Analysis of ATP Synthase Genes within *Elizabethkingia anophelis* R26

GRP# 27

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ABSTRACT

This poster begins to analyze five different genes of the *Elizabethkingia anophelis* R26 genome that function to perform ATP synthase. Our task was to find the amount of RNA transcribed within the genes we explored and to compare the number of transcripts of a controlled environment to the number of transcripts of two environments with antibiotics present, as well as finding the location of the genes. We found that, in the addition of cefotax, only two changes in transcription were observed, but the transcriptions all increased. However, with the addition of imipenem, four significant changes were observed but the changes in transcription both increased and decreased, giving us inconclusive results.

INTRODUCTION

Elizabethkingia anophelis, a gram negative bacteria, is responsible for causing human disease in dozens of people across the US per year and is quite resistive to many antibiotics. By looking at similar, specific genes within the bacteria, we aim to better understand *Elizabethkingia anophelis* R26. Five unique genes within the bacteria are responsible for the coding of ATP synthase. In exploring the enzyme, we hoped to find the amount of RNA transcribed within the different genes that ATP synthase is comprised from and interpret its meaning as it relates to the genome. In addition, we used data that illustrated the gene's ability to transcribe DNA in a controlled environment, with the antibiotic cefotax, and the antibiotic imipenem in order to find any change in the transcription with the addition of the antibiotics.

MATERIALS AND METHODS

1. We navigated to the RAST database (3) from Brightspace.
2. We searched the database for genes that function with ATP.
3. From the genes listed, we selected gene 154, gene 155, gene 156, gene 157, and gene 159 as our five genes for this project.
4. We used Wikipedia (2) to determine the overall function of all five genes and the RAST database (3) to determine the function of each gene.
5. We found an image to portray our genes' function in ATP synthase.
6. We returned to the RAST database (3), selected our genes, and then selected "sequence."
7. We recorded each gene's DNA sequence and then proceeded to the BLAST database (1) to determine how each DNA sequence was transcribed into RNA.
8. At the BLAST database (1), we copied and pasted each DNA sequence--in FASTA format--into the box, selected "search," and then recorded the results for each gene.
9. We navigated to the spreadsheet titled "E.anoR26_RNAseqData_FoldChanges.xls" from Brightspace, located each of our genes in the spreadsheet, and recorded our results in the form of a table (Table 1).
10. We navigated back to the RAST database (3), selected each gene, and scrolled to "Visual Region Information."
11. We recorded the location of each gene in the genome.

RESULTS

Table 1

Gene Name	No. of Transcripts (Control)	No. of Transcripts (Cefotax)	No. of Transcripts (Imipenem)	Total No. of Transcripts (all conditions)	Fold Change in Transcripts (Cefotax/ Control)	Fold Change in Transcripts (Imipenem/ Control)
Gene 154	120	244	78	442	2.0	-1.5
Gene 155	126	146	117	389	1.2	-1.1
Gene 156	105	106	232	443	1.0	2.2
Gene 157	36	47	23	106	1.3	-1.6
Gene 159	182	281	102	565	1.5	-1.8

Figure 1

Location of Our Genes in the *E. anophelis* R26 Genome

1. Gene 154 (red)
2. Gene 155 (green)
3. Gene 156 (orange)
4. Gene 157 (blue)
5. Gene 159 (yellow)

Function of Our Genes in the E. anophelis R26 Genome

1. Gene 154 serves as the gamma subunit of the ATP synthase chain.
2. Gene 155 serves as the alpha subunit of the ATP synthase chain.
3. Gene 156 serves as the delta subunit of the ATP synthase chain.
4. Gene 157 serves as the "b" subunit of the F0 sector of the ATP synthase chain.
5. Gene 159 serves as the "a" subunit of the F0 sector of the ATP synthase chain.

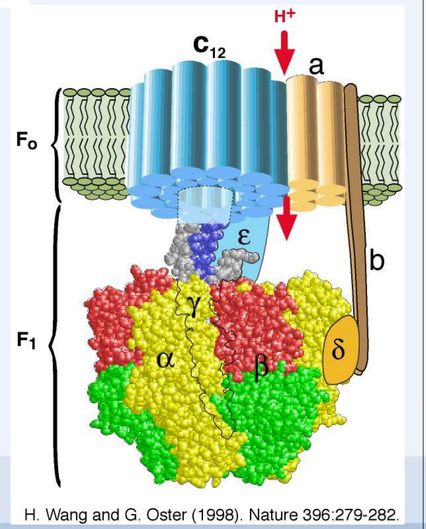

Figure 2

DISCUSSION

Because our genes were located in front of and behind one another, we were lead to speculate that our genes form an operon. Together, these genes function in ATP synthase, which means that the genes function as enzymes that produce ATP for energy that the bacteria can utilize. From the results in the table and the previous information, we speculated that the bacteria needed energy in imipenem, cefotax, and the control, so it transcribed RNA to achieve this purpose. For example, while the cell was living in cefotax, the gene needed to synthase ATP for energy, so it transcribed gene 154 and gene 159, with a fold change of 2.0 and 1.5, to achieve this. So, in cefotax, gene 156 and gene 157 were not needed in producing ATP for energy, so transcription decreased, creating a fold change of 1.0 and 1.3. While living in imipenem, the cell needed to make ATP for energy as well, so it transcribed gene 156 to make a fold change of 2.2. In imipenem, the cell did not need to use gene 154, gene 157, and gene 159 to produce ATP for energy, so transcription decreased to allow the fold change to be -1.5, -1.6, and -1.8. Gene 155 was not needed in cefotax or imipenem to help make ATP for energy, so no significant changes in the increase and decrease of transcription were found because the fold changes were only 1.2 in cefotax and -1.1 in imipenem. Overall, the data we found supported our original goal of understanding the DNA of *E. anophelis* better and discovering how much RNA was transcribed in each condition. However, since our genes are located near one another, our results are inconclusive because all genes were transcribed in different amounts even though the genes serve relatively the same purpose. This revelation would lead us to research why certain genes were transcribed in higher or lower amounts since they all perform ATP synthase.

REFERENCES

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2. N.d. ATP synthase. *Wikipedia, The Free Encyclopedia*.
3. The RAST Server: Rapid Annotations using Subsystems Technology. Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formsma K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil LK, Paarmann D, Paczian T, Parrello B, Pusch GD, Reich C, Stevens R, Vassieva O, Vonstein V, Wilke A, Zagnitko O. 2008. *BMC Genomics*. PubMed.

Background:

http://www.pptbackgrounds.org/classy-and-authoritative-backgrounds.html

Image:

https://users.soe.ucsc.edu/~hongwang/ATP_synthase.html