SCIENCE EDUCATION PARTNERSHIP AWARI Annotation of the Helicobacter pylori 83 Genome from DNA Coordinates ted by the National Institutes of Healt (82463 to 83719), (89946 to 90623) and (90605 to 91042) 75 Wesley Dorow and Lawrence Hohl. East Rochester High School, East Rochester, New York and The Western New York Genetics in Research University and Health Care Partnership at Buffalo Abstract Methods This year, I annotated 4 genes from Helicobacter pylori 83 Modules of the GENI-ACT (http://www.geni-act.org//were using the modules given by GENI-ACT. Following the used to complete Helicobacter pylori 83 genome instructions given in our GENI-ACT manual, we went to many annotation. The modules are described below: different sites that aided us in annotating our genes. These included BLAST, CDD, T-coffee, WebLogo, Gram Stain, Modules Questions Investigated Module 1- Basic Information DNA Coordinates and Figure 3- example of the TMHMM, SignalP, Psort, Phobius, IMG EDU, TIGRfam, Pfam, What is the sequence of my Module Sequence, Protein Sequen gene and protein? Where is results given, when I PDB, KEGG, MetaCyc and Rfam. I recorded these findings on it located in the genome attempted to annotate the online GENI-ACT lab notebook. My results were Module 2- Sequence-Based Blast, CDD, T-Coffee Is my sequence similar to HMPREF4062 0083 and established using all 4 annotations. Finally I am presenting our Similarity Data WebLogo other sequences in Genbank? HMPREF4062 0091 showing results on this trifold poster. I added pictures and diagrams to Module 3- Cellular Gram Stain, TMHMM, Is my protein in the negative results for the help show what our genes do, and the processes used to SignalP, PSORT, Phobiu cytoplasm, secreted or embedded in the presence of a signal peptide annotate them. The most frustrating part about this year, was membrane? by TMHMM and negative that three of my four genes were hypothetical proteins. This Module 4- Alternative Open Has the amino acid IMG Sequence Viewer For Alternate ORF Search sequence of my protein been results for a signal peptide Reading Frame meant that most websites provided little info on the gene. My 4 called correctly by the and transmembrane helixes genes were HMPREF0462 0083. HMPREF0462 0090. computer? by Phobius HMPREF0462 0091 and HMPREF0462 0095. Only 83's Module 5- Structure-Based TIGRfam, Pfam, PDB Are there functional domains Evidence in my protein? annotation remained the same, while the others changed Module 6- Enzymatic KEGG, MetaCyc, E.C. In what process does my slightly, and sometimes dramatically. In 90, I learned it Function Number protein take part contained a nucleotide binding protein domain, 91 was Figure 1- a snippet of the weblogo of HMPREF0462_0090. This Module 7- Gene Duplication/ Are there other forms of my Paralog, Pseudogene weblogo is extremely well conserved. This shows the the hypothetical, but I learned it was transmembrane, and 95 was Gene Degradation gene in the bacterium? Is ParAprotein is a crucial part of Helicobacter pylori 83 annotated as a hypothetical, but I learned it may be a DNA my gene functional? Module 8- Evidence for Phylogenetic Tree. Has my gene co-evolved topoisomerase. Horizontal Gene Transfer with other genes in the genome? **Topoisomerase I Mechanism** Introduction Does my gene encode a functional RNA? Module 9- RNA REAM Conclusion The gram negative Helicobacter pylori 83 bacterium can alter the human regulatory mechanisms for gastric acid production. CCCCCC Initial proposed Product after Results During initial, Helicobacter pylori 83 can decrease acid secretion product levels in the stomach. This can result in ulcers in the stomach, and even in the duodenum. For many years, people believed HMPREF0462 0083 HMPREF4062 0083 Hypothetical protein Hypothetical protein that smoking, stress, spicy food, and other lifestyle caused This gene was initially proposed as Hypothetical Proteins, stomach ulcers. It was later found that Helicobacter pylori 83 and this remained consistent throughout. This gene have was ingested through unclean food. The pylorus is the sphincter had very little information on them. Few results came up muscles between the duodenum and the stomach. This On binding to DNA, When the strand is The reaction is HMPREF4062 0090 ParA protien ParA nucleotide on most sources. research is very important because it will help us learn new TopoI cleaves one cleaved, it rotates in a completed by religation binding domain strand of the DNA controlled manner of the cleaved strand ways to fight diseases and bacteria, such as Helicobacter pylori HMPREF0462 0090 orotein through a Tyr (Y) around the other This relaxes the DNA! 83. residue attacking a strand The proposed annotation of this gene was that it was a HMPREF4062 0091 Hypothetical protien Still hypothetical: phosphate Of the four genes that I was given, 2 of them were hypothetical ParA nucleotide binding domain protein. This gene is the but most likely proteins. This unfortunately meant that little information was gene that separates and partitions the two chromosomes transmembrane. known about them. This made it extremely difficult to complete in a chromosome pair. The ParA protein helps with Figure 2- This shows the actual function of a Dna topoisomerase. HMPREF4062 0095 the task of annotating them. These hypothetical proteins are Hypothetical protien Dna topsemirase It cleaves a strand of DNA, then it realigns them, making a relaxed chromosomal replication in helicobacter pylori 83. The proteins that have had very little work in research done on them. strand of dna initial proposition of the gene remained constant through I used the resources given to on the geni-act website, I tried to validate the initial proposed annotation of the genomes. the study. Through this, I also learned the new things about the genes that HMPREF0462 0091 TMHMM posterior probabilities for HMPREF0462 009 I annotated. Below shows the ortholog neighborhood of the This was initially proposed as Hypothetical Proteins, and References genes I annotated. this remained consistent throughout. This gene have had 2005-2016 WebMD, LLC HMPREF0462 0090 very little information on them. Few results came up on Geni-act.org binding domain ParA most sources. I did learn that HMPREF4062 0091 was HMPREF0462 0083 nucleotide binding Hypothetical protein transmembrane protein Acknowledgments HMPREF0462 0095 Supported by an NIH Science Education Partnership (SEPA) Award 0.2 - 5R250D010536 The initial proposed annotation of HMPREF0462 0095 Thank you to Stephen T. Koury, Ph.D. University at Buffalo was actually a hypothetical protein. Using Blast, IMG. 150 200 250 300 350 400 100 Thank you to Rama Dey-Rao, Ph.D. University at Buffalo MetaCyc and ExPASy ENZYME, determined that it inside outside E.R. Tech department. actually was a DNA Topoisomerase. The DNA Figure 3, even though HMPREF4062 0091 was a Hypothetical Jennifer R.Cooke, MPS, CSA (Program coordinator) WNY R-AHEC topoisomerase in an enzyme that aids in the breakage and protein. Tmhmm said that it very likely is transmembrane. www.buffalo.edu HMPREF0462_0095

rejoining of single stranded DNA.

HMPREF0462 0095

A Dna topoisomerase

Hypothetical protein