Annotation of the *Kytococcus sedentarius* Genome from DNA Coordinates 512848 to 515799

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### Abstract

A group of consecutive 7 genes from the microorganism *Kytococcus sedentarius* (Ksed_05160 – Ksed_05190) 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, and potential alternative open reading frames. The Genbank proposed gene product name did not significantly differ 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.

### Introduction

*Kytococcus sedentarius* is a strictly aerobic, non-motile, non-encapsulated, and non-endospore forming gram positive coccoid bacterium, found predominantly in tetrat 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), *Kytococcus sedentarius* is a microorganism of interest for several reasons. This bacterium is a natural source of the oligoketide antibiotics monensin A and monensin 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 as the etiological agent of a number of opportunistic infections including valve endocarditis, hemorrhagic pneumonia, and pitted keratolysis. This research group is interested in the genes involved in the resistance mechanisms of *Kytococcus sedentarius*.

### Methods and Materials

#### Modules

- **Module 1: Basic Information**
  - Activities
    - DNA Coordinating and Sequence
    - Protein Sequence
  - Questions Investigated
    - What is the sequence of my protein?
  - **Module 2: Sequence-Based Similarity Data**
    - Blast, CDD, T-Coffee, WebLogo
    - **Module 3: Cellular Localization**
      - Green Stain, TIGRFAMs, PSI-PRT
    - **Module 4: Alternative Open Reading Frame**
      - BLOG Sequence Viewer For Alternate ORF Search
    - **Module 5: Structure-Based Evidence**
      - TCGRam, Pfam, PDB

### Results

#### *Kytococcus sedentarius* Ksed_05160

**Basic Information**
- DNA Coordinates: 512848 - 512859
- DNA Length: 1566 Base Pairs

**Sequence Based Similarity**
- COG: COG0651: HyfB
- T-Coffee and Weblogo alignments show that the protein product of Ksed_05160 is well conserved. Data supports this protein has not been changed much through time. COG results indicate this protein to be a sodium antiporter, which is inferred to be electrogenic (produces a change in electrical potential of a cell). Cellular localization data supports an integral transmembrane protein because it has three helices, and no signal peptides.

**Cellular Localization**
- Transmembrane Helices: Well conserved in the middle from amino acid 185 to 447.
- Signal Peptide: No signal peptide
- PSORTB Final Prediction: Cytoplasmic Membrane
- Alternative ORFs: None
- Structure Based Evidence: HMM Logo Key Residues: E12, K92, W101, K168, A172, S174, F212, N283

**Structure Based Evidence**
- TCGRam: [Image]
- Pfam: [Image]
- PDB: [Image]

### References


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**Figure 1** – Cellular Localization Data for *Kytococcus sedentarius* 05160, 05170, 05180, and 05190. All are predicted to be transmembrane proteins. Due to the predicted functions, it is probable that these proteins are involved in reactions within the membrane as well as inside and outside the bacterial cell.