

Annotation of the *Kytococcus sedentarius* Genome from Locus Tags Ksed_09730 to Ksed_09760

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Abstract

A group of four consecutive genes from the microorganism *Kytococcus sedentarius* (Ksed_09730 – Ksed_09760) were annotated using the collaborative genome annotation website GENI-ACT. The proposed gene product name for each gene was assessed in terms of the general genomic information, amino acid sequence-based similarity data using BLAST, CDD, T-Coffee, and WebLogo analysis, structure-based evidence from the amino acid sequence, cellular localization data (TIGRFAM and Pfam), 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 in the r database.

Methods

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?

Introduction

Kytococcus sedentarius is a strictly aerobic, non-motile, non-encapsulated, and non-endospore forming gram positive coccoid bacterium, found usually in tetrad formation. This organism is classified as a chemoheterotroph, since it requires several 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%.

Kytococcus sedentarius is of interest for several reasons. It is a source of the antibiotics monensin A and monensin B (Sims et al., 2009). It has also been found to be the cause of a number of opportunistic infections including valve endocarditis, hemorrhagic pneumonia, and pitted keratolysis (Sims et al., 2009). Finally, the evolutionary history of *K. sedentarius* is of interest because it is a member of the family Dermacoccaceae, which has not yet been thoroughly studied using bioinformatic analysis (Sims et al., 2009).

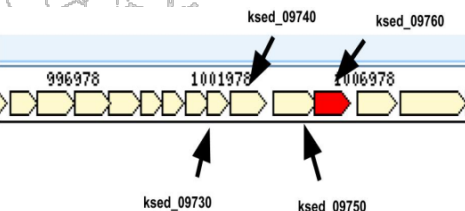


Figure 1. The locus tags and relative position of the genes under investigation in this research.

Results

Ksed_09730:

The initial proposed product of this gene by GENI-ACT was a Phosphoribosyl-AMP cyclohydrolase. This product proposal was supported by the top BLAST hits, the cellular location of, and the enzymic function of the amino acid sequence. This protein is involved in the 2nd and 3rd steps of the triggering of a gene that synthesizes the amino acid L-histidine from the enzyme 5-phospho-alpha-D-ribose-1-diphosphate

Ksed_09740:

The initial proposed product of this gene by GENI-ACT was a cysteine desulfurase family protein. This gene product proposal was supported by the top BLAST hits for the amino acid sequence, the cellular location of the amino acid sequence, the results from TMHMM website, Phobius and other resources we used. As such, the results confirmed that Ksed_09740 was in fact a cysteine desulfurase family protein.

Ksed_09750:

The initial proposed product of this gene by GENI-ACT was HNH endonuclease. This product proposal was supported by the first PFAM hit HNH endonuclease is found in bacteria and viruses. This family includes pycocins, colicins and anaredoxins.

Ksed_09760:

The initial proposed product of this gene by GENI-ACT was a tRNA methyltransferase. This gene product proposal was supported by the top BLAST hits for the amino acid sequence, the cellular location of the amino acid sequences. This enzyme transfers one-carbon group methyltransferases, and helps with different steps of protein synthesis, such as the reinforcement of the codon-anticodon interaction, the regulation of wobble base pairing, and the stabilization of tRNA structure.

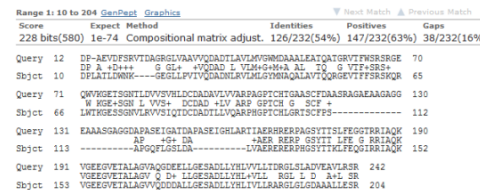


Figure 2 - Ksed_09730 BLAST hit using Swiss-Prot that shows the basic information of this specific alignment of *Kytococcus sedentarius* i.e. Alignment length, score, e-value, etc.

Prediction of

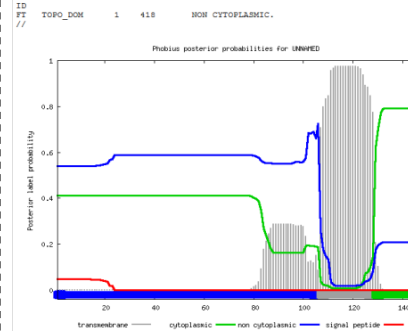


Figure 3 - Phobius graph of Ksed_09740. This graph indicates that the Ksed_09740 protein is found inside the cytoplasm.

212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227

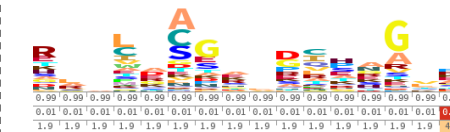


Figure 4 - HMM Logo for Ksed_09750 showing an area of high variability, shown by the large number of amino acids at each location.

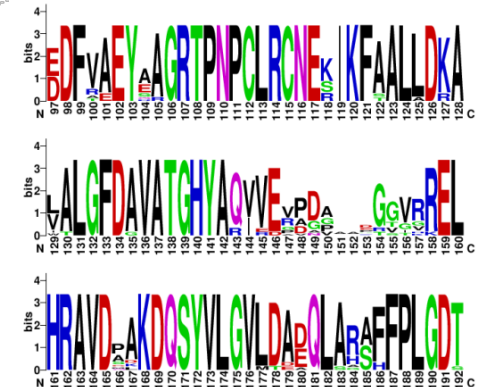


Figure 5 - WebLogo result for Ksed_09760. This portion of the WebLogo shows an area where the amino acids are highly conserved. This is indicated by a single large letter at a specific location. Areas of higher variability have many amino acid symbols stacked at the same location.

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
09730	Cyclohydrolase	Cyclohydrolase
09740	Cysteine desulfurase family protein	Cysteine desulfurase family protein
09750	HNH Endonuclease	HNH Endonuclease
09760	Methyltransferase	Methyltransferase

References

Sims et al. (2009). Complete genome sequence of *Kytococcus sedentarius* type strain (541T). Standards Genomic Sciences, 12 - 20.

Acknowledgments

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