Annotation of the *Kytococcus sedentarius* Genome from 06900 to 06940
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Abstract
A group of three genes from the microorganism *Kytococcus sedentarius* (Ksed_06900 – Ksed_06940) were annotated using the collaborative genome annotation website G ENI-A CT. 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 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.

*Kytococcus sedentarius* is a microorganism of interest for several reasons. Its bacterium is a natural source of the glycolipid antibiotics monacins A and B. *Kytococcus sedentarius* has been implicated as the etiological agent of a number of opportunistic infections including valve endocarditis, hemolytic pneumonitis, and pitted keratolysis. This bacterium 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

Figure 2. Gene neighborhood containing the locus tag region Ksed_06900

Results
*Kytococcus sedentarius* 06900:
The initial proposed product of this gene by G ENI-A CT was a leucine auxotroph. This gene product proposed 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 topology of the amino acid sequence, and the cellular location of the amino acid sequence. As such, the proposed annotation is a pantothenate permease-like transporter.

*Kytococcus sedentarius* 06910:
The initial proposed product of this gene by G ENI-A CT was a putative protein. This gene product proposed 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, 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* 06930:
Gene 06940 is made of 346 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 tuberculosum. 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 a membrane protein. PSORT-B confirmed that this gene is not in the cytoplasm of *Kytococcus sedentarius*, but in the cell membrane itself.

Proposed Products
*Kytococcus sedentarius* 06900:
The initial proposed product of this gene by G ENI-A CT was a putative permease-like transporter. This gene product proposal was supported by the top 3 BLAST hits for the amino acid sequence, the presence of well-curated protein functional domains within 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 cytoplasm and this is supported by the phoU model.

*Kytococcus sedentarius* 06910:
The initial proposed product of this gene by G ENI-A CT 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 biosynthetase-domain-containing protein 2. This protein is involved in the metabolism and nicotinamidase, converting nicotinic acid to nicotinic acid and ammonia in the pyridine nucleotide cycle. It also contains isochores mase, an enzyme that catalyzes the conversion of isochores to 2,3-bisphosphoglycerate and pyruvate, via the hydration of the 3-phosphoglycerate.

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

Ksed_06910

Ksed_06900

References
1. Complete genome sequence of *Kytococcus sedentarius* type strain (2014).

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