Gene Annotation of Ksed_04930, a Putative Signal Transduction Histidine Kinase in *Kytococcus sedentarius*

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**Abstract**

*Kytococcus sedentarius* is a Gram-positive bacterium that is arranged in packets of eight in a cubical shape (1). *Kytococcus sedentarius* was found on a partially submerged swing set in San Diego California (2). It is a coccoid or spherical shaped bacterium that can live on the skin (1).

The genome of *Kytococcus sedentarius* 541,278,024 bp long and codes for 2,703 genes. Of the 2,703 genes predicted, 2,639 were identified proteins by DIAMANT. The remaining ones were annotated as hypothetical genes. 72.1% of these genes were assigned with a predicted function while the remaining ones were annotated as hypothetical proteins.

The purpose was to look for a signal transduction histidine kinase involved in adding a phosphate group to a protein. A section of the bacteria’s genome was annotated by the GENI-ACT database for original research. 2,785,024 bp long and codes for 2,703 genes. The gene that we investigated was Ksed_04930, Ksed_04930, a gene product in the cytoplasmic membrane. This protein-coding gene codes for 389 amino acids.

**Introduction**

*Kytococcus sedentarius* is a Gram positive bacterium that is arranged in packets of eight in a cubical shape (1). *Kytococcus sedentarius* was found on a partially submerged swing set in San Diego California (2). It is a coccoid or spherical shaped bacterium that can live on the skin (1).

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**Results**

**Materials and Methods**

Modules of the GENI-ACT (http://www.geni-act.org/) were used to complete *Kytococcus sedentarius* genome annotation. The modules are described below:

- **Module 1 - Basic Information** Gene Coordinates and Protein Sequences
- **Module 2 - Sequence-Based Similarity Data** Blast, CDD, T-Coffee, WebLogo
- **Module 3 - Cellular Localization Data** Gram Stain, TMHMM, SignalP, G-Find, Phobius
- **Module 5 - Structure-Based Evidence** TDIWeb, P3D, PDB
- **Module 6 - Enzymatic Function** KEGG, MetaCyc, E.C. Number
- **Module 7 - Gene Duplication and Gene Degradation** Polarity, Pseudogene
- **Module 8 - Evidence for Horizontal Gene Transfer** Phylogenetic Tree
- **Module 9 - RNA** Rfam

**Results continued**

**Figure 1.** Top BLAST hit in UniProtKB/SwissProt database (histidine protein kinase, (e-value 3-48)).

**Figure 2.** TMHMM graph predicting 2 transmembrane helices in Ksed_04930.

**Figure 3.** This graph is the Web logo for the T-COFFEE of the orthologs of Ksed_04930. It shows that the gene is conserved except at the C-terminus.

**Figure 4.** This is the Pfam-B section of the gene notebook, and this shows the location of the gene product in the cytoplasmic membrane. A protein with transmembrane helices should be found in cytoplasmic membrane.

**Figure 5.** Phylogenetic tree for Ksed_04930. It shows Micrococcus as the closest neighbor. *Kytococcus* and *Micrococcus* are the classified the same to the family level. This indicates Ksed_04930 likely did not arise in *Kytococcus* by lateral gene transfer.

**Figure 6.** This is the ortholog neighborhood viewer of the gene Ksed_04930. It shows evidence of transfer by heredity. The neighborhood is conserved in close relatives of *Kytococcus*.

**Conclusions**

The Gene product for ksed_04930 appears to be a Histidine protein kinase and its main purpose is to catalyze the reaction bonding a phosphate group to a protein.

**Literature Cited**


2. (http://biocyc.org/KSED478801/organism-Fummary?object=KFED478801)

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