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

David Personius, Amelia Schaeffer, and Paul Weber
Amherst Central High School and the Western New York Genetics in Research Partnership

Abstract

A group of 3 conserved genes from the microorganism *Kytococcus sedentarius* (Ksed_06970 – Ksed_06980) was annotated using the collaborative genome annotation website GENI-ACT. These genes were analyzed based on their general genomic information, amino acid sequence-based similarities, 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 in their database.

Introduction

*Kytococcus sedentarius* is a strictly aerobic, non-motile, non-endospore forming gram-positive acid resistant bacterium, found predominantly in soil formation. This organism is classified as a chemoheterotroph, as it requires glucose and several other amino acids for growth. Originally isolated from a microscope slide submerged in seawater in 1944, *Kytococcus sedentarius* grows well in sodium chloride 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 oligoketide antibiotics menenin A and menenrin 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 Dermacoccaceae within the adinobacter suborder Micrococcineae, which has yet to have been thoroughly studied utilizing bioinformatics (Sims et al., 2009).

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:

**Genome Database**

Ksed_06970, Ksed_06971, and Ksed_06980 from the Ksed_06970 and other versions of transposase. Base sequences provide a key tool for understanding functions.

**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, the transmembrane topology of the amino acid sequence, and the cellular localization 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 Phosphate-transporting ATPase. A 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 localization 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 is a specific amenity 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.

**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.

**References**


**Acknowledgments**

Dr. Rama Dey, Rao, Dr. Stephen Koury
Supported by NSF ITEST Strategies Award Number 1311902