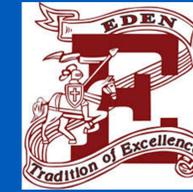


Annotation of the *Kytococcus sedentarius* Genome from Locus Tags

Ksed_26420 to Ksed_26460

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Abstract

A group of five consecutive genes from the microorganism *Kytococcus sedentarius* (Ksed_26420 – Ksed_26460) 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 in the computer 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), *K. sedentarius* is of interest for several reasons. It is known for the production of oligoketide antibiotics as well as for its role as an opportunistic pathogen causing valve endocarditis, hemorrhagic pneumonia, and pitted keratolysis. It is strictly aerobic and can only grow when several amino acids are provided in the medium. The strain described in this report is a free-living, nonmotile, Gram-positive bacterium, originally isolated from a marine environment. (Sims et al., 2009).

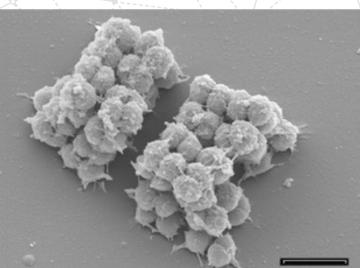


Figure 1. Scanning electron micrograph of *K. sedentarius* strain 541T (Manfred Rohde, Helmholtz Centre for Infection Biology, Braunschweig)

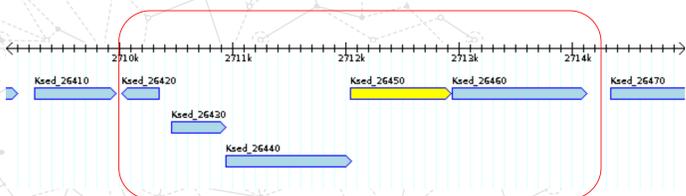


Figure 2. The locus tags of Ksed_26420 – Ksed_26460 and relative position of the genes under investigation in this research

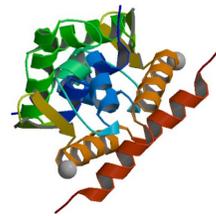
Methods

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?
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

Ksed_26420: The initial proposed product of this gene by GENI-ACT was a transcriptional regulator, ArsR family. This gene product proposal was supported by the top BLAST hits for the amino acid sequence with several ArsR family transcriptional regulator genes across many different Genera. Pfam supported this with only one result and the PDB gave us the possible structure of a transcriptional regulator for arsenical resistance



As such, the proposed annotation is most likely a transcriptional regulator, ArsR family

Ksed_26430: The initial proposed product of this gene by GENI-ACT was a lactoylglutathione lyase-like lyase. Pfam-Glyoxalase/Bleomycinresistanceprotein/Dioxygenase Superfamily. This was heavily supported by BLAST results.

Sequence producing significant alignments

Accession	Score	E	Query Start	Query End	Subject Start	Subject End	Description
U00000	128	100	14	117	100	117	Escherichia coli
U00000	101	17%	14	117	100	117	Escherichia coli
U00000	100	17%	14	117	100	117	Escherichia coli
U00000	176	17%	14	117	100	117	Escherichia coli
U00000	177	17%	14	117	100	117	Escherichia coli
U00000	178	17%	14	117	100	117	Escherichia coli
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