Annotation of the *Kyctococcus sedentarius* Genome for Ksed_07190- Ksed_07240

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Abstract

A group of conserved 8 genes from the microorganism *Kyctococcus sedentarius* (Ksed, 07190 - Ksed, 07240) 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 sequences, cellular location data, potential alternative open reading frames and the possibility of horizontal gene transfer. The Genbank proposed gene product name did not differ significantly from the proposed gene annotation for most of the genes in the group. Ksed, 07190 is a ho-rodialc gene. Otherwise, the genes appear to be correctly annotated by the database.

Introduction

The *Kytococcus* is a sedentarius bacterium is an aerobic, free-living, non-motile bacterium. It has a high GC content of 72%. The gram positive and isolated from an marine environment, Methionine, along with other a minor acid in the medium, are essential for growth. *Kytococcus sedentarius* is found in the Dermacoccaceae family. It is known for the production of lipopolysaccharide. It is an opportunistic pathogen, causing various endocarditis, hemorrhagic pneumonia, and pitted arthritis. The optimal growth temperature is around 25-35 degrees celcius in a NaCl (sodium chloride) concentrations up to 10%. It does not form spores, and its GPC in the bradich.

The main purpose of the study was to annotate the assigned genes (Ksed, 07190-07240). Through annotation, cell location and establishment of whether the genes were hypothetical or functional, were determined. Another purpose of this project was to add further knowledge regarding *Kytococcus sedentarius* to the science community.

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:

**Module 1: Basic Information Module**
- DNA Coordinates and Sequence Information
- The name of the gene and protein
- Where is the nucleotide position?

**Module 2: Gene Product Module**
- Predicted ORF (Open Reading Frame)
- Gene name
- Methionine, Threonine, Phosphorylation, Hydroxylation
- The protein is secreted or secreted in the extracellular space?

**Module 3: Evidence for Homologous Gene Transfer**
-blast of the region near the homologous genes
- Amino acid sequence
- Phylogenetic Tree
- The observation for the homologous genes

**Kytococcus sedentarius 07190**
- Protein BLAST resulted in a top hit including a hypothetical protein; an organism known as *Tannarococcus sp. S76*. BLAST hit 42 agreed with the predicted gene product by Geni-ACT, an ABC transporter permease protein. Pfam results indicated the gene was part of the T7 family with 4 domains. THMM had 10 predicted transmembrane helixes. PSORT-B showed a cytoplasmic membrane score of 100, the highest possible score. RhoBisogen generated a graph illustrating the tRNA membrane. The absence of a signal peptide predicted in SignalP indicating it does not have a cell.

**Kytococcus sedentarius 07200**
- according to BLAST the top hit is a marrode ABC transporter ATP-binding protein and the organism is *Tannarococcus sp. S76*. The second top hit is marrode ABC transporter ATP-binding protein and the organism is *Propionibacterium propionicum*. The Weblogo sequence logo for this gene is well conserved. The Gram stain of the marrode is Gram-Positive. PSORT-B hit 1 predicted is a Cytoplasmic membrane.

**Results**

**Kytococcus sedentarius 07190**
- The predicted gene product by GENI-ACT was histidine kinase. BLAST results from SeaPort correlate with the predicted gene. Signal transduction histidine kinase was the top hit from COG. **Kytococcus sedentarius 07220**
- The original gene predicted by GENI-ACT was a response regulator with a Che Y-repressor domain and HTH DNA-binding domain. The Pfam prediction was a response regulator, repressor domain, bacterial regulatory proteins, LuxR family. The assessment of the BLAST resulted in the top gene product hit of DNA-binding response regulator. The COG was the same family as the original genes predicted. The WEBLOGO was well conserved indicating a match.

**Conclusion**

The GENI-ACT proposed gene product did not differ significantly from the proposed gene annotation for most of the genes in the group and as such, the genes appear to be correctly annotated as the database. Ksed_07190 is the exception and may be a hypothetical gene.

**References**

ATP-binding domain of ABC transporters from Wikipedia, 2016

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