Annotation of the *Kytococcus sedentarius* Genome from Ksed_09090 - Ksed_09130 and Ksed_09100

Kaia Skurzewski, Jeffery Rashko, Cristian Swiatek, and Ashley Vohwinkel

John F Kennedy High School and The Western New York Genetics in Research Partnership

**Abstract**

A group of organisms 5 genes from the microorganism *Kytococcus sedentarius* (Ksed_09090 - Ksed_09130) were annotated using the collaborative genome annotation website GENI-ACT. The Genbank proposed gene product name for each gene was used in terms of the general gene 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, 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 database.

**Methods and Materials**

Using Web Log, we compared our assigned genes to our top hits. Sequences 3, 4, 8, 11, 16, 17, 18, 20, and 21 resemble Kaia’s gene Ksed_09130 the most; 1, 27, 29, 30, and 31 resemble her gene the least.

**Results**

Using Web Log, we compared our assigned genes to our top hits. Sequences 3, 4, 8, 11, 16, 17, 18, 20, and 21 resemble Kaia’s gene Ksed_09130 the most; 1, 27, 29, 30, and 31 resemble her gene the least.

**Conclusion**

The GENI-ACT 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 database.

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The alignment shows that my protein amino acid sequence easily matches the translation of the DNA sequence at MG/EDU. Therefore there is no evidence of a frameshift mutation or a premature stop codon. Ksed_09100 is gene product is a histidine-rich protein is detected by reverse transcription. The protein that is encoded by this gene is highly conserved in organisms closely related to Kytococcus. Therefore there was no evidence of horizontal transfer. The characteristic GC percent was 72% and the average GCs of the gene was 69%. There was also no evidence of a frameshift mutation or stop codon.

**References**