GRP# 28

Multidrug Resistance in *Elizabethkingia Anophelis*

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ABSTRACT

Elizabethkingia Anophelils is a bacteria that has shown to be resistant to multiple antibiotics, which in turn is a danger to the human population. The focus of our research was to determine whether our genes play a roll in the bacteria's ability to survive under antibiotics. Using the RAST and BLAST databases we concluded that our genes did not have a significant fold change or enough RNA to determine if our genes were significant to the bacteria's ability to survive under antibiotic conditions.

INTRODUCTION

Elizabethkingia Anophelis is a gram negative bacteria that has shown the ability to live in multiple environments. Studies have shown that the bacteria is resistant to multiple antibiotics making it difficult to treat. Bacteria does not transcribe genes if they are not needed in a particular environment. In our research we are looking to see if our particular genes are being transcribed under control, cefotax, and imipenem conditions.

MATERIALS:

1. A computer with access to Firefox in order to access the RAST and BLAST databases.

2. An electronic notebook (through Microsoft Word) in order to keep a record of our results, methods, and discussions for future rederence.

METHOD:

We began by researching and picking a specific group of genes through the RAST database. Our specific gene group was part of the multi-drug efflux pump subsystem. Once we picked our genes we began research on them through the RAST Database to find out how they relate to each other and work together to perform tasks to resist antibiotics. We obtained the DNA sequencing of each gene through RAST, and then used each sequence in BLAST to determine whether or not our genes were transcribed through RNA. We then used the data sheet provided to us to determine whether the fold changes in our genes where significant or not.

RESULTS

Figure 1 shows the mapping of gene 87, and 88. To the left is a transcriptional regulator, and to the right is a hypothetical protein.

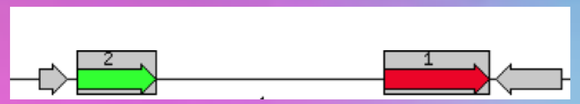

Figure 2 shows the mapping of genes 576, and 577. To the left is a hypothetical protein, and to the right is a Glycerophosphoryl diester phosphodiesterase protein.

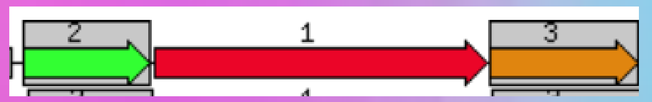

Figure 3 shows the mapping of gene 811. To the left probable RND efflux membrane fusion protein. To the right is an outer membrane protein.

Table 1. Shows the amount of mRNA transcribed under a controlled condition, a Cefotax condition, and an Impinem condition. It also shows the Fold changes in Cefotax and Impinem, which where calculated by comparing the mRNA of each antibiotic condition back to the controlled condition.

Gene #	mRNA Control	mRNA Cefotax	mRNA imipenem	Total mRNA	Fold Changes in Cefotax	Fold Changes in Imipenem
87	6	3	8	17	-2.0	1.3
88	3	3	8	14	-1.0	2.7
576	8	7	18	33	-1.1	2.3
577	3	3	4	10	-1.0	1.3
811	9	13	16	38	-1.4	1.8

DISCUSSION

The purpose of this research was to determine whether efflux pumps played an important role in the ability of the bacteria to survive in the presence of antibiotics. We did this by obtaining our specific genes DNA sequence and used it to see if our genes were transcribed from RNA. We then looked at the fold changes from the RNA sequenced data and determined if the fold changes were significant or not. By determining whether or not the fold changes are significant, and if there are enough total mRNA we can infer that our genes are either being used or not being used under these specific conditions. Our specific genes had a very low amount of RNA present and insignificant fold changes. However, there is not enough data present to determine the significance of these genes. Further testing would have to gather more information on the importance of the genes under antibiotic conditions.

REFERENCES

- RAST Database http://rast.nmpdr.org/rast.cgi?page=Jobs

- BLAST Database http://darwin.biochem.okstate.edu/blast/blast1990.html