

Annotation of the *Kytococcus sedentarius* Genome from DNA Coordinates 06970 to 06980

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Abstract

A group of 3 consecutive genes from the microorganism *Kytococcus sedentarius* (Ksed_06970 – Ksed_06980) was annotated using the collaborative genome annotation website GEN-FACT. These genes were analyzed based on their 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 annotation for any of the genes in the group and as such, the genes appear to be correctly annotated by in their database.

Introduction

Kytococcus sedentarius is a strictly aerobic, non-motile, non-encapsulated, and non-endospore forming gram-positive coccoid bacterium, found predominantly in tetrad formation. This organism is classified as a chemoheterotroph, as it requires methionine and several other amino acids for growth. Originally isolated from a microscope slide submerged in sea water in 1944, *Kytococcus sedentarius* grows well in sodium chloride at concentrations less than 10% (w/v).

According to Sims et al. (2009), *Kytococcus sedentarius* is a microorganism of interest for several reasons. This bacterium is a natural source of the oligopeptide antibiotics monensin A and monensin B (Sims et al., 2009). *Kytococcus sedentarius* has been implemented as the etiological agent of a number of opportunistic infections including valve endocarditis, hemorrhagic pneumonia, and pitted keratolysis (Sims et al., 2009). Finally, the phylogeny of this microorganism is a source of interest, as it is a member of the family *Dermaoocaceae* within the actinobacterial suborder *Micromonosorales*, which has yet to have been thoroughly studied utilizing bioinformatics (Sims et al., 2009).

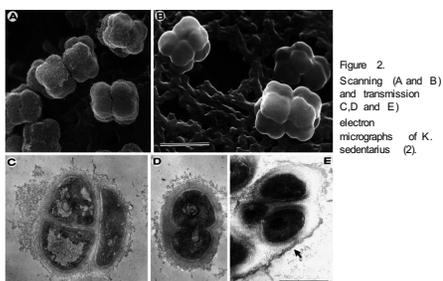
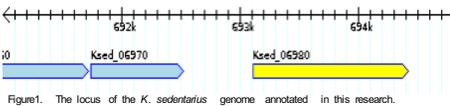


Figure 2. Scanning (A and B) and transmission (C, D and E) electron micrographs of *K. sedentarius* (2).

Methods and Materials

Modules of the GENI-ACT (<http://www.geni-act.org/>) were 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* 06970:** The initial proposed product of this gene by GENI-ACT was a Phosphate transport protein family. 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, and the cellular location of the amino acid sequence. As such, the proposed annotation is a Phosphate-transporting ATPase.

***Kytococcus sedentarius* 06980:** The initial proposed product of this gene by GENI-ACT was a transposase family protein. 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 transposase. A gene for transposase in an organism like *Kytococcus sedentarius* codes for the production of transposons. Transposons are sections of DNA that can move around to different parts of a specific chromosome to increase the rate of mutation of an organism. They also play a vital role to researchers while altering the DNA of a living organism.

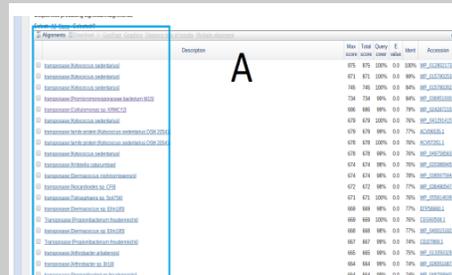


Figure A: Results of an amino-acid base comparison search for Ksed_06980 show the high levels of aa similarity between Ksed_06980 and other versions of transposase. Base sequences provide a key tool for understanding function.

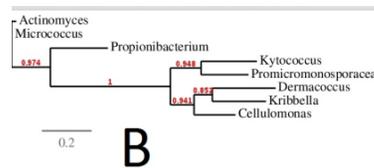


Figure B: This is a simple evolutionary relationship map between *Kytococcus sedentarius* and other organisms that through searches were revealed to have similar amino acid sequences.

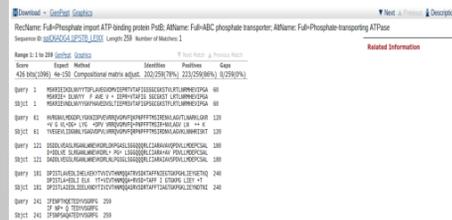


Figure C: A BLAST of Ksed_06970. The low e value of 4e-150 makes it very likely that Ksed_06970 is for a Phosphate transport protein.

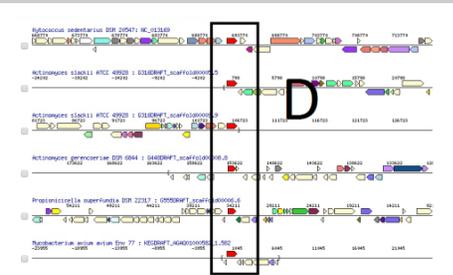


Figure D: Analyzing similar genes in related organisms allows the conclusion to be drawn that this gene, Ksed_06980, was a result of vertical rather than horizontal transfer. This means that in its evolution, *Kytococcus sedentarius* got this gene from ancestral organisms, not other contemporary organisms that it interacted with.

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
06970	Phosphate Transport family protein	Phosphate-transporting ATPase
06980	Transposase family protein	Transposase

References

- Sims et al. (2009). Complete genome sequence of *Kytococcus sedentarius* type strain (541T). *Standards in Genomic Sciences* 12 - 20.
- Can. J. Microbiol. 44: 1007-1011 (1998)

Acknowledgments

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