Annotation of the Campylobacter jejuni Genome from DNA Coordinates from locus tags CJE0008 to CJE0010 Janette Tatum, Wahida Jannat, Mi Rasa and Dana Pryor Moncrieffe Frederick Law Olmsted School and the Western New York Genetics in Research and Health Care Partnership

Abstract

Students in the research group of Frederick Law Olmsted's Science Club have been assigned to Three consecutive locus tags to annotate in the organism, Campylobacter jejuni. The genome annotation website GENI-ACT allows us to research basic information, sequence based similarity data, cellular localization data, alternative open reading frame, and structure based evidence. Interpretations of data are depicted by information given from BLAST results, using the amino acid sequence of Campylobacter jejuni. A hypothesis of whether the predicted product name is well suited for the gene is found at the very end of the research. According to the overall data of this group, our findings did not contradict the Genbank product names of the geness, except for Locus Tag CJE0010. Introduction

Campylobacter jejuni was noticed in 1886 by Theodor Escherich in kitten's' stool. The studies that progressed after that tells us that researchers discovered that Campylobacter jejuni was present in untreated and filtered lake water, unpasteurized milk, etc. It is known as the leading cause of bacterial food-borne diarrhoeal disease throughout the world. Campylobacter jejuni was also known as the most frequent antecedent to a form of neuromuscular paralysis known as Guillain-Barré syndrome in 2000.

Current studies tell us that Campylobacter jejuni is currently the leading cause of bacterial gastroenteritis in humans, that disease in humans is mainly caused by the zoonotic pathogen Campylobacter jejuni and that chickens and poultry meat are common hosts for the bacteria.. Campylobacter jejuni targets C-type lectin (SIGNR1, SIGNR3) and immunoglobulin-like receptors (TREM2, TREM3, LMIR5, LMIR8) causing gastroenteritis and Guillain-Barré syndrome.

Our team annotated three different gene sequences from the Campylobacter jejuni genome. After analyzing the sequences, we have determined the gene products: a small sub unit of glutamate synthase and ribonuclease HII to have been named correctly by the GENI-ACT.



Scanning electron microscopic view of *Campylobacter jejuni* present in chickens, wild animals, and humans.

Methods and Materials

Modules of the GENI-ACT (http://www.geni-act.org/) were used to complete Campylobacter jejuni 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- Cellular Localization Data	Gram Stain, TMHMM, SignalP, PSORT, Phobius	Is my protein in the cytoplasm, secreted or embedded in the membrane?
Module 4- Alternative Open Reading Frame	IMG Sequence Viewer For Alternate ORF Search	Has the amino acid sequence of my protein been called correctly by the computer?
Module 5- Structure-Based Evidence	TIGRfam, Pfam, PDB	Are there functional domains in my protein?

Results

Campylobacter jejuni CJE0008:

The initial proposed product of this gene by GENI-ACT was, small subunit of glutamate synthase. Numerous BLAST hits determined the gene product to be the same a the initial gene product predicted by GENI-ACT, using the amino acid sequence, the presence of wellcurated functional domains within the amino acid sequence, the cellular location of the amino acid sequence, and the enzymatic function of the amino acid sequence. Therefore final annotation is a small subunit of glutamate synthase.

Campylobacter jejuni CJE0009:

GENI-ACT initially proposed the product of this gene to be ribonuclease HII. The top BLAST hits for the amino acid sequence, the presence of well-curated protein functional domains within the amino acid sequence, the trans membrane topography of the amino acid sequence, and the cellular location of the amino acid sequence supported these proposals. In conclusion, the gene product is ribonuclease HII. Ribonuclease HII is involved in the degradation of the ribonucleotide moiety on RNA-DNA hybrid molecules carrying out endonucleolytic cleavage to 5'-phospo-monoester (5).

Campylobacter jejuni CJE0010:

The initial proposed product of the gene predicted by GENI-ACT was competence protein ComEA. The top BLAST hits for the amino acid sequence were multispecies DNA-binding protein. The top COG hit was COG1555: ComEA, with the descrioription of DNA uptake protein ComE and related DNA-binding proteins. Competence is the ability of a cell to take up exogenous DNA from its environment, resulting in transformation. It is widespread among bacteria and is probably an important mechanism for the horizontal transfer of genes. ComEA has been shown to be an integral membrane protein, as predicted from hydropathy analysis, with its C-terminal domain outside the cytoplasmic membrane (6). TMHMM predicts CJE0010 to have one transmembrane helx (Figure IV) and Psortb predicts CJE0010 to be a membrane protein (Figure V) consistent with ComEA being an intergral membrane protein.





0.15
9.82
0.01
0.01
0.01
9.82

Gene Locus	Geni-Act Gene Products	Proposed Annotation
008	glutamate synthase, small subunit	glutamate synthase, small subunit
009	ribonuclease HII	ribonuclease HII
010	competence protein ComEA	competence protein ComEA