Annotation of the *Kytococcus sedentarius* Genome from DNA Coordinates 06950 to 06960

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Abstract

A group of seven genes from the microorganism *Kyococcus sedentarius* (Ksed_06950 – Ksed_06960) were annotated using the collaborate genome annotation website GENI-AC. The Genbank proposed gene product name for each gene was assessed in terms of the general genome information, amino acid sequence similarity, blast hit, signal transduction function, putative activity opens 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 nr database.

Introduction

*Kyococcus sedentarius* is a strictly aerobic, non-motile, non-encapsulated, and non-endospore forming gram positive co-coid bacterium, found predominantly in leaf litter. This organism is classified as a chromobacterium, or a rickettsi-like parasite and an overall amino acid for growth. Originally isolated from a mesocline slide submerged in sea water in 1944, *Kyococcus sedentarius* grows well in sodium chloride concentrations less than 10% (w/v).

According to Sims et al. (2009), *Kyococcus sedentarius* is a microorganism of interest for several reasons. This bacterium is a natural source of the antibiotic amoxicillin and menanthen B (Sims et al., 2009). *Kyococcus sedentarius* has been implemented as a biological 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 Dermatococccaeae within the actinobacterial suborder Micrococcaceae, which has yet to have been thoroughly studied utilizing bioinformatics (Sims et al., 2009).

This research poster contains information about two genes in *Kyococcus sedentarius*. Ksed_06950 and Ksed_06960. As seen above, they are next to each other in the gene sequence. Their proposed products are actually similar. They are both ABC-type transporters. Also, as seen above, the genes are about the same length and pointing in the same direction. If the arrows are pointing to the right, it means the genes are on the forward strand of the DNA. The products proposed by the computer for the other surrounding genes are similar to these proposed products. This area of the genome seems to have to do with phosphorus binding and transport.

Methods and Materials

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

**Ksed_06950**

The top gene product was Phosphate transport protein from *Mycobacterium* (with an alignment length of 284). And a 

**Ksed_06960**

Also, results were found in BLAST in the swissprot database with low e-values that support the proposed product, and swissprot has less information but more reliable information than nr.

This next image shows the domains of the amino acid sequence that are transmembrane, intracellular and extracellular. There are many places, seen in red, where the protein crosses the membrane. There are a few large gaps between these crossings, however, where the protein is outside of the membrane.

**Ksed_06960**

The initial proposed product of this gene by GENI-AC was a phosphate ABC transporter membrane protein. This gene product proposal was supported by the top BLAST hits for the amino acid sequence. The image below shows the amino acid sequence for this gene compared with the amino acid sequence for phosphate ABC transporter permease (Cithh coa sp. CH26A) With a very low e-value, these proteins are very similar to one another, though they are found in different organisms.

**Ksed_06950**

The following image is another BLAST hit with a very low e-value. This protein from another organism is similar to what the computer predicted for Ksed_06960’s product, both in name and sequence.

**Ksed_06960**

The top gene product was Phosphate transport protein from *Mycobacterium* (with an alignment length of 284). And a 

**Ksed_06950**

The Cytoplasmic membrane score in PSORT-B was also relatively high. It was 10.00, while Cytoplasmic, Cell wall and Extracellular scores were all zero. The PSORT-B final prediction was Cytoplasmic membrane 10.00. There is a Shine-Dalgarno sequence 5 to 15 bases upstream of the start codon. Also, names bound in TGIFAM COG names and names of paralog gene products in *Kyococcus sedentarius* were found that are similar to the name of the proposed product.

Conclusion

The GENI-AC 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.

For Ksed_06950, the proposed product is the same as what the computer called: phosphate ABC transporter membrane protein. The blast hits with low e-values support this conclusion. The TMHMM posterior probability graph supports the idea that the protein is bound in the membrane. The large gaps could have biological functions or be places where the amino acid wrap around, putting certain transmembrane sections next to each other that aren’t shown next to each other in the graphical representation. Also, the shine-dalgarno sequence 5 to 15 bases upstream of the start codon suggests that the amino acid sequence of the protein has been called correctly by the computer.

References


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