To begin our experiment, we chose a set of genes in the Patric Fold Change*. The delta chain gene helps keep the F1 stationary as the rotary 36 S, Kagawa Y (Dec 1993). “Gene structure of human mitochondrial ATP synthase The last gene in the table is a hypothetical protein but appear to be 20 Rast database names: ATP synthase Delta Chain-fig|1246994.3.peg.3544 ATP synthase Gamma Chain-fig|1246994.3.peg.3547 ATP synthase F0 sector Subunit-fig|1246994.3.peg.3547

Using the Rast database names and the excel sheet provided by Dr. Cannan we then recorded the transcription patterns for each genome. (Shown in the table below)

The last gene is a hypothetical but because the genes are so close to the other it can be inferred that it is part of an operon. The genes have a mathematically high significance but no biological outcome/significance. The genes are not highly expressed maybe due to a repressor.

**RESULTS**

We first gathered information on each genome in the photosynthesis pathway and found that: ATP synthase Beta chain- Produces ATP from ADP in the presence of a proton gradient.[5][6] ATP synthase Gamma chain- Produces ATP from ADP and is also important in regulating ATPase activity and the flow of protons through the CF0 complex.[1]

All genes in the photosynthesis pathway work together in some way to form ATP, the cells energy source, during the process of photosynthesis.

After translating the Patric database name for the genomes through Blast were able to obtain the Rast database names:

<table>
<thead>
<tr>
<th>RAST Name</th>
<th>Fold Change*</th>
</tr>
</thead>
<tbody>
<tr>
<td>ATP synthase Beta Chain-fig</td>
<td>1246994.3.peg.2583 ATP synthase Delta Chain-fig</td>
</tr>
<tr>
<td>1.5</td>
<td>2.0</td>
</tr>
</tbody>
</table>

We evaluated their RNA sequences as well as if they played a key role in evaluating the transcription of our genes under the conditions of Cefotax and Imipenem and overall learn more about how the bacteria operates.

**DISCUSSION**

- In the ATP pathway, the alpha and beta genes help create energy for the cells inside the Elizabethkingia anophelis bacteria.[4][9]
- The delta chain gene helps keep the F1 stationary as the rotary motor is in motion.[8][11]
- The gamma chain connects the motor on the portions of the alpha and beta genes, that provides energy for the Elizabethkingia bacteria, where the gamma chain serves almost like a bridge connecting the two.[4][5][9][6]
- When we converted our gene sequences from Patric to Rast we were able to evaluate the transcription of our genes under the conditions of Cefotax and Imipenem and overall learn more about them and if they are effected by them.
- The last gene in the table is a hypothetical protein but appear to be a part of another operon.

**MATERIALS AND METHODS**

- To begin our experiment, we chose a set of genes in the Patric database and described briefly what each gene’s assignment was.
- From there, we had to convert our gene name into the appropriate gene name for the RAST database in order to find out whether or not the genes are turned on when introduced to antibiotics.
- In order to convert the genes, we logged into the RAST database and plugged our Patric names into the BLAST system which gave us the same gene name for both databases.
- We searched through the RNAseq spreadsheet, provided on D2L by Dr. Canaan, where we found our genes, located in the 550th to 554th rows, and recorded the transcription pattern observed from our group of genes and placed our results in a table.
- After this, we went back to the RAST database and found a picture of each of the genes being observed.
- To conclude, we made our interpretations as to if our genes were turned on when introduced to antibiotics or not.