Abstract

The annotation of 5 gene-coding genes from the microorganism Kyococcus sedentarius (Ksed, 08070 - Ksed, 08110) was completed with the use of the 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, potential alternative open reading frames, enzymatic function, presence or absence of gene duplication and degradation, and the possibility of horizontal gene transfer. The annotation of Kyococcus sedentarius by computer software was verified through manual annotation with results recorded in the GENI-ACT lab notebook.

Introduction

Kyococcus sedentarius is a gram positive, strictly aerobic bacterium that resides in various environments such as human skin and marine habitats. The bacteria resides in temperatures of 25-37°C and is a chemooxygenotrophic-organism, requiring methane and other amino acids to grow. It thrives in sodium chloride concentrations less than 10% (w/v), and it is a spherical accoci that occurs predominantly in tetrads. In addition, the organism is non-motive, non-encapsulated, and non-endospore forming.

Kyococcus sedentarius was studied due to the fact that it has several advantageous uses in biotechnology. It is known for the production of polyethylene (alkanes A and B) as well as its role as an opportunistic pathogen. It may be harmful to humans be cause it can cause phlebitis, wound infections, and hemorrhagic pneumonia.

Ksed, 08070 is a transcriptional regulator of the Arf family. Ksed, 08070 is an arabinose efflux permease family protein.

Methods and Materials

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

- **Modules of GENI-ACT**: The proposed gene product name for each gene was assessed in terms of its general genomic information, amino acid sequence-based similarity data, structure-based evidence from the amino acid sequence, cellular localization data, potential alternative open reading frames, enzymatic function, presence or absence of gene duplication and degradation, and the possibility of horizontal gene transfer. The annotation of Kyococcus sedentarius by computer software was verified through manual annotation with results recorded in the GENI-ACT lab notebook.

- **Results**: The initial proposed product of these genes by GENI-ACT was a transcriptional regulator of the Arf family. Thigene product proposal was supported by the top BLAST results and the putative transcriptional location of the products predicted by PSORT-B. The amino acid sequence of this gene tends to be well conserved across species. No signal peptide was predicted and the probability of any transmembrane regions was low. The start and stop codons were accurately called, and there was a Shine-Dalgalno sequence 5-15 bases upstream of the start codon. The domain of the product was annotated in the database. The domain of the product was annotated in the database. The domain of the product was annotated in the database. The domain of the product was annotated in the database. The domain of the product was annotated in the database. The domain of the product was annotated in the database. The domain of the product was annotated in the database. The domain of the product was annotated in the database.

- **Figure 1**: Scanning electron micrograph of the Kyococcus sedentarius (Manfred Rohlfs, Helmholtz Center for Infection Biology, Braunschweig).

- **Figure 2**: Gene neighborhood from IMGedU. The five consecutive genes that were studied are labeled.

- **Figure 3**: Probabilistic results for Ksed, 08070 demonstrating the probabilities for the location of the protein. Although there appears to be a high probability for the location to be non-epitolytic, PSORT-B reported a non-epitolytic score of 7.5, predicting that the gene is located in the epitolytic.

- **Figure 4**: Ksed, 08070 HMM LOGO results show that there were key functional residues at 19, 44, and 45 with the amino acid sequence.

- **Figure 5**: Graph for Kyococcus sedentarius, 08100 showing the C-score, S-score, and Y-score. The results indicate that there is no signal peptide and hereby no signal peptide.

- **Figure 6**: Graph for Kyococcus sedentarius, 08110 showing the C-score, S-score, and Y-score. The results indicate that there is no signal peptide and hereby no signal peptide.

- **Figure 7**: Protein structure of the initial proposed product of these genes by GENI-ACT was a transposase. The protein product was supported by the top BLAST results and the putative transcriptional location of the products predicted by PSORT-B. The amino acid sequence of this gene tends to be well conserved across species. No signal peptide was predicted and the probability of any transmembrane regions was low. The start and stop codons were accurately called, and there was a Shine-Dalgalno sequence 5-15 bases upstream of the start codon. The domain of the product was annotated in the database. The domain of the product was annotated in the database. The domain of the product was annotated in the database. The domain of the product was annotated in the database. The domain of the product was annotated in the database. The domain of the product was annotated in the database. The domain of the product was annotated in the database. The domain of the product was annotated in the database. The domain of the product was annotated in the database.

References


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