23Sr RNA Purpose *In Elizabethkingia anophelis* Genome

GRP# 16

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ABSTRACT

Elizabethkingia anophelis is an organism that is gram negative and has a rod shape. We were interested in 23Sr RNA proteins in *E. anophelis*. What we wanted to find was if the seven 23Sr RNA were transcribed in the presence of two antibiotics. We used the RAST data base, BLAST data base, and an Excel spreadsheet to find this out. Also we used RAST to see what surrounded each of the seven proteins. Due to the fact that 23Sr RNA is necessary, it was transcribed in each of the antibiotics. Although all the proteins were transcribed only three pegs were significant. Also, only one peg for each of the antibiotics was up significantly.

INTRODUCTION

Elizabethkingia anophelis is a rod shaped, single celled, gram negative organism (7,8). It originally found in the gut of a mosquito; it causes meningitis in people who are immunocompromised, and is also dangerous to infants and elderly people (7,8). However, one of the important characteristic is that it is antibiotic resistant (8). We were interested in 23Sr RNA proteins, which are a part of the large subunit of the ribosome and are in charge of making polypeptide bonds. (1) We researched to see if the 23Sr RNA proteins were transcribed in two antibiotics, Cefotaxime and Imipenem. Cefotax is a parenteral cephalosporin, that is used for infections found mainly in the lungs, throat, ears, or urinary tract. Imipenem is a large spectrum beta-lactam antibiotic. The main goal was to then see if the proteins that we picked, 23Sr RNA, were transcribed in the two antibiotics; if they were then if there was significant fold change in the proteins of interest.

MATERIALS AND METHODS

- First thing needed was to access the RAST data base (4)
  - This is what shows all the proteins that exist in *E. anophelis*.
  - http://rast.nmpdr.org/seedviewer.cgi?page=BrowseGenome&organism=1246994.5
- To see the seven proteins we were focused on, we searched 23Sr RNA in the function part of the data base, this resulted in seven proteins.
  - We were interested in these genes due to the fact that they are an important part of making any organism be able to function.
- Then, to get a closer view of each of the proteins, we clicked on each of the seven proteins.
- After clicking on the protein, we clicked the sequence which would display the DNA sequence for the protein.
- With the DNA sequence, we accessed the BLAST data base, that expressed whether the sequence is transcribed in Cefotaxime and Imipenem.
  - http://darwin.biochem.okstate.edu/blast/blast1990.html (2)
- Then using the Excel spread sheet, we looked at each of the seven proteins to see if the change expressed in the gene was significant in the two antibiotics.
  - https://online.okstate.edu/d2l/le/content/51884/viewContent/452214/View (3)
- Lastly, we went back to the RAST data (4) and look at what proteins surrounds each of the seven proteins of interest.

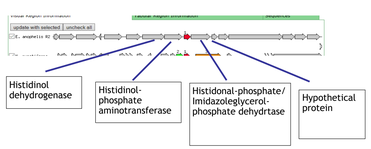
RESULTS

Our results show that the seven genes of 23Sr RNA are expressed in the presence of both antibiotics. In other words, in the presence of the antibodies, the proteins were expressed, meaning they are needed for the cells survival, and are unaffected by the antibiotics. Although all of the genes were expressed, only **peg 424 in Cefotax, peg 490 in both Cefotax and Imipenem, and peg 797 in Imipenem had significant changes**. Also, through our research we found that each of the seven genes, although they had the same functions, were located at different places. They were also surrounded by different proteins that ranged significantly different (in function) from one of the seven proteins to another of the proteins.

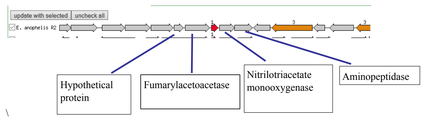
Peg Number	Fold Change (Cefotax/Control)	Fold Change (Imipenem/ Control)	Total of all three	MRNA Count Control	MRNA Count Cefotax	MRNA Count Imipenem
Peg 424	2.0	-1.0	4	1	2	1
Peg 490	-1.6	1.8	237	56	35	103
Peg 797	-1.0	-4.0	9	4	4	1
Peg 1307	-1.0	-1.0	3	1	1	1
Peg 2122	1.2	-1.0	7674	2413	2936	2325
Peg 2943	1.4	1.4	80	21	29	30
Peg 3487	-1.1	1.1	112	37	35	40

(Significant changes are ≤ -1.5 or ≥1.5)

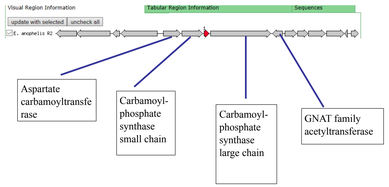
For peg 490



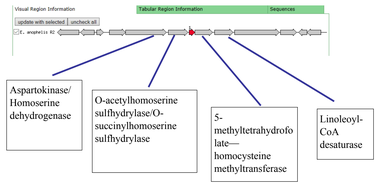
For peg 424



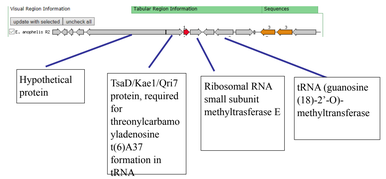
For peg 797



For peg 1307



For peg 2122



DISCUSSION

23Sr RNA is necessary to make an organism function, due to the fact that it is in charge of making polypeptide bonds (1). If the proteins that we researched were not being made, the organism would not be surviving. This is because if the production of the bonds stopped, then it would stop the other necessary functions of the proteins in the organism. With the pegs that are significant this means that they are either less or more needed to make the *E. anophelis* function in the presence of the antibiotics. In peg 424, it was produced more in Cefotax, and therefore had a greater affect in Cefotax than the control. This would be because that peg is much more need to help *E. anophelis* in Cefotax survive. In peg 490, it was produced less in Cefotax and more in Imipenem. This means that although in Cefotax it was not needed like it was in Imipenem. In peg 797 it was needed less in Imipenem than in the control. All the pegs were expressed but the others were not significant changes between the antibiotics and the control. *E. anophelis* was surviving in the presence of the antibiotics, which shows by the seven 23Sr RNA proteins being produced. In conclusion, the proteins of 23Sr RNA are being produced and therefore the *E. anophelis* in the presence of antibiotics is growing. In Cefotax, only peg 424 is up significantly therefore that is the only 23Sr RNA needed for it to survive. In Imipenem, only peg 490 is up significantly therefore that is the only 23Sr RNA needed for it to survive.

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