

Annotation of Locus Tags Ksed_07750, Ksed_07840, Ksed_07810, Ksed_07790 of the *Kytococcus sedentarius* Genome

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Abstract

A group of genes from the microorganism *Kytococcus sedentarius* (Ksed_07750, Ksed_07840, Ksed_07810, and Ksed_07790) 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. 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 nr database.

Introduction

Kytococcus sedentarius is a marine dwelling, Gram positive bacterium that produces the polyketide antibiotic against pathogens. It is aerobic and can only grow when certain amino acids are present. It is in the *Dermaoocaceae* family and is primarily found as part of human skin and groundwater. It is well-known as a producer of antibiotics such as monesin A and monesin B. Its optimum growth temperature is between 25-37 degrees Celsius (Figure 1).

Kytococcus sedentarius is mostly known as a pathogen that creates pitted keratolysis which commonly affects feet and hands (Figure 2). The benefit of actually annotating genes of *Kytococcus sedentarius* is that it can help us better understand how genetic causes damage.

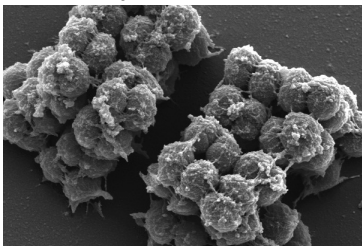


Figure 1. A scanning electron micrograph of *Kytococcus sedentarius* (Taken from Sims et al., 2009)



Figure 2. An image of a food showing the appearance of pitted keratolysis. (Taken with <http://www.medhealth.net/Pit-the-keratolysis.html>).

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?

Results

Kytococcus sedentarius 07750:

The initial proposed product of this gene by GENI-ACT was an alcohol dehydrogenase [*Nocardia vinacea*]. 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 an alcohol dehydrogenase. I have discovered that my protein has two transmembrane helices as seen in Figure 3.

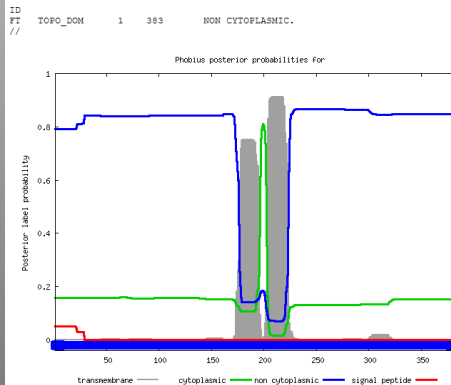


Figure 3- Phobius probability graph for *Kytococcus sedentarius* 07750 showing the presence of 2 transmembrane helices.

Kytococcus sedentarius 07810:

The initial proposed product of this gene by GENI-ACT was a phosphoribosylaminoimidazolecarboxamide formyltransferase. 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 phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase.

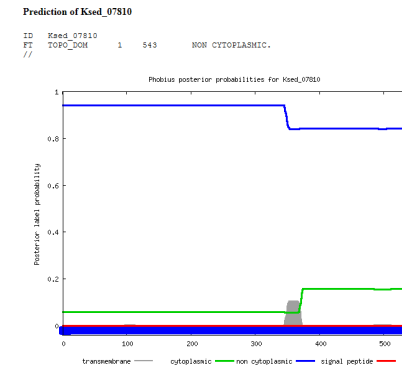


Figure 4- Phobius probability graph for *Kytococcus sedentarius* 07810, showing the protein lacks both transmembrane helices and an signal peptide.

Kytococcus sedentarius 07790:

The initial proposed product of this gene by GENI-ACT was Peptidase A24. 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 Peptidase A24. I have discovered that my protein strand is within the Cytoplasmic Membrane, with seven transmembrane helices, as shown on my Phobius Probability Graph (Figure 5).

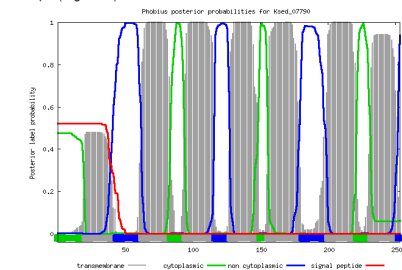


Figure 5- Phobius probability graph for *Kytococcus sedentarius* 07790, showing it has 7 transmembrane helices.

Kytococcus sedentarius 07840:

The initial proposed product of this gene by GENI-ACT was malate dehydrogenase. 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 malate dehydrogenase.

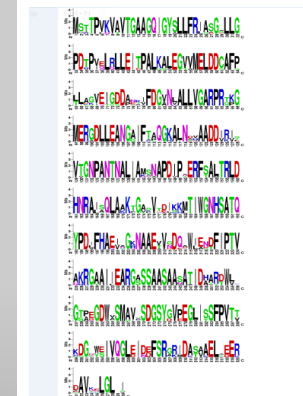


Figure 6. WebLogo of Ksed_07840. From the amino terminus to the carboxyl terminus, the letters are mainly big telling us that the amino acids are mainly similar between the divisions in the sequence. The amino acid sequence is conserved (mainly big letters). The protein is found somewhere in the bacteria. It won't be found in the cytoplasmic membrane.

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
07750	Alcohol dehydrogenase [Nocardia vinacea]	Alcohol dehydrogenase [Nocardia vinacea]		
07840	Malate dehydrogenase	Malate dehydrogenase		
07810	phosphoribosylaminoimidazolecarboxamide formyltransferase	phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase		
07790	Peptidase A24	Peptidase A24		

References

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

Acknowledgments

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