Annotation of 2 Kytococcus sedentarius genes: Ksed_19620 and 25490 that encode an aspartate kinase

Meghan Francis, Xiaoying Xu, and Margaret Diamond, Ph.D.
The Park School of Buffalo and the Western New York Genetics in Research Partnership

Abstract
Two genes from the microorganism Kytococcus sedentarius (Ksed_19620 and 25490) were annotated using the collaborative genome annotation website GENI-ACT. The GENI-ACT proposed gene product identification for each gene was examined in terms of the general genomic information, amino acid sequence-based similarity data (BLAST, CDD, T-Coffee, and WebLog), structure-based information from the amino acid sequence (TIGRHam and Pfam), cellular localization data (TMMHM, SigmaP, and Phobius), enzymatic function (KEGG, MetaCyc, E.C. number), gene duplication (paralog), and evidence for horizontal gene transfer. The GenBank proposed gene product name did not differ significantly from the proposed gene annotation for each of the two genes studied. Therefore, the genes appear to have been correctly identified by the computer program.

Introduction
Kytococcus sedentarius is a gram-positive bacterium that produces certain antibiotics. It is aerobic and requires some amino acids for growth. This bacterium was originally found in a marine environment. Even though it is often overlooked, it is known to have caused serious illnesses such as valve endocarditis and pneumonia. It also causes foot odor and pitting of foot calluses (pitted keratolysis) (Sims 2009; James 2012).

Figure 1. Left panel, scanning electron micrograph of Kytococcus sedentarius. Right panel, pitted keratolysis of the sole of the foot, caused by K. sedentarius.

Ksed_19620 was identified as an aspartate kinase protein. Its function is to transfer a phosphate group from ATP to L-aspartate. BLAST showed that this protein is most similar to other partate kinases identified in many other bacterial species. In addition to BLAST, other programs (as listed in Materials and Methods) were used to analyze and annotate the gene Ksed_19620, including WebLog, cellular localization, duplication, and enzymatic function. Ksed_25490 was also identified as an aspartate kinase. It was found to be most similar to a protein sequence from Holopaga foetida, with a high degree of similarity to many other bacterial protein sequences as shown by the e-value 1e-148. This gene was characterized using the same methods as for Ksed_19620.

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
Comparison of the amino acid sequence of Ksed_25490 to the non-redundant protein database using BLAST showed that Ksed_19620 is most similar to other identified aspartate kinase proteins and that it has an e-value of 2e-171. This is a very high value which means that the compared protein sequences are very similar. WebLog also illustrated that it was highly conserved throughout. It is most likely in the cytoplasm since no transmembrane domains or signal sequence were identified.

Conclusion
The GENI-ACT proposed gene products did not differ significantly from the proposed gene annotation for each of the genes analyzed and as such, the genes appear to have been correctly identified by the computer program as follows:

References

Acknowledgments
Supported by NSF ITEST Strategies Award Number 1311902. Thanks to Dr. Stephen Koury and Dr. Patricia Masso-Welch for their invaluable help.