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Annotation of the *Kytococcus sedentarius* Genome from 06900 to 06940

Kyle Glenn, Jaylen Greene, Maheer Sayeed and Dennis Bauer

Amherst Central High School and the Western New York Genetics and Research Partnership

Abstract

A group of three genes from the microorganism *Kytococcus sedentarius* (Ksed_06900 – Ksed_06940) 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, cellular localization data, potential alternative open reading frames, enzymatic function, presence or absence of gene duplication and degradation, the possibility of horizontal gene transfer, and the production of an RNA product. 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 in the database.

Background

Kytococcus sedentarius is an airborne and immobile gram positive coccoid bacterium, found predominantly in tetrad formation. Originally isolated from a playground slide submerged in salt water in the year 1944, *Kytococcus sedentarius* grows well in salt water at low concentrations[1].

Kytococcus sedentarius is a microorganism of interest for several reasons. This bacterium is a natural source of the oligoketide antibiotics monensin A and monensin B. *Kytococcus sedentarius* has been implemented as the etiological agent of a number of opportunistic infections including valve endocarditis, hemorrhagic pneumonia, and pitted keratolysis[1]. This bacteria causes foot infections for a lot of people, that makes their feet release a bad odor. Research for this genome is important so that humans can rid the world of these infesting bacteria, or at the very least to figure out if they have a positive purpose hidden in their DNA.

Figure 1. *Kytococcus sedentarius colonies on an agar plate*

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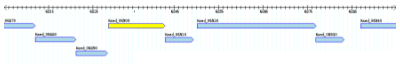


Figure 2. Gene neighborhood containing the locus tags analyzed in this study: Ksed_06900, Ksed_06910, Ksed_06940

Modules of GENI-ACT

(http://www.geni-act.org/) was used to complete *Kytococcus sedentarius* 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?
Module 6- Enzymatic Function	KEGG, MetaCyc, E.C. Number,	In what process does my protein take part?
Module 7- Gene Duplication/ Gene Degradation	Paralog, Pseudogene	Are there other forms of my gene in the bacterium? Is my gene functional?
Module 8- Evidence for Horizontal Gene Transfer	Phylogenetic Tree,	Has my gene co-evolved with other genes in the genome?
Module 9- RNA	RFAM	Does my gene encode a functional RNA?

Results

Kytococcus sedentarius 06900:

The initial proposed product of this gene by GENI-ACT was. This gene product proposal was supported by the top BLAST hits for the amino acid sequence, the presence of well-curated protein functional domains within the amino acid sequence, the transmembrane topography of the amino acid sequence, and the cellular location of the amino acid sequence. As such, the proposed annotation is a purine-cytosine permease-like transporter.

.*Kytococcus sedentarius* 06910:

The initial proposed product of this gene by GENI-ACT was a Xenopus laevis.This gene product proposal was supported by the top BLAST hits for the amino acid sequence, the presence of well-curated functional domains within the amino acid sequence, the cellular location of the amino acid sequence, and the enzymatic function of the amino acid sequence. As such, the proposed annotation is a Nicotinamidase-Like Amidase.

Kytococcus sedentarius 06920: No Data

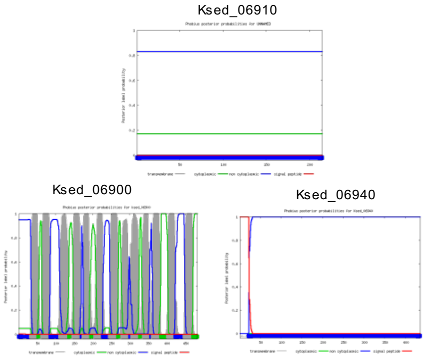
Kytococcus sedentarius 06940:

Gene 06940 is made of 436 nucleotides and it is found in the DNA of Kytococcus sedentarius. During sequence based similarities, the protein encoded by this gene was most similar to a protein *Mycobacterium tuberculosis*. However, in the structure based evidence section, Pfam predicted it to be part of the periplasmic binding protein clan. Cellular localization data deemed the protein gram-positive. PSORT-B confirmed that this gene is not in the cytoplasm of kytococcus sedentarius, but in the cell membrane itself. Gram-positive bacteria usually have a cell wall called peptidoglycan. Since PSORT-B also gave a high score for the gene to be located in the cell wall, the gene may also exists in the outer barrier off *Kytococcus sedentarius*. Finally, during the Enzymatic Function section, the gene map in kegg showed that gene 06940 is a phosphate and amino acid transporting gene involved in membrane transport. In conclusion, gene 06940 is a gram-positive phosphate transporting gene that is found in the cell membrane of *Kytococcus sedentarius.*

Web Logo

Proposed Interpretation

- The letters show how many times the amino acid appeared in the sequence.
- The larger letters represent amino acids repeated throughout the sequence.
- The different colored letters showed differences in the sequence.
- Different letters with the same color show different amino acids with the same function.



Ksed_06910

Ksed_06900

Ksed_06940

Figure 3. Phobius results for Ksed_06910, Ksed_06940 and Ksed_06900. Ksed_06910 had no transmembrane helixes, Ksed_06900 showed 13 transmembrane helixes and Ksed_06940 was predicted to have a signal peptide.

Proposed Products

Kytococcus sedentarius 06900:

The initial proposed product of this gene by GENI-ACT was a purine-cytosine permease-like transporter. This gene product proposal was supported by the top BLAST hits for the amino acid sequence, the presence of well-curated functional domains within the amino acid sequence, the cellular location of the amino acid sequence, and the enzymatic function of the amino acid sequence. This aids in the transport of nucleotides and metabolism. It transports from the membrane to the transmembrane to the cytoplasm and this is supported by the phobius model.

Kytococcus sedentarius 06910:

The initial proposed product of this gene by GENI-ACT was nicotinamidase-like amidase. After running a BLAST of the amino acid sequence for this gene, it can be surmised that this gene codes for Isochorismatase domain-containing protein 2. This protein is involved in creatine metabolism and nicotinamidase, converting nicotinamide to nicotinic acid and ammonia in the pyridine nucleotide cycle. It also contains isochorismatase, an enzyme that catalyzes the conversion of isochorismate to 2,3-dihydroxybenzoate and pyruvate, via the hydrolysis of the vinyl ether bond, and other related enzymes with unknown function.

Kytococcus sedentarius 06920:

N.A

Kytococcus sedentarius 06940:

Kytococcus Sedentarius 06940 is a phosphate transporting protein. It aids in the transportation of phosphates from the cytoplasm to the cell membrane. As a result, it is predominantly found active in the cell membrane. Its function may be used during cellular respiration for the recycling of ATP.

The GENI-ACT proposed gene product did not differ much from the proposed gene annotation for each of the genes.

Gene Locus	Geni-Act Gene products	Proposed Annotation
06900	Purine-cytosine permease-like transporter	Purine-cytosine permease-like transporter
09610	nicotinamidase-like amidase	nicotinamidase-like amidase
06920	DNA Helicase	DNA Helicase
06940	Phosphate binder	Phosphate transporter

References

1. Complete genome sequence of *Kytococcus sedentarius* type strain (541T).

Acknowledgments

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