Annotation of the *Kytococcus sedentarius* Genome from DNA Coordinates 764347 to 773451

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**Abstract**

Five genes (Ksed_07600, Ksed_07610, Ksed_07640, Ksed_07650, Ksed_07660) from the microorganism *Kytococcus sedentarius* were annotated using the collaborative genome annotation website GENI-ACT. The Genbank proposed gene product name did not differ significantly from the proposed annotation (based on Modules 1-6) for Ksed_07600. Ksed_07600 and the remaining genes mentioned above were not annotated to completion however. It is proposed, therefore, that further study of these genes is needed to determine their function.

**Introduction**

To annotate genes is a non-trivial function to them. While supercomputers do this, a person, in our case, has the unique ability to make connections between genes that a computer cannot. An investigator who manually annotates genes can also catch errors made by a computer. In this project, we participated in the manual annotation of genes from the bacteria, *Kytococcus sedentarius*. This experience has allowed us and others to contribute our findings to the scientific community regarding genes and their functions. Learning more about genes and their functions may lead to the treatment and prevention of disease.

According to Sims et al. (2009), *Kytococcus sedentarius* is a strictly aerobic, free-living, nonmotile, actinomycete, non-sporing Gram-positive bacteria originally isolated from a marine environment. *K. sedentarius* is known for the production of oligoketone antibiotic candidates for its role as an opportunistic pathogen causing endocarditis, hemorrhagic pneumonia, and piliated keratitis. It has a genome of interest because of its localization in *Deinococcus*, a poorly studied family within the actinobacterial suborder Mycobacterales (Sims et al., 2009). Our study of the genes of *K. sedentarius* comes after its complete genome sequencing as part of the Genomic Encyclopedia of Bacteria and Archaea (GEBA) project. With the complete sequencing of this genome, we can look at genes in question and compare them to other genes in the database and understand their functions. This is what the authors of this study did.