

Beta-lactamase In a Specific Genomic Sequence From *Elizabethkingia anophelis* R26

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ABSTRACT

Elizabethkingia anophelis, is a bacteria found heavily in the environment which but has been known to rarely make people sick. In this lab, we specifically looked at the genes contained in the *Elizabethkingia anophelis* R26 strand that were related to Beta-lactamase. Through data research, we were able to narrow down the production of beta-lactamase in the R26 strand and we were also able to determine how specific antibiotics were able to affect the production of the Beta-lactamase related genes.

INTRODUCTION

The *Elizabethkingia anophelis* is a genus of bacteria that is gram-negative. It is most often found in the mosquito *Anopheles gambiae*, as well as a human pathogen that has recently caused an outbreak in Central Africa and Singapore. The bacteria has a broad antibiotic resistance which is caused by beta-lactamase. To better understand this, we studied the beta-lactamase by the use of the PATRIC (Pathosystems Resource Integration Center) system.

MATERIALS AND METHODS

To find our beta-lactamase gene group we used the RAST genome database. With this database we were able to find and connect genes using key words. Along with finding the gene group we used RAST to find the sequencing and positions of the genes within our beta-lactamase gene group. Using the database to go from gene to gene taking screenshots showing how we gained our information. By searching google we were able to find what beta-lactamase does to help a move proteins within the genes. Wikipedia web page helped connect some dots for how the lactamase genes worked. In order for us to get the DNA sequencing we went back to the RAST database. By clicking on the genes we could select a link to show the genes sequence.

RESULTS

To start our research, our group obtained basic information found in the RAST Database of genes related to Beta Lactamase which provided us with the Data in the table below. Through the database we were able to find a total of 12 genes the were associated with beta-lactamase.

Shortly after obtaining the table above, we were provided a table that displayed the mRNA counts for every gene within *Elizabethkingia anophelis* R26 in three different categories of control, Cefotax, and Imipenem. With the provided table, we were able to narrow down the complete table to just display the genes we had initial interests in above which is represented in the table below.

Column1	Column2	Column3	Column4	Column5	Column6	Column7	Column8	Column9	Column10
RAST Name	Description	Fold Change ^a (Cefotax/Control)	Fold Change ^a (Imipenem/control)	TOTAL mRNA ^{**} from all 3 conditions	mRNA Counts Control	mRNA Counts Cefotax	mRNA Counts Imipenem		
fig 1246994.5.peg.29	Beta-lactamase [EC 3.5.2.6]	-1.2	1.3	22	7	6	9		
fig 1246994.5.peg.194	Beta-lactamase [EC 3.5.2.6]	1.1	-1.1	357	116	132	109		
fig 1246994.5.peg.399	Beta-lactamase [EC 3.5.2.6]	-1.0	-1.0	3	1	1	1		
fig 1246994.5.peg.503	Beta-lactamase [EC 3.5.2.6]	-1.3	-2.2	159	71	56	32		
fig 1246994.5.peg.519	Beta-lactamase [EC 3.5.2.6]	-2.5	-1.3	104	48	19	37		
fig 1246994.5.peg.605	Beta-lactamase [EC 3.5.2.6]	1.7	1.5	1953	471	797	685		
fig 1246994.5.peg.1010	Beta-lactamase [EC 3.5.2.6]	-2.1	1.0	177	71	34	72		
fig 1246994.5.peg.1724	Beta-lactamase [EC 3.5.2.6]	-1.2	2.5	61	14	12	35		
fig 1246994.5.peg.1915	Beta-lactamase	1.6	-1.3	302	89	144	69		
fig 1246994.5.peg.1934	Metal-dependent hydrolases of the beta-lactamase superfamily; PnP protein	1.3	1.2	317	91	118	108		
fig 1246994.5.peg.2536	Beta-lactamase	1.1	-1.3	45	16	17	12		
fig 1246994.5.peg.3527	Beta-lactamase [EC 3.5.2.6]	-1.3	-1.1	64	24	19	21		

With the results provided above the only genes that provided a noticeable change from control to cefotax were peg.519, peg.605, peg.1010, peg.1915. Peg.519 decreased by 29 counts, Peg.605 increased by 326 counts, peg.1010 decreased by 106 counts, peg.1915 increased by 55 counts. The only genes that provided a noticeable change from control to Imipenem were peg.503, peg.605, peg.1724. Peg.503 decreased by 39 counts, peg.605 increased by 214 counts, peg.1724 increased by 21 counts. The genes listed as noticeable, are listed as so because they achieved a 50% change from control to variable at least in each.



DISCUSSION

From our results we are able to see the effects that the antibiotics have on the beta-lactamase related genes within the *E. Anophelis* R26 strand. When cefotax was added to the R26 strand peg.605 and peg.1915 mRNA counts that both increased significantly. This shows that beta-lactamase produced from these genes is need more to fight the effects of the cefotax antibiotic when added. Also when the cefotax is added to the R26 strand peg.519 and peg.1010 are decreased significantly in terms of mRNA counts. Displaying that other genes are sacrificed for other genes to be produced making these genes less important to fight the cefotax antibiotic. When the Imipenem antibiotic is added to the R26 strand peg.605 and peg.1724 were significantly increased in terms of mRNA counts displaying that the beta-lactamase produced from these genes are more heavily required to fight the Imipenem antibiotic. Also when the Imipenem antibiotic was added to the R26 strand peg.503 decreased by a significant amount in terms of mRNA production displaying that the beta-lactamase produced within this gene is less important in fighting the Imipenem antibiotic. From this data we have received that we are better able to get a firmer understanding on which genes inside the R26 strand are actually active and which genes only activate when an outside force or antibiotic is introduced to our R26 strand possibly supplying introduction to which antibiotics can be used to fight and or kill this strand of bacteria, or specific ways DNA in the gene itself could be edited in a way to make the bacteria more susceptible or to have it kill itself from the inside.

REFERENCES

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Release of 02-Nov-16 (5858 active entries)