acid Sequence Length	847 aa
Sequence-based Similarity	COGS	No significant hit
	T-Coffee	No orthologs present
	Web-Logo	Not well conserved
Structure-based Evidence	TIGRFAMs	No significant TIGERFAM hits
	PFAMs	No significant PFAM hits
	HMM Logo Key Residues	No HMM Logo Key Residues
	PDB	Alanyl-tRNA synthetase
	Transmembrane Helices	none
Cellular Localization	Signal Peptide	none
	PSORTb Final Prediction	cytoplasmic

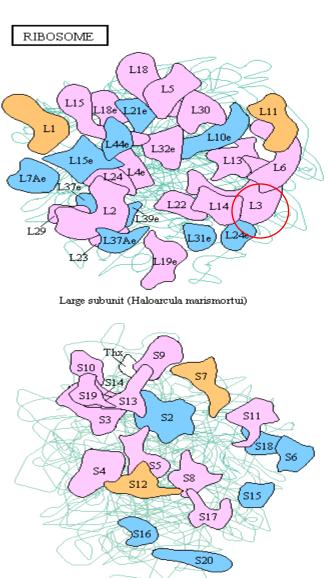


in protein synthesishttp://www.dna.neu.edu

Helicobacter pylori HP1241:

Although there is little evidence provided, PDB data supports HP1241 to be an alanyl-tRNA synthetase. This protein catalyzes the attachment of an amino acid to its transfer RNA molecule for the process of protein synthesis. No orthologs shown in the BLAST database. Cellular localization predicts that this protein functions in the cytoplasm.





Se

Helicobacter pylori HP1319:

COG, TIGRFAM, PFAM, and PDB data suggests that HP1319 is a ribosomal protein. Ribosomal proteins function in the translation of RNA in protein synthesis. Cellular localization data predicts that HP1319 functions in the cytoplasm.

Figure 3 shows the large and small subunit of a ribosome. Circled in red is the L3 domain making up part of the large subunitwww.genome.jp/kegg/

	Gene Locus: HP1450	
	DNA Coordinates	complement(15179061519549)
sic Information	DNA Length	1644 nt
	Amino Acid Sequence Length	547 aa
	COGS	COG0706: YidC-Membrane protein insertase Oxa1/YidC/SpoIIIJ
equence-based Similarity	T-Coffee	well conserved until very end
Chimany	Web-Logo	well conserved from position 1- 30 then not well conserved until the end
tructure-based	TIGRFAMs	yidC_oxa1_cterm:membrane protein insertase,. [Protein fate, Protein and peptide secretion and trafficking]
Evidence	PFAM	pfam02096:60KD_IMP
	HMM Logo Key Residues	Y149
	PDB	EM fitted model of bacterial holo- translocon
	Transmembrane Helices	6
ular Localization	Signal Peptide	none
	PSORTb Final Prediction	cytoplasmic membrane

Helicobacter pylori HP1450: COG, TIGRFAM, PFAM, and PDB data suggests that HP1450 is a membrane protein insertase that is required for the insertion and or proper folding of membrane proteins. Cellular localization data predicts that HP1450 has 6 transmembrane helices, residing in the cytoplasmic side of the cell membrane.

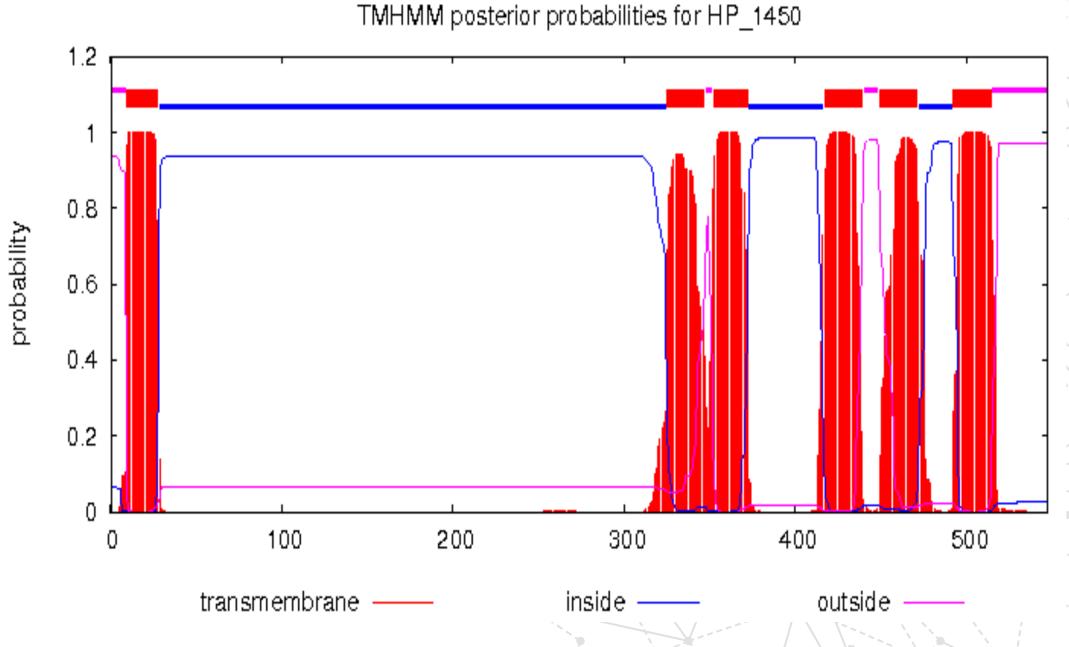
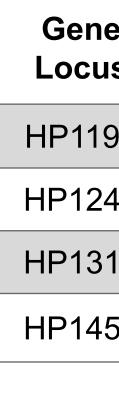


Figure 4 – TMHMM data for *Helicobacter pylori* HP1450. The cellular localization data shows the presence of 6 transmembrane helices

Conclusion

The GENI-ACT proposed gene product did not differ significantly from the proposed gene annotation for each of the genes in the group and as such, the genes appear to be correctly annotated by the computer database. All proteins annotated seem to be involved with the processes of transcription and translation in *H. pylori*.





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e Is	Geni-Act Gene Products	Proposed Annotation
98	RNA polymerase	RNA polymerase
41	Alanyl-tRNA synthetase	Alanyl-tRNA synthetase
19	Ribosomal protein L3	Ribosomal protein L3
50	Membrane protein insertase	Membrane protein insertase

References

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