Expression of Genes Involved with Carotenoid Biosynthesis in *Elizabethkingia anophelis*

GRP# 34

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ABSTRACT

In this experiment, we examine the genes found in the *Elizabethkingia anophelis* bacteria. By examining these genes, we are able to see which are active in the pathway of carotenoid biosynthesis. We found that some genes are more expressive than others as well as observed how these genes would react towards certain, specific conditions. By observing these sequences, we have a better understanding of the *Elizabethkingia anophelis* bacteria, as well as its ability to synthesize carotenoids.

INTRODUCTION

Elizabethkingia anophelis bacteria is responsible for outbreaks of infections throughout the midwest. There have currently been fifty-nine cases related to this organism; twenty of which have caused death. Symptoms of this bacteria include: shortness of breath, fever, chills, nausea, etc. The bacteria has caused meningitis in infants and respiratory infections in people with weak immune systems. The bacteria is currently being investigated by the CDC (Center for Disease Control) to better understand the organism, as well as find new ways to prevent its spreading.

Researchers have performed numerous test on the *Elizabethkingia anophelis* bacteria to discover new things and help prevent potential outbreaks. By using tests involving Cerofax or Imipenem, researchers have observed that the bacteria expresses certain genes differently. With these procedures, we become closer to finding the best way of preventing the spread of *Elizabethkingia anophelis.*

MATERIALS AND METHODS

Materials:

- Computer

Methods:

1. We used RAST program to locate the gene browser of the *Elizabethkingia anophelis* bacteria.
2. We checked the pathways and examined the "Carotenoid Biosynthesis" pathway, as well as researched its importance to the organism.
3. With the use of the PATRIC database, we found all the genes associated with this pathway and recorded their sequences.
4. We translated the PATRIC sequences with the use of the BLAST program to see how expressive that gene was
5. We then used an excel spreadsheet and recorded how the genes reacted under certain conditions onto a table (SEE RESULTS SECTION)

RESULTS

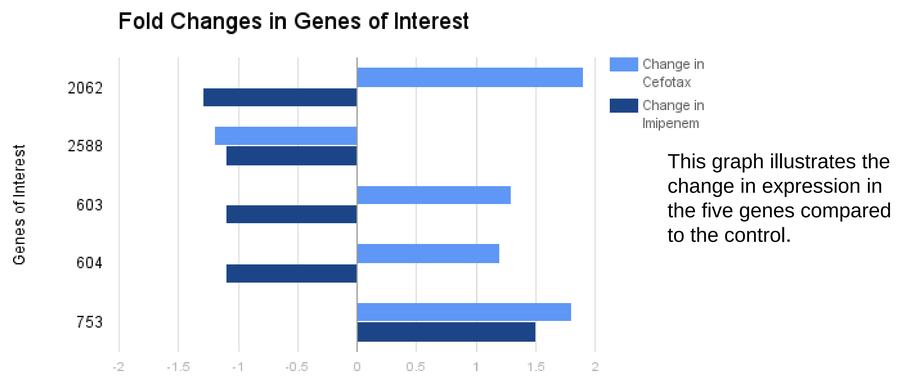
Using databases, such as RAST, PATRIC, and BLAST, we can closely examine the pathways and genes of the bacteria. There are 5 genes associated with the carotenoid biosynthesis pathway in *Elizabethkingia anophelis*.

For each gene, we recorded:

1. # of transcripts observed grown under Control conditions
2. # of transcripts observed grown with Cefotax
3. # of transcripts observed grown with Imipenem
4. Total # of transcripts observed across all three conditions tested
5. Fold change in transcription in Cefotax compared to the control
6. Fold change in transcription in Imipenem compared to the control

By creating the table seen below, we can see that some genes are transcribed less often than others under certain conditions. This table shows that 3 of the 5 genes are very expressive in carotenoid biosynthesis.
When these 3 genes are grown with Cefotax and Imipenem, they are switched on and are expressed throughout the pathway. We can tell that this process happens due to the fact that Cefotax and Imipenem increases the amount transcripts produced by the bacteria.

	peg.2062	peg.2588	peg.603	peg.604	peg.753
Control	175	17	392	538	4
Cefotax	340	14	491	652	7
Imipenem	133	16	356	512	6
All 3 conditions	648	47	1239	1702	17
Fold change in Cefotax	1.9	-1.2	1.3	1.2	1.8
Fold change in Imipenem	-1.3	-1.1	-1.1	-1.1	1.5



This graph illustrates the change in expression in the five genes compared to the control.

DISCUSSION

By researching and examining this bacteria, we are able to see that these genes are affected by Cefotax and Imipenem. These conditions can either inhibit the gene, or cause it to be expressed more. With the use of RAST, PATRIC, and BLAST, we are able to observe the genes and sequences associated in the pathway of carotenoid biosynthesis. With this information, researchers are able to better examine *Elizabethkingia anophelis* as well as prevent its spreading.

When one views the gene fold changes, it can be seen that only two of the genes changed significantly in their expression. That is, the overall change in the expression of the gene was more than 1.5, or 50%. However in Gene 753, the expression was limited to only a few transcripts and so cannot demonstrate any significance. This suggests that of all the genes examined, the only significant change in expression is the increased expression of Gene 2062 in the presence of Cefotax.

If Gene 2062 is significantly expressed under these conditions, it can be reasonably concluded that this gene is required for the survival of the bacteria. Further experimentation is required to determine if this is the case, and if so, how the gene might be exploited for the treatment of infections.

REFERENCES

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