Annotation of the *Kyctococcus sedentarius* Genome from DNA Coordinates 08030 to 08060

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**Abstract**

4 genes from the microorganism *Kyctococcus sedentarius* (Kcd, 08030 – Kcd, 08060) were annotated using the computer program Genomics Education National Initiative Annotation Collaboration Toolkit (GENI- ACT). The proposed gene product for each gene was manually annotated with GENI-ACT to modules including Cellular Localized Data, Structure-Based Evidence, and Sequence-Based Similarity Data. For all 4 genes, the Genbank proposed gene product did not differ from the proposed annotation. Genes 08030 and 08060 were found to code for transmembrane transport proteins; gene 08040 codes for a transcriptional regulator; gene 08050 codes for an enzyme that is involved in DNA-deacetyl and cell division.

**Introduction**

*Kyctococcus sedentarius* is a skin bacterium that is usually harmless but can cause serious infections such as septic arthritis, endocarditis, meningitis, and puerperal sepsis (Sim et al., 2009). However, it is also a producer of the cephalosporin antibiotic, aminopenicillin A, which is widely used in the poultry and cattle industries (Lowod et al., 2013). This organism must be researched to further clarify its virulence and determine whether beneficial modifications can be achieved.

*Kyctococcus sedentarius* is a nonmotile, Gram-positive bacterium, originally found in marine environments. Gram positive bacteria are usually aerobic, and can only grow when amino acids are provided on the medium. It is a producer of the cephalosporin antibiotics, aminopenicillin A and B, and DNA analysis revealed no close relationship to Streptomyces cinnamomeus, a typical meningococcal producer (Popperl et al., 1998). It is a part of the family Dermatopneumococcaceae, which is not very well studied (Sim et al., 2009).

The current study of *Kyctococcus sedentarius* focuses on using the computer annotating program, Genomics Education National Initiative Annotation Collaboration Toolkit (GENI-ACT), to manually annotate the genes of the bacteria. Through this approach, the gene products can be confirmed or be marked for further investigation based on data obtained from the GENI-ACT. Thus, our proposed gene products include TMHM, a program that predicts the probability of transmembrane helices, Phobius, which predicts the probability of transmembrane helices, signal peptides, cytoplasmic and non-ribosomal protein families, and MetaCyc, which shows maps of enzymatic pathways in which the gene product may participate.

**Methods and Materials**

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

**Results**

**08030:** The gene product for *Kcd, 08030* is an arabinoside efflux permease that functions in cellular transport of the monosaccharide arabinose. This product is supported by investigations in the *Cellular Localized Data module* of GENI-ACT. TMHM and Phobius both predict 12 transmembrane helices, and Phobius predicted a very low chance of the presence of a signal peptide, so the protein is highly unlikely to be secreted from the cell. This leads to the conclusion that the gene product is an integral transmembrane transport protein.

**08050:** The gene product for *Kcd, 08050* is TmcC relaxase, which is an enzyme that has DNA cleavage and strand transfer activities during cell division. This enzyme is supported through the results of Tigrfam, Pfam B, and the HMM logo. According to Tigrfam, we found that the gene is involved in the transmembrane helices which support the conclusion because it can bind to DNA. The TMHM test also predicted this as having three helices.

**08060:** The gene product of *Kcd, 08060* is an arabinoside efflux permease family protein which functions in the transport of arabinose; a sugar of the pentose class. This is supported by the PSORT-B prediction because only the cytoplasmic membrane score was zero. The TMHM test also predicted this as having two helices. The signal peptide probability was listed as not likely as well and indicates that it is a transmembrane protein and not likely to be secreted by the cell. The PFAM investigation also did not support the function of the gene. Its PFAM name is listed as Major Facilitator Superfamily. The major facilitator superfamily (MFS) is a class of membrane transport proteins that facilitate movement of small solutes across cell membranes. This test led us to believe that the following gene product is a transporter protein reinforcing the idea that it transports arabinose across the membrane.

**Conclusion**

The Genbank proposed gene products were all confirmed:

<table>
<thead>
<tr>
<th>Gene Locus</th>
<th>Genbank Product</th>
<th>Proposed Annotation</th>
</tr>
</thead>
<tbody>
<tr>
<td>08030</td>
<td>Arabinoside efflux permease</td>
<td>Arabinoside efflux permease</td>
</tr>
<tr>
<td>08040</td>
<td>Transcriptional regulator</td>
<td>Transcriptional regulator</td>
</tr>
<tr>
<td>08050</td>
<td>TmcC relaxase</td>
<td>TmcC relaxase</td>
</tr>
<tr>
<td>08060</td>
<td>Arabinoside efflux permease</td>
<td>Arabinoside efflux permease</td>
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**References**


Sim et al. (2009). Complete genome sequence of *Kaucaurus sedentarius* type strain (KST). Standards in Genomic Science. 12-25

**Acknowledgments**

Special thanks to Dr. Rama Dey-Rao and Dr. Stephen Koury from University at Buffalo. Supported by NSF ITEST Strategies Award Number 1311902