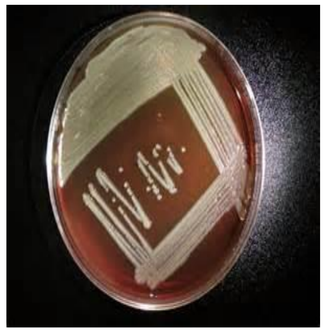

tRNA & Its Affects on Antibiotic Resistance

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GRP# 15

ABSTRACT

In this experiment, we conducted research on a bacteria known as *Elizabethkingia anophelis*. This bacteria is known to cause meningitis and has had many outbreaks, occurring primarily in Michigan. To begin our research, we explored the online database RAST where we found RNA genes consisting on the same pathway. Using these genes we could then determine the amount of transcription that occurred when compared to two known antibiotics. Using our results, we determined if the change in transcription was significant.

INTRODUCTION

Elizabethkingia anophelis is a bacteria that is found primarily in wet environments. This is a disease that causes meningitis in individuals that have a weaker immune system. Since Michigan is a wetland state, there is a higher prominence of the *anophelis* strain causing more people to become infected. Since it has immunity to multiple antibiotics, there have been multiple outbreaks of *E. anophelis* in Michigan. The possibility of these outbreaks could be due to its immunity to antibiotics; this would make sense if *E. anophelis* has an increase in tRNA that transcribes for an increase in biotin synthase then, the cells overall immunity would be stronger towards antibiotics.

MATERIALS AND METHODS

To obtain research on *Elizabethkingia anophelis*, we accessed online databases. For our group, we used the online database RAST. We used this database to complete many of the steps to find out information on *E. anophelis.* To begin our research, we first looked at two genes within the *E. anophelis* R26 genome. After choosing the genes for Biotin Synthase and Nitric-Oxide reductase, we conducted further research with the aid of Wikipedia. After furthering our knowledge on these specific genes, we chose a pathway of genes that code for the production of cellular wall growth. We chose the genes fig|1246994.5.rna.14 - fig|1246994.5.rna.18 on the same pathway that code RNA We then used this information to determine the sequences for all five RNA genes on our pathway of interest. After retrieving all sequences, we used the provided spread sheet to determine the amount of mRNA counts for *Elizabethkingia anophelis* on three different conditions for our specific pathway. Using the spread sheet, we were able to determine if the number of transcription for the conditions Cefotax and Imipenem were significant changes from the level of control. Finally, we used all this information to determine if *E. anophelis* is resistant to the specific antibiotics.

RESULTS

After looking over the spreadsheet of tRNA data sequences for *Elizabethkingia anophelis* we can conclude that the strains of fig|1246994.5.rna.14 through fig|1246994.5.rna.18 do have a significant change in the tRNA that transcribes for *E. anophelis.*

		Fold Change*		TOTAL mRNA **	mRNA Coun	RNA Coun	RNA Counts
RAST Name	Descriptio	fotax/Cont	penem/control)	from all 3 conditions	Control	Cefotax	Imipenem
fig|1246994.5.rna.14	tRNA-Trp-C	2.5	4.0	15	2	5	8
fig|1246994.5.rna.15	tRNA-Thr-C	-1.0	3.0	5	1	1	3
fig|1246994.5.rna.16	tRNA-Gly-T	-1.0	1.5	6	2	1	3
fig|1246994.5.rna.17	tRNA-Tyr-C	2.0	5.0	8	1	2	5
fig|1246994.5.rna.18	tRNA-Thr-T	1.3	2.0	17	4	5	8

Figure 2

As seen in figure two, there is a change of over 50% from the control, Cefotax, and Iminipenem in fig|1246994.5.rna.14. changes of over 50% implies that there was a significant change. Also seen in figure two is the strain fig|1246994.5.rna.18. This strain only has a significant change from the Cefotax to the Imipenem. There are changes in the strains between fig|1246994.5.rna.14 and fig|1246994.5.rna.18 but they are not huge changes.

Display fasta sequences

DNA Sequence: DNA Sequence with flanking: 500 bases Protein Sequence

Download Sequences Show Fasta

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>fig|1246994.5.rna.18 tRNA-Thr-TGT [Elizabethkingia anophelis R26]
gcctccatagctcagttggccagagcacgtgatttgtaatctcggggtcgtgggttcgaa
tccctctggaggct
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DNA sequence for fig|1246994.5.rna.18

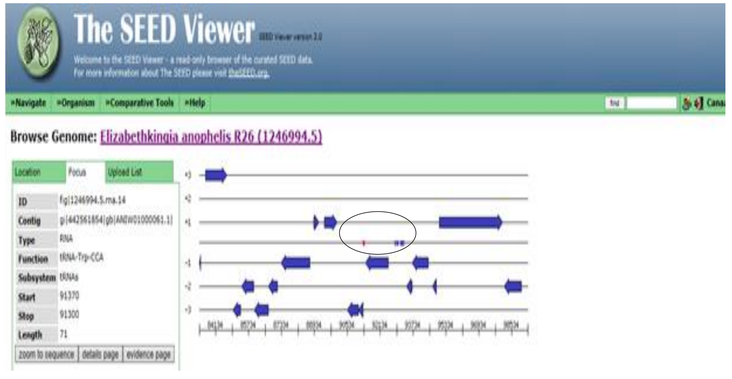
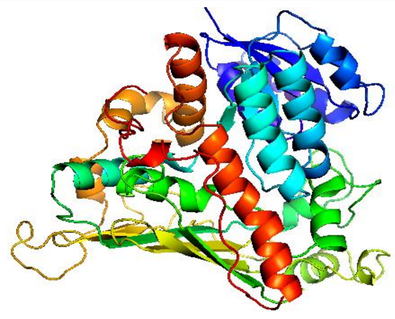


Figure 3. The circled group of genes is fig|1246994.5.rna.14 through fig|1246994.5.rna.18

DISCUSSION

For this experiment our purpose was to conduct research on *Elizabethkingia anophelis* and determine what factors are causing it to have an increased resistance to most know antibiotic resistance. Throughout this experiment, the research we conducted, lead to the conclusion that *Elizabethkingia anophelis*' resistance is due to an increased production of Biotin Synthase, and Nitric-Oxide reductase. This increased production can interpreted from the data to be from an increase in the transcription of specific genes within *Elizabethkingia anophelis* genome; these genes are fig|1246994.5.rna.14 through fig|1246994.5.rna.18, and have transcribed for genes that increase the resistance to antibiotic drugs such as Cefotax, and Imipenem. The production and transcription of these genes have increased by 50% when compared to control experiments. More research is required to determine if these genes work in tandem are turned on separately to increase antibiotic resistance within *E. anophelis.*



REFERENCES

1. Shiuan D, Campbell A (1998). "Transitional regulation and gene arrangement of Escherichia coli, Citrobacter freundii and Salmonella typhimurium biotin operons". *Gene.* 67 (2): 203-11
2. Wikipedia contributors. 19 Sept. 2016 "Transfer RNA." *Wikipedia, The free Encyclopedia*. Wikipedia, The Free Encyclopedia.
3. http://www.cdc.gov/elizabethkingia/about/index.html