

Annotation of *Campylobacter jejuni* at Locus Tags CJ0035c, CJ0809c, CJ0309c, CJ0025c, and CJ0765c

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Abstract

A group of genes from the microorganism *Campylobacter jejuni* 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

Campylobacter jejuni is a gram-negative bacteria and is a main cause for food poisoning and bacterial infections. *Campylobacter* comes from two Greek words, campylos and baktron, which mean "curved" and "rod". *Campylobacter* itself is in the shape of a curved rod and contains a single flagellum. It belongs to a genus of bacteria that often cause many bacterial infections worldwide. However, the genus is very diverse. Each of the species are so genetically and metabolically different from one another that some scientists believe they do not fit under the same genus at all. *Campylobacter jejuni* is considered to be one of the most significant species in its genus.

Campylobacter jejuni is commonly found in animal excrements. Disease usually results from the ingestion of contaminated food or water which can be treated with antibiotics. Under-prepared meat and poultry is also a primary source of the bacteria. However, *C. jejuni* can be killed by properly cooking chicken, pasteurizing milk, and chlorinating drinking water. *C. jejuni* participates in natural genetic transformation, so it exchanges DNA with other bacterium. It openly welcomes foreign DNA, which is how certain strains become resistant to antibiotics. *Campylobacter jejuni* may cause some serious health issues, but it is relatively treatable.



Scanning electron micrograph of *Campylobacter jejuni*. Credit: De Wood, Pooley, USDA's Agricultural Research Service. medicalxpress.com

Methods

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- 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?

Results

Gene Locus: CJ0035c		
Basic Information	DNA Coordinates	complement(52665..53867)
	DNA Length	1203 bp
	Amino Acid Sequence Length	400 aa
Sequence-based Similarity	COGS	AraJ- Predicted arabinose efflux permease, MFS family [Carbohydrate transport and metabolism]
	T-Coffee	Some conservation throughout
	Web-Logo	Sporadically conserved
Structure-based Evidence	TIGRFAMs	efflux_Bcr_CfiA; drug resistance transporter
	PFAMs	MFS_1: transporter, major facilitator family
	HMM Logo Key Residues	G60, G96, G133, W150
	PDB	Crystal structure of E. coli multidrug transporter MdfA in complex with deoxycholate
Cellular Localization	Transmembrane Helices	12
	Signal Peptide	None
	PSORTb Final Prediction	Cytoplasmic membrane

Campylobacter jejuni CJ0035c:

Data from the TIGRFAM, PFAM, and PDB databases support CJ0035c to be an efflux transporter that is possibly involved with drug resistance. Evidence from the TMHMM database indicate that this transporter is found in the membrane with 12 transmembrane helices.

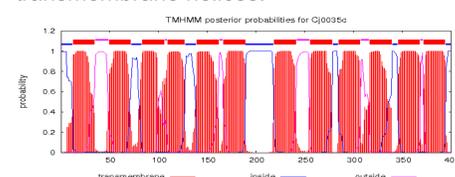


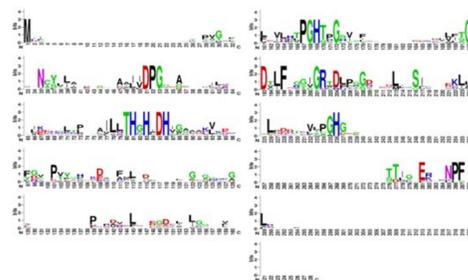
Figure 1 – TMHMM data for *Campylobacter jejuni* CJ0035c. The image on the left shows the cellular localization data from the TMHMM database indicating the presence of 12 transmembrane helices.

Gene Locus: CJ0809c		
Basic Information	DNA Coordinates	complement(760734..761330)
	DNA Length	597 bp
	Amino Acid Sequence Length	198 aa
Sequence-based Similarity	COGS	COG0491: GloB- Glyoxylase or a related metal-dependent hydrolase, beta-lactamase superfamily II
	T-Coffee	sporadically conserved
	Web-Logo	sporadically conserved
Structure-based Evidence	TIGRFAMs	GSH_gloB hydroxyacylglutathione hydrolase
	PFAMs	Lactamase_B- Metallo-beta-lactamase superfamily
	HMM Logo Key Residues	D21, T51, H52, H54, D56, H57, G149, D150, H197
	PDB	2ZWR: Entity 1 containing Chain A, B
Cellular Localization	Transmembrane Helices	none
	Signal Peptide	none
	PSORTb Final Prediction	cytoplasmic

Campylobacter jejuni CJ0809c:

COG, TIGRFAM, PFAM, and PDB data support CJ0809c to be a hydrolase protein whose main function is to catalyze the hydrolysis of a particular substrate. Cellular localization data predicts that this enzyme functions within the cytoplasm of the cell. Due to the presence of many orthologs, it can be inferred that this is a common protein in many different species of bacteria.

Figure 2 – WebLogo data for *Campylobacter jejuni* CJ0809c showing sporadic conservation throughout the middle of the protein and less conservation at the beginning and end.



Gene Locus: CJ0309c		
Basic Information	DNA Coordinates	complement(281311..281625)
	DNA Length	315 bp
	Amino Acid Sequence Length	104 aa
Sequence-based Similarity	COGS	COG2076- EmrE Multidrug transporter EmrE and related cation transporters [Defense mechanisms]
	T-Coffee	Well conserved at beginning and middle
	Web-Logo	Well conserved at beginning and middle
Structure-based Evidence	TIGRFAMs	no tigrfams given
	PFAMs	pfam00893- Multi_Drug_Res Small Multidrug Resistance protein; This family is the Small Multidrug Resistance (SMR) family
	HMM Logo Key Residues	Y59, G66
	PDB	no results given
Cellular Localization	Transmembrane Helices	4
	Signal Peptide	none
	PSORTb Final Prediction	cytoplasmic membrane

Campylobacter jejuni CJ0309c:

BLAST, COG, and PFAM data support CJ0309c to be a multidrug transporter in the membrane. This transporter acts as a pump to remove antibiotics harmful to the bacteria. Cellular localization data predicts that this protein is found in the membrane and contains 4 transmembrane helices.

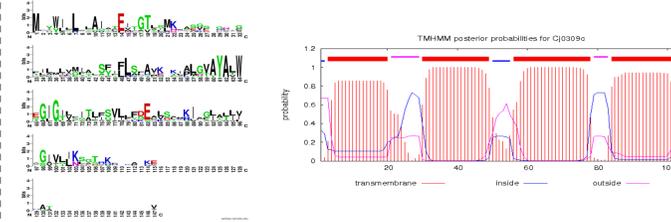


Figure 3 – WebLogo data and TMHMM data for *Campylobacter jejuni* CJ0309c

The Weblogo image on the top left shows that the protein was fairly well conserved in the beginning and middle, but then less conserved at the end. The cellular localization data on the top right from the TMHMM database shows the presence of 4 transmembrane helices.

Gene Locus: CJ0025c		
Basic Information	DNA Coordinates	32134..33519
	DNA Length	1386 bp
	Amino Acid Sequence Length	461 aa
Sequence-based Similarity	COGS	COG1823: L-cystine uptake protein TcyP, sodium:dicarboxylate symporter family [Amino acid transport and metabolism]
	T-Coffee	Fairly well conserved in the middle
	Web-Logo	Fairly well conserved in the middle
Structure-based Evidence	TIGRFAMs	None given
	PFAMs	SDF: transporter, dicarboxylate/amino acid:
	HMM Logo Key Residues	G12, G16, P45, G149, P185, S257, P263, G294, D369, T373, N376
	PDB	4KY0: Entity 1 containing Chain A, B, C
Cellular Localization	Transmembrane Helices	11
	Signal Peptide	none
	PSORTb Final Prediction	cytoplasmic membrane

Campylobacter jejuni CJ0025c:

COG, PFAM, and PDB data support Cj0025c to be an uptake protein found in the cellular membrane. It transports cystine that allows proteins to keep a three-dimensional structure. Cellular localization data supports the prediction that this is a membrane protein with 11 transmembrane helices. Due to the presence of many orthologs, it can be inferred that this is a common protein in many different species of bacteria.

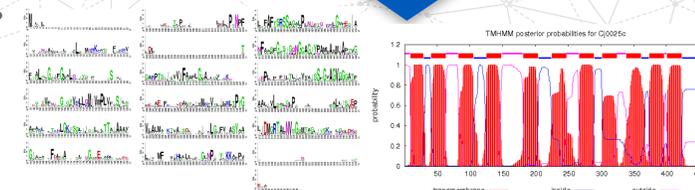


Figure 4 – WebLogo data and TMHMM data for *Campylobacter jejuni* CJ0025c

The Weblogo image on the top left shows that the protein was well conserved throughout the middle. The cellular localization data on the top right from the TMHMM database shows the presence of 11 transmembrane helices.

Gene Locus: CJ0765c		
Basic Information	DNA Coordinates	Complement(716609..717835)
	DNA Length	1227 bp
	Amino Acid Sequence Length	408 aa
Sequence-based Similarity	COGS	COG0124-HisS-Histidyl-tRNA synthetase [Translation, ribosomal structure and biogenesis]
	T-Coffee	Well conserved throughout
	Web-Logo	Well conserved in middle and end
Structure-based Evidence	TIGRFAMs	TIGR00442- hisS
	PFAMs	pfam13393-tRNA-synt_His
	HMM Logo Key Residues	Y29, G115, E117, G285, Y287
	PDB	2EL9: Entity 1 containing Chain A, B, C, D
Cellular Localization	Transmembrane Helices	none
	Signal Peptide	none
	PSORTb Final Prediction	cytoplasm

Campylobacter jejuni CJ0765c:

COG, TIGRFAM, PFAM, and PDB data support CJ0765c to be a tRNA ligase enzyme which makes sure the tRNA is appropriately bound to its amino acid, in this case histidine. Cellular localization data predicts this protein to function within the cytoplasm further supporting its role in the process of translation.

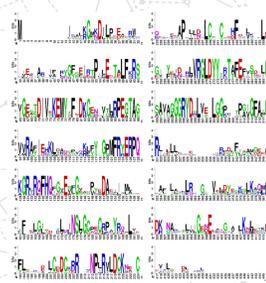


Figure 5 – WebLogo data for *Campylobacter jejuni* CJ0765c showing that the protein is mostly well conserved, and then less conserved at the beginning and end.

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.

Gene Locus	Geni-Act Gene Products	Proposed Annotation
CJ0035c	Drug resistance transporter	Drug resistance transporter
CJ0809c	Metal-dependent hydrolase	Metal-dependent hydrolase
CJ0309c	Multidrug transporter	Multidrug transporter
CJ0025c	Cystine uptake protein	Cystine uptake protein
CJ0765c	Histidyl-tRNA synthase	Histidyl-tRNA synthase

References

Campylobacter jejuni. (2018, May 11). Retrieved from https://en.wikipedia.org/wiki/Campylobacter_jejuni

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