A-T-P, Easy as 1-2-3

GRP# 10

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ABSTRACT

Elizabethkingia anophelis R26 is a subunit of the Elizabethkingia bacteria genome that contains thousands of genes and proteins residing in it. These genes can cause different types of antibiotics to resist the effect to the antibiotics, Cefotaxime and Imipenem, and what the genes functibacteria. The experiment we conducted searched for what genes had a negative ons were to the bacteria genome. The genes we tested were ATP synthase F0 subunit b genes, ATP synthase delta chain, ATP synthase gamma chain, ATP synthase alpha chain, and ATP Synthase beta chain. We looked further into the genes and evaluated their RNA sequences as well as if they played a key role in how the bacteria operates.

INTRODUCTION

Elizabethkingia Anophelis is a gram-negative bacterium from coming from the Anopheles Gambia Mosquito. This bacterium can cause neonatal meningitis and in 2016 the states of Wisconsin, Michigan and Illinois had an outbreak with 61 confirmed cases with 21 fatalities. Although deaths occurred in the very old and very young it remains difficult to treat due to it being resistant to the majority of antibiotics. [2][3]After getting the results of the DNA sequence we began to study the ATP synthase to determine if there was any change under new conditions, and if so what.

MATERIALS AND METHODS

- To begin our experiment, we chose a set of genes in the Patric database and described briefly what each gene's assignment was.
- From there, we had to convert our gene name into the appropriate gene name for the RAST database in order to find out whether or not the genes are turned on when introduced to antibiotics.
- In order to convert the genes, we logged into the RAST database and plugged our Patric names into the BLAST system which gave us the same gene name for both databases.
- We searched through the RNAseq spreadsheet, provided on D2L by Dr. Canaan, where we found our genes, located in the 550th to 554th rows, and recorded the transcription pattern observed from our group of genes and placed our results in a table.
- After this, we went back to the RAST database and found a picture of each of the genes being observed.
- To conclude, we made our interpretations as to if our genes were turned on when introduced to antibiotics or not.

RESULTS

We first gathered information on each genome in the photosynthesis pathway and found that:
ATP synthase Beta chain- Produces ATP from ADP in the presence of a proton gradient.[5][6]
ATP synthase Gamma chain- Produces ATP from ADP and is also important in regulating ATPase activity and the flow of protons through the CF0 complex.[1]
ATP synthase Alpha chain- Works alongside the Beta chain to form an ATP catalase[4][5]
ATP synthase Delta chain- Holds the F1 complex stationary and links the Alpha and beta chains
ATP synthase F0 factor- Is the primary function of the enzyme is to hydrolyze ATP to generate this potential difference.[7]
All genes in the photosynthesis pathway work together in some way to form ATP, the cells energy source, during the process of photosynthesis.

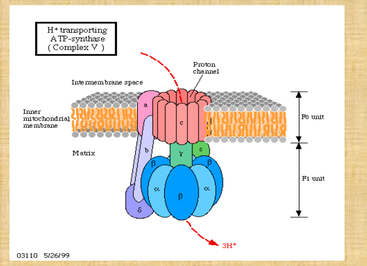
After translating the Patric database name for the genomes through Blast were able to obtain the Rast database names:
ATP synthases Beta Chain - fig|1246994.3.peg.2583
ATP synthase Delta Chain-fig|1246994.3.peg.3546
ATP synthase Alpha Chain-fig|1246994.3.peg.3545
ATP synthase Gamma Chain-fig|1246994.3.peg.3544
ATP F0 Sector Subunit-fig|1246994.3.peg.3547

Using the Rast database names and the excel sheet provided by Dr. Cannan we then recorded the transcription patterns for each genome. (Shown in the table below)

The last gene is a hypothetical but because the genes are so close to the other it can be inferred that it is part of an operon. The genes have a mathematically high significance but no biological outcome/significance. The genes are not highly expressed maybe due to a repressor.

RAST Name	Fold Change* (Cefotax/Control)	Fold Change* (Imipenem/control)	TOTAL mRNA ** from all 3 conditions	mRNA Counts Control	mRNA Counts Cefotax	mRNA Counts Imipenem
ATP synthases Beta Chain – fig|1246994.3.peg.3548	-1.5	-1.2	23	15	20	58
ATP synthase Delta Chain- fig|1246994.3.peg.3546	2.0	-1.7	36	10	20	6
ATP synthase Alpha Chain- fig|1246994.3.peg.3545	1.5	1.8	17	4	6	7
ATP synthase Gamma Chain- fig|1246994.3.peg.3544	-1.4	1.1	20	7	5	8
ATP F0 Sector Subunit- fig|1246994.3.peg.3547	1.3	-1.0	20	6	8	6

DISCUSSION



- In the ATP pathway, the alpha and beta genes help create energy for the cells inside the Elizabethkingia anophelis bacteria.[4][9]
- The delta chain gene helps keep the F1 stationary as the rotary motor is in motion[8][11]
- The gamma chain connects the motor on the portions of the alpha and beta genes, that provides energy for the Elizabethkingia bacteria, where the gamma chain serves almost like a bridge connecting the two together.[4][5][9][6]
- When we converted our gene sequences from Patric to Rast we were able to evaluate the transcription of our genes under the conditions of Cefotax and Imipenem and overall learn more about them and if they are effected by them
- The last gene in the table is a hypothetical protein but appear to be a part of another operon.

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