Genome Characterization and Annotation of a Cluster S Bacteriophage

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Introduction

Bacteriophages (phages) are viruses that infect their host and cannot reproduce independently outside of them. The application of bacteriophages in the biotechnology and medical sectors has recently increased, including uses as a potential antibacterial agent and CRISPR technology. In this project, genes 87-98 of the Corazon phage genome were annotated by five student researchers at Purdue University in addition to genes 74-83 of the Krili genome, and genes 89-99 of the Smooch genome. Our goal for this project was to determine the locations and functions of select genes within these phage genomes.

Summary and Conclusion

Genes 87-98 in the Corazon phage, genes 74-83 in Krili, and genes 89-99 in Smooch were annotated. Based on the evidence collected through various bioinformatics softwares, base pair locations of the genes were called by the group. After determining the gene location, gene functions were called based on alignments and comparison with other analogous genes. Many functions were unknown due to lack of evidence, but other functions included endonucleases and DNA Polymerase III subunits.

Results

Comparison of Known vs Unknown Functions

<table>
<thead>
<tr>
<th>Genome</th>
<th>Known Function</th>
<th>No Known Function</th>
</tr>
</thead>
<tbody>
<tr>
<td>Corazon</td>
<td>10</td>
<td>8</td>
</tr>
<tr>
<td>Krili</td>
<td>10</td>
<td>8</td>
</tr>
<tr>
<td>Smooch</td>
<td>10</td>
<td>8</td>
</tr>
</tbody>
</table>

Figure 1: DNAMaster possible start sites for Corazon Gene 88.

Summary and Conclusion

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Literature


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