Annotation of the Kytococcus sedentarius Genome from Locus Tag Ks ed_07330 to Ks ed_07370
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Abstract
A group of five core bio genes from the microorganism Kytococcus sedentarius (Ksed, 07330 – 07370) were annotated using the collaborative genome annotation website GENI-ACT. The Genome project produced name for each gene was assessed in terms of the general genomic information, amino acid sequences and data, structure-based evidence from the amino acid sequence, cellular localization data, potential, or absence of gene duplication and degradation, and enzymatic function. The Genome project produced gene names did not differ significantly from the proposed gene annotations for four of the five genes in the group, which appear to be correctly annotated by the database. The fifth gene, Ksed_07370, had conflicting results.

Introduction
First discovered in 1944, Kytococcus sedentarius is a gram-positive, marine dwelling organism. As an opportunistic pathogen, this bacterium can easily infect a wounded or weakened host. It lays dormant, not displaying pathogenic qualities until a viable host is discovered. K. sedentarius cannot grow unless a multitude of pre-existing amino acids, such as methionine, are present in the environment at the temperature ranges between 25 and 36 degrees Celsius. K. sedentarius can produce two different, extracellular enzymes that can breakdown natural, insoluble human collagens.

Stains of this species are frequently found residing in human skin. It is non-motile, non-saprophytic, and non-endospore forming. K. sedentarius cells are spherical or coiled in nature and are typically arranged in tetrads, which, in turn, can be arranged similar to that of a table. Its genome is 2785,652 bp long with its central, circular chromosome consisting of 71% genes.

K. sedentarius primarily causes pod rot keratolysis, a skin infection of the feet caused by wearing tight, restricting footwear and sweating profusely. It appears as crater-like depressions in the feet and toes, primarily found in weight-bearing areas. People of any age, race, or gender can suffer from the disease as though it is found more commonly in men. People who sweat and walk on an exacted walk rate are most at risk of contracting the disease.

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

Results
Kytococcus sedentarius 07330:
Initial proposed results for Ksed_07330 is pantetheine kinase, which was determined by the Genebank database is cytoplasmic in nature. This gene does not possess transmembrane helices as determined by use of TMHMM and associated transmembrane topology graph. The data found would indicate a location in the cytoplasm.

Kytococcus sedentarius 07350:
No data acquired beyond initial BLAST results suggesting glutamine–fructose-6-phosphate transaminase, which is also suggested as the suspected protein by initial Genebank results.

Kytococcus sedentarius 07360:
The initial proposed product of these genes by GENI-ACT was phosphopantetheine-protein transerase. This gene product proposal was supported by the top BLAST hits for the amino acid sequences, the presence of well-conserved functional domains within the amino acid sequences, the cellular location of the amino acid sequences, and the ensemble function of the amino acid sequences. The crystal lattice structure of this protein in direct correlation with the proposed product and family of phosphopantetheinetranseras.

Kytococcus sedentarius 07370:
Top BLAST hits, as well as a result from T-Coffee and PD B suggest that this gene is responsible for producing repair proteins such as NAD(P)H-hydride repair enzymes, which are most likely located in the cytoplasm. Phobius and Signal IP results are conflicting and suggest further research is needed to pinpoint the location as transmembrane or cytoplasmic. This enzyme allows for the repair of both epimers of NAD(P)H, a damaged form of NAD(P)H that is a result of enzymatic or heat-dependent hydration. The YafF-like protein selected by the initial Genebank results are similar in nature and cytoplasmic, but each with different roles in the metabolic pathway. Collected data indicates a need for more research. The HMM Logo below suggests the protein is an NAD(P)H-hydride repair enzyme.

Conclusion
The products proposed by GENI-ACT did not differ significantly from the proposed gene annotation for four of the genes in the group and as such, these genes appear to be correctly annotated by the computer database. One gene, Ksed_07370, did show a slight difference from the proposed gene annotation through use of information extracted during the GENI-ACT research project.

References

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