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Our group annotated 4 con secutive genes from Helicobader pylori83 using the modules given by GENI-ACT. Following the instructions given in our GENI-ACT manual, we went to many different sites that aided us in annotating our genes. These included BLAST, CDD, Tcoffee, WebLogo, Gram Stain, TMHMM, SignalP, Psort, Phobius, IMG EDU, TIGR fam, P fam, PDB, KEGG, MetaCvc and R fam, We recorded these findings on the online GENI-ACT lab notebook. Our results were established using all 4 students annotations. Finally, as you can see, we are presenting our results on this trifold poster. We added pictures and diagrams to help show what our genes do . In the end, most of the proposed annotations for the sequenced genomes were the same. The purpose of our research was to annotate specific genes then compare the results to those already given by GEN I-ACT and see if the data proposed annotations were either correct or incorrect. All of our genes were as proposed except for HMPREF0462 0043.

#### Introduction

The gram negative Helicobacter pylori 83 bacterium can alter the human regulatory mechanisms for gastric acid production. During initial, Helicobacter pylori 83 can decrease acid secretion levels in the stomach. This can result in ulcers in the stomach, and even in the duodenum. For many years, people believed that smoking, stress, spicy food, and other lifest le caused stomach ul cers. It was later found that Helicoba der pylori 83 was ingested through undean food. The pylorus is the sphinder musdes between the duodenum and the stomach. This research is very important because it will help us learn new ways to fight disea ses and bacteria, such as Helicobader pylor i 83.

Our bioinformatics group has been working to analyze and annotate eight different genomes, that make up Helicobacter pylori 83.We split into two groups of four, who each annotated parts of the genome. We used websites such as Pfam, Tigrfam, Kegg, T-Coffee, to di scover what our genes do, and what purpose they serve a in Helicobacter pylori 83



Above is a snippet from the Helicobacter pylori 83 ortholog gene neighborhood showing the locus tags under investigation by East Rochester students

## Methods and Materials

#### Modules of the GENI-ACT (http://www.geni-act.org/) were used to complete Helicobacter pylori 83 genome ann otation . The modules are described below: Modules Activities Questions Investigated

| Module 1- Basic Information<br>Module              | DNA Coordinates and<br>Sequence, Protein Sequence | What is the sequence of my gene and protein? Where is it located in the genome?           |
|--|---|---|
| Module 2- Sequence-Based<br>Similarity Data        | Blast, CDD, T-Coffee,<br>WebLogo                  | Is my sequence similar to<br>other sequences in<br>Genbank?                               |
| Module 3- Cellular<br>.ocalization Data            | Gram Stain, TMHMM,<br>SignalP, PSORT, Phobius     | Is my protein in the<br>cytoplasm, secreted or<br>embedded in the<br>membrane?            |
| Module 4- Alternative Open<br>Reading Frame        | IMG Sequence Viewer For<br>Alternate ORF Search   | Has the amino acid<br>sequence of my protein been<br>called correctly by the<br>computer? |
| Module 5- Structure-Based<br>Evidence              | TIGRfam, Pfam, PDB                                | Are there functional domains<br>in my protein?  |
| Module 6- Enzymatic<br>Function                    | KEGG, MetaCyc, E.C.<br>Number,                    | In what process does my<br>protein take part?   |
| Module 7- Gene Duplication/<br>Gene Degradation    | Paralog, Pseudogene                               | Are there other forms of my gene in the bacterium? Is my gene functional?                 |
| Module 8- Evidence for<br>Horizontal Gene Transfer | Phylogenetic Tree,                                | Has my gene co-evolved<br>with other genes in the<br>genome?                              |
| Module 9- RNA                                      | RFAM  | Does my gene encode a<br>functional RNA?  |

## Helicobacter pylori 83 HMPREF0462\_0041:

The initial proposed product of the gene by GENI-ACT was a response regulator receiver domain. This gene function is supported by the top BLAST hit in Swissprota swell as data and results collected in T-Coffee, TIGRFAM, CDD, and PDB results. This specific genes function for the whole organism is to receive the signal from the sensor partner bacterial two-component systems. It is u sually found Nterminal to a DNA binding effector domain.

### Helicobacter pylori 83 HMPREF0462 0042

The initial proposed product of the gene by GENI-ACT was a Histidine Kinase domain protein and the data that supports this is Swissprot BLAST, TIGRFAM, and T-Coffee. The function of this gene for the whole organism is to help send an enzyme that helps play a role in signal transduction across the cellular membrane.

#### Helicobacter pylori 83 HMPREF0462 0043:

The original gene proposed was Bifunctional N AD(P)H-hydrate repair enzyme. This evidence was supported by a swissprot BLAST search. CDD results, and T-Coffee results. This search later returned as a sugar kinase, supported by Pfam results, TIGRFAM results, and also, PDB results.

## Helicobacter pylori 83 HMPREF0462 0044

This gene was proposed as a DNA Replication gene. The top swissprot hits on B.L.A.S.T. and the results returned from T-coffee, IMG/EDU, and Pfam. This gene is controls the parts of Helicobacter pylori 83 that regulate its replication. It can be found working to replicate DNAprior to cell division.



Figure 1 - Picture of the ortholog gene neighborhood of Helicobacter pylori 83, HMPREF0462\_0041 showing very similar organisms meaning there is no horizontal gene transfer.



Figure 2: This is a picture of a WEBLogo from HMPREF0462 0044. Its shows well conserved amino acids in other dosely related species.



| A STATE CONTRACTOR | 10000000000 | The Constraint region, the other particulation in table teration, E. Con part that for the part | 200-004 |          |
|--------------------|-------------|---|---------|----------|
| [+] y(oF ntorm     | TIGR00197   | yieF N-terminal region. The protein region corresponding to this model shows no clear homology  | 1-201   | 6.08e-76 |
| [+] Carb_kinase    | ptam01256   | Carbohydrate kinase; This family is related to pfam02110 and pfam00234 implying that it also    | 236-463 | 7.79e-68 |
| [+] Nnr1           | C0G0052     | NAD(P)H-hydrate repair enzyme Nnr, NAD(P)H-hydrate epimerase domain [Nucleotide transport and   | 1-193   | 9.54e-52 |
| [+] Nn/2           | C0G0053     | NAD(P)H-hydrate repair enzyme Nnr, NAD(P)H-hydrate dehydratase domain (Nucleotide transport     | 193-464 | 2.66e-53 |
| [+] Y]eF_N         | ptam03853   | YjeF-related protein N-terminus; YjeF-N domain is a novel version of the Rossmann fold with a   | 23-177  | 8.58e-37 |
| [+] PLN03050       | PLN03050    | pyridovine (pyridovamine) 5'-phosphate ovidase; Provisional                                     | 10-163  | 3.04e-09 |
| [+] PRK10565       | PRK10565    | putative carbohydrate kinase; Provisional   | 6-443   | 1,44e-33 |
|                    |             |   |         |          |
|                    |             |   |         |          |
|                    |             |   |         |          |

Figure 3 - The above picture is the result from the C.D.D. search through blast. This shows the different domains that are similar to the blast results for HMPREF0462 0044.



### Figure 4 : Here is a diagram of a kegg pathway map for Helicobacter pylori 83 replication helicase. It shows how the replication helicase system works in Helicobacter pylori 83

| Conclusion               |   |   |  |  |  |
|--------------------------|---|---|--|--|--|
| Locus Tag Numbers        | Proposed annotation                               | Most likely annotation                            |  |  |  |
| HMPREF0462_0041:         | Response Regulator<br>Reœiver Domain.             | An N-terminal to a<br>binding effector<br>domain. |  |  |  |
| HMPREF0462 0042:         | Histidine Kinase<br>domain protein.               | Histidine kinase<br>domain protein.               |  |  |  |
| <u>HMPREF0462 0043</u> : | Bifunctional<br>NAD(P)H-Hydrate<br>repair enzyme. | Sugar kinase.                                     |  |  |  |
| HMPREF0462 0044:         | DNAReplication gene.                              | DNAReplication gene.                              |  |  |  |

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