Our Little Piece of Elizabethkingia

Naima Afrin. Haley Riley. Madison Clark, and Zomaree McNac
Dr. Patricia Canaan. William Johnson, and Nathan Torres

ABSTRACT

Elizabethkingia anophelis is the cause of many disease outbreaks in the United States which makes it a crucial bacteria to research and investigate. Our study focuses on whether certain antibiotics have a significant effect on the RNA transcription levels in five genes involved in the Shikimate pathway. Using the UniPROTdb, RASTdb, and BLAST databases, along with RNA sequencing we were able to find data to aid in our investigation. Ultimately, we found that exposing bacteria to these specific antibiotics leads to significant changes in the transcription levels in two of the five genes we have studied.

INTRODUCTION

Elizabethkingia anophelis is a gram negative human pathogen that is resistant to most antibiotics (10). Bacteria such as E. anophelis is known to respond to changes in environment often through gene expression (9). In correlation to that, five genes in E. anophelis were subjected to exposure to antibiotics such as Cefotax and Imipenem in order to research whether a change in environment could lead to a change in the transcription levels of these genes. The results indicated that the antibiotics do indeed have an effect on the RNA transcription levels of the five genes we have chosen.

MATERIALS AND METHODS

Starting with the UniPROT database, search through the genes (2). Click on the number beside a metabolic pathway name to open a page and table with those genes listed.

Click the (+) symbol to expand each pathway name and scroll down to sub pathways.

Explore additional Views by clicking on the “Gene Ontology” or “Enzyme Class” in the menu on the left.

After navigating through the UniPROT database, use BLAST to convert the genes to the RAST database (1, 3).

Use the RAST database to obtain details of each specific gene (1).

Log into the RAST database.

Find Elizabethkingia anophelis R26 at the top of the table.

Click “view details” on the right side of the table.

Click browse annotated genome in “seed viewer”

Click the (∞) symbol to expand each pathway name and scroll down to sub pathways.

Finalized by our genes, we found that they were subjected to significant changes in transcription when exposed to either Cefotax or Imipenem.

RESULTS

We identified five genes related to the Shikimate pathway.

- 3-dehydroquinate dehydratase II (RAST ID: 1424)
- Shikimate kinase I (RAST ID: 222)
- Chorismate synthase (RAST ID: 1591)
- 3-dehydroquinate synthase (RAST ID: 3399)
- 5-Enolpyruvylshikimate-3-phosphate synthase (RAST ID: 1737)

Table 1. The Shikimate Pathway

<table>
<thead>
<tr>
<th>RAST ID</th>
<th>Description</th>
<th>Control (Fold)</th>
<th>3-Dehydroquinate dehydratase II</th>
<th>Chorismate synthase</th>
<th>3-Dehydroquinate synthase</th>
</tr>
</thead>
<tbody>
<tr>
<td>1424</td>
<td>Shikimate kinase I</td>
<td>1.5</td>
<td>2.8</td>
<td>2.2</td>
<td>2.0</td>
</tr>
<tr>
<td>222</td>
<td>Chorismate synthase</td>
<td>1.5</td>
<td>2.4</td>
<td>4.5</td>
<td>2.0</td>
</tr>
<tr>
<td>3399</td>
<td>5-Enolpyruvylshikimate-3-phosphate synthase</td>
<td>1.4</td>
<td>1.6</td>
<td>2.0</td>
<td>1.0</td>
</tr>
</tbody>
</table>

Figure 1. The Shikimate Pathway

Figure 2. The Shikimate Pathway

Figure 3. The Shikimate Pathway

Figure 4. The Shikimate Pathway

Figure 5. The Shikimate Pathway

Figure 6. The Shikimate Pathway

DISCUSSION

Based on our results, we have concluded that our genes do, in fact, respond to their environment. Two of our five genes experienced a significant change in transcription when exposed to either Cefotax or Imipenem.

- 3-dehydroquinate dehydratase II, when exposed to Imipenem, decreased by 50%. When it was exposed to Cefotax, there was a 50% increase.
- Shikimate kinase I experienced a 80% decrease when exposed to Cefotax, and a 220% increase when exposed to Imipenem.

We believe that these significant changes represent the organism’s attempt to adapt when its survival is put at risk.

When we examined the genes surrounding our genes of interest, we found that they were unrelated in function. This means our genes are not operating, and they do not rely on each other, instead they function independently.

REFERENCES