The Effects of Cefotax and Imipnem on mRNA Transcription in ATP Synthase Related Genes

GRP# 1

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ABSTRACT

We researched the bacterium *Elizabethkingia anophelis*, focusing specifically on a group of genes pertaining to ATP synthase. We used the RAST database to find the genes, and determine the gene sequences. We then used the chart provided to determine if two drugs (Imipenem and Cefotax) had an impact on mRNA transcription. According to the chart, cefotax increased mRNA translation in two of the six genes, and imipenem reduced mRNA translation in four of the six genes. This indicates that imipenem would be a better treatment option for Elizabethkingia anophelis than cefotax.

INTRODUCTION

Elizabethkingia anophelis is a gram-negative, rod-shaped bacterium which was originally isolated in the gut of the malaria vector mosquitoes, *Anopheles gambiae* (5). Although there are three different subcategories of this bacterium our main focus was the *E. Anopheles* genome due to it's resistance to antibiotics(4). It is commonly found in the environment and has been detected in soil and certain water sources such as river water and reservoirs(6). In order to treat this strain of bacterium, combination antibiotics therapies are recommended (3). These medicines affect the way that the disease/bacteria work. Under these conditions the mRNA would either transcribe more or less often, and that's what we were looking at.

MATERIALS AND METHODS

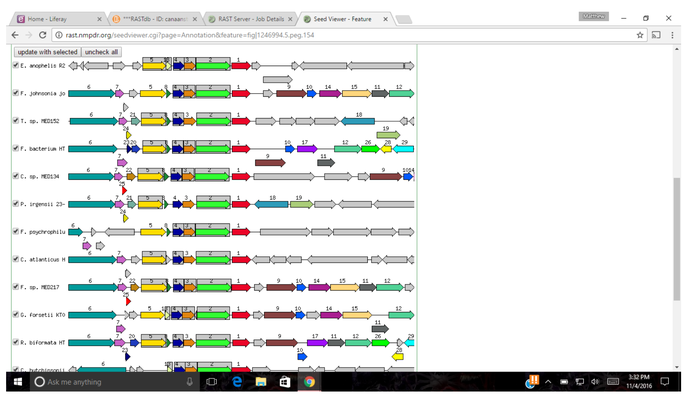
The experiment began with identifying a group of interesting genes within the *Elizabethkingia anophelis* R26 genome. The genes researched and genomic sequences we gathered all came from the RAST database (1,2,7). Based off of the gene identifications and placement on the gene itself, we could tell these few genes were consecutively next to each other and were working hand and hand with each other. Next, we went back to the RAST database and pulled up DNA sequences for the six genes. Looking at the sequences, the length of each gene could be determined. Afterwards, we searched through a spreadsheet that contained the RNA sequence data that was provided on D2L. We recorded the level and number of transcripts grown under control conditions, Cefotax, Imipenem, and the total transcription patterns observed across all of the three conditions from the spreadsheet.

RESULTS

Using the chart below, we determined that all of our chosen genes were active and necessary for Elizabethkingia anophelis to properly function; all six of our genes experienced mRNA transcription when no drug was present. The fold change between cefotax and the control group was only significant in genes 154 and 159. Both of these changes were positive, indicating that while grown in the presence of cefotax transcription of mRNA for these genes increased. The fold change between imipenem and the control group had significant changes in genes 154, 156, 158, and 159. All of these changes were negative, indicating a lower number of mRNA transcription in the drug-treated group than in the control group.

AST Name	Description	Fold Change* (Cefotax/Control)	Fold Change* (Imipenem/control)	TOTAL mRNA ** from all 3 conditions	mRNA Counts Control	mRNA Counts Cefotax	mRNA Counts Imipenem
g1246994.5.peg.149	hypothetical protein	-1.0	1.5	515	147	143	225
g1246994.5.peg.150	FIG01129619: hypothetical protein	1.5	-1.4	13089	4129	6005	2955
g1246994.5.peg.151	hypothetical protein	1.5	-1.7	8909	2885	4287	1737
g1246994.5.peg.152	Magnesium and cobalt efflux protein CorC	1.1	-1.1	513	171	181	161
g1246994.5.peg.153	acetyltransferase (putative)	1.0	1.0	628	207	212	209
g1246994.5.peg.154	ATP synthase gamma chain (EC 3.6.3.14)	2.0	-1.5	442	120	244	78
g1246994.5.peg.155	ATP synthase alpha chain (EC 3.6.3.14)	1.2	-1.1	389	126	146	117
g1246994.5.peg.156	ATP synthase delta chain (EC 3.6.3.14)	1.0	2.2	443	105	106	232
g1246994.5.peg.157	ATP synthase F0 sector subunit b	1.3	-1.6	106	36	47	23
g1246994.5.peg.158	ATP synthase F0 sector subunit c	1.1	-1.1	332	110	125	97
g1246994.5.peg.159	ATP synthase F0 sector subunit a	1.5	-1.8	565	182	281	102
g1246994.5.peg.160	hypothetical protein	1.4	-1.8	1325	447	623	255
g1246994.5.peg.161	hypothetical protein	1.1	1.6	597	164	176	257
g1246994.5.peg.162	FIG00935709: hypothetical protein	1.1	1.8	934	239	263	432
g1246994.5.peg.163	hypothetical protein	1.4	2.0	241	54	78	109
g1246994.5.peg.164	NADH-ubiquinone oxidoreductase chain A (EC 1.6.5.3)	1.4	-1.1	1196	364	505	327
g1246994.5.peg.165	NADH-ubiquinone oxidoreductase chain B (EC 1.6.5.3)	1.4	1.0	990	290	408	292
g1246994.5.peg.166	NADH-ubiquinone oxidoreductase chain C (EC 1.6.5.3)	-1.2	1.5	507	155	125	227

In this chart, the rows highlighted in yellow are the genes that pertain to our research; the values highlighted in green and orange show how the two drugs impact transcription. Fold change values equal to or above 1.5 or equal to or below -1.5 are considered to be significant.



DISCUSSION

We chose these specific genes because ATP Synthase is vital for a cell to function (8), and is therefore important to study when researching the effects of drugs on different genes. When imipnem was introduced, the genes underwent less translation, potentially because of drug resistance. When the cefotax was introduced, mRNA transcription increased in our chosen genes; this shows that cefotax is most likely not effective in treating Elizabethkingia anophelis. More research should be done regarding both these drugs and other possible treatments in order to find an effective way to treat Elizabethkingia anophelis; based on our results, imipenem could possibly be used to treat or reduce the effects of E. anophelis, but again, more research is needed.

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