RNA Sequencing of our Interesting Genes in the *Elizabethkingia anophelis* R26

GRP# 32

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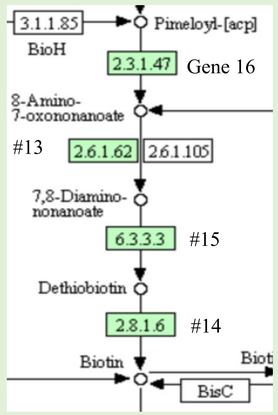
ABSTRACT

The main focus of our class is to work as a group and find genes of interest, and research them in the RAST date base. With our interesting genes we were asked to find the RNA sequencing. With the RNA sequencing we were asked to look at the surrounding genes. Professor Canaan gave us a spread sheet to find the counts for the control, cefotax, and imipenum. We were asked to state whether there was a significant change or insignificant change, and also to state if it was up regulated or down regulated.

INTRODUCTION

- *Elizabethkingia anophelis* R26 is a strain of bacteria that is found in the gut mosquitoes.
- The bacteria is drug resistant to many medications. (1)
- We are researching genes that are involved in the production of Biotin Synthesis (fig. 1).
- The enzymes we chose are an important part in the production of vitamins
- We also researched how the genes reacted when exposed to antibiotics.

Fig. 1 Biotin Pathway



MATERIALS AND METHODS

For this research we used mainly the RAST database (2) and the BLAST database (3) and all of the functions that it offers. This database provided us with the tools to finish each aspect of the research. It also provided graphs and other visual representations of the genes in the sequence that we chose. Another very helpful thing in our research was the teaching assistants and the professors guidance. They helped move us along the right path when completing each task we were given, because they have actual experience in the field that we are studying. Also, our scientific notebook is the guideline that we used in putting our research together. It houses all of the pictures and visual representations, along with additional information that we gathered on the subject of *Elizabethkingia Anophelis* R26.

RESULTS

Table 1. The fold change between to control, Cefotax, and Imipenem. It also shows the counts that we had on each variable. Significant changes are less than or equal to -1.5, or greater than or equal to +1.5.

Gene #	Fold Change (Cefotax)	Fold Change (Imipenem)	Control	Cefotax	Imipenem
13	+2.0	-1.0	1	2	1
14	-1.5	+1.1	21	14	24
15	-1.3	-1.3	5	4	4
16	+1.7	+1.1	7	12	5
2056	+1.4	-1.3	399	565	305

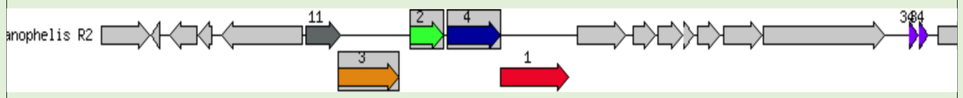


Fig. 2 The visual representation of the strand is shown above. We found that all of our genes fall in line within our pathway. Except gene 2056. Dark Green is a hypothetical protein, Orange is gene 16, Light Green is gene 15, Blue is gene 14, and Red is gene 13. The gene to the right is gene 12 (Alkaline phosphodiesterase). (2)

Fig. 3 The visual representation is the strand of gene 2056. We found that the gene is somewhere on it's own. Red is gene 2056, the gene to the left of 2056 is gene 2055(Diphosphomevalonate decarboxylase), and the gene to the right of 2056 is gene 2057 (Dihydroflavonol-4-reductase). (2)

DISCUSSION

- We found that gene 13, 15, and 16 need further research to be able to determine if the gene was up or down regulated when it was exposed to antibiotics. (Table 1)
- Gene 14 when exposed to Cefotax was down regulated by 50%, we hypothesis cefotax interferes with the production of gene 14, or it might not need as much gene 14 within this treatment. With imipenum the environment didn't change enough for need of the production of gene 14, the imipenum didn't interfere with the production of gene 14.
- Gene 2056: Although there wasn't a significant change between the control, cefotax, and imipenum we can hypothesize that cefotax interferes with the production of gene 2056, or that it needs more of gene 2056. Due to the fact that we had 399 counts form control and 565 counts from cefotax. The environment with the imipenum we can hypothesize that gene 2056 isn't need, or it interfered with the product of gene 2056.
- Four of our five genes are part of a operon, because the genes are all next to each other (Fig. 2).
- That gene 2056 is not related by function to the gene on either side (Fig. 3).
- For future research we could test our hypotheses for gene 14, and gene 2056.

REFERENCES

1. Center for Disease Control (2016). *Elizabethkingia. Aviable from http://www.cdc.gov/elizabethkingia/ 11/2/2016.*
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3. Altschul SF, Gish W, Miller W, Myers EW, and Lipman DJ (1990). *Basic local alignment search tool.* J. Mol. Biol. 215:403-410