Gene Annotation of Ksed_04890, a Hypothetical Protein of Unknown Function in Kytococcus sedentarius

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Abstract

Kytococcus sedentarius is an aerobic, gram positive organism found on a partially submerged slide. Students at Westfield Academy and Central School have annotated individual genes in order to further understand the function of this organism. Eight modules on GENI-ACT were completed in order to reach conclusions on the function of each gene. It is through these steps that the gene product Ksed_04890 was found to be a hypothetical protein of un-known function. However, a hypothesis was formulated that it can that Ksed_04890 may be a new transposase or a non-functional mutation of a transposase based on multiple sequence alignment of Ksed_04890 with a number of short transposase sequences found in the Kytococcus genome.

Introduction

Kytococcus sedentarius cells are spherical and occur predominantly in tetrads. K. sedentarius is Gram-positive, nonmotile, non-encapsulated, and not endospore-forming. Kytococcus sedentarius is strictly aerobic, requires methionine and grows well in NaCl at concentrations up to 10%.

The genome of Kytococcus sedentarius has 2,785,024 base pairs coding for 2703 genes. 2,639 genes code for proteins. 1948 of the genes have predicted functions. This means that almost 700 genes have no predicted function. 64 are RNA genes.

Results

Figure 1. The results of a protein BLAST using the Non-redundant database shows a Cytochrome C biogenesis protein as the top hit (non significant e-value of 1.6). Students at Westfield Academy and Central School have annotated individual genes in order to further understand the function of this organism. The gene product Ksed_04890 was found to be a hypothetical protein of unknown function. However, a hypothesis was formulated that it can that Ksed_04890 may be a new transposase or a non-functional mutation of a transposase based on multiple sequence alignment of Ksed_04890 with a number of short transposase sequences found in the Kytococcus genome.

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:

Results continued

Figure 7. This graph is the phylogenetic tree for the Kytococcus and Arthrobacter as the closest neighbor. Kytococcus and Arthrobacter are the same down to taxonomic family. Kytococcus and Propionibacterium are the same down to class. These indicate transmission by Heredity and not Lateral gene transfer.

Conclusions

According to the website used gene Ksed_04890 is a hypothetical protein of unknown name and unknown function. After looking closely at this gene product it was found that may not be the case. After running a BLAST search of Ksed_04890, the first hit was a cytochrome C biogenesis protein. However, the gene product for Cytochrome C has already been found (Ksed_16240 & Ksed_16250). Ksed_04890 was then compared to several known transposase gene products. Ksed_04890 seemed to have some conservation of domains found in transposase gene products found in the Kytococcus genome. We hypothesize that Ksed_04890 could be a new transposase or one that has mutated and lost the functional part of the gene.

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Literature Cited


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