Analyzing ATP Synthase Gene Activity in *Elizabethkingia anophelis*

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ABSTRACT

Elizabethkingia anophelis is a gram-negative bacteria that causes blood stream infections in the human body. In this study, databases were used to study genes associated with ATP synthase. Each of the subunits investigated serve a specific function in the ATP synthase reaction. The expression of genes was analyzed under the influence of Cefotax and Imipenem antibiotics in order to determine what specific genes were harmed under antibiotics. It was concluded that ATP synthase gamma chain was expressed heavily under Cefotax and that ATP synthase delta chain was expressed heavily under Imipenem which could indicate a possible disruption to the ATP synthase reaction.

INTRODUCTION

The Elizabethkingia anophelis bacteria was discovered in 1959 by bacteriologist Elizabeth King ¹ and is a gram-negative rod that does not form spores, and is not motile². However, it causes bloodstream infections in humans that are difficult to source, diagnose and treat. Recent outbreaks in the United States this year have increased interest in the bacteria because it is highly resistant to a number of traditional antibiotics that are used to treat routine bacteria in spreading, and by analyzing how different antibiotics affect the gene expression of genes involved in ATP synthase, one could be able to identify how to harm the energy production, and thus kill the bacteria. Gene location and expression under the influence of antibiotics was investigated in order to reach a possible cure.

MATERIALS/METHODS

1) Genes were found by navigating to the PATRIC database $^{\rm 3}$ through the link given.

- 2) The Photosynthesis pathway was chosen, revealing 7 genes involved in ATP synthase.
- 3) Genes were sequenced and matched to the RAST database⁴.

4) The "Visual Image" for each gene was found in order to determine gene location.

5) The gene expression was also determined under the influence of Cefotax and Imipenem antibiotics.

RESULTS

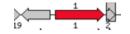


Figure 1. The gene location of (1) ATP synthase beta chain⁴. It is located between the Riboflavin kinase gene (left) and the ATP synthase epsilon chain (right).

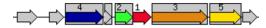


Figure 2. The gene location of (1) ATP synthase delta chain, (2) ATP synthase F0 subunit b, (3) ATP synthase alpha chain, (4) ATP synthase F0 subunit a, (5) ATP synthase gamma chain.⁴

| Gene Number | Gene | Control | Cefotax | Imipenem | Total | Cefotax Fold | Imipenem Fold |
|------------------------|------------------------------|---------|---------|----------|-------|-----------------|------------------|
| fig 1246994.5.peg.1117 | ATP Synthase beta chain | 13 | 20 | 9 | 42 | +1.5 | -1.4 |
| fig 1246994.5.peg.154 | ATP Synthase gamma chain | 120 | 244 | 78 | 442 | +2.0 | -1.5 |
| fig 1246994.5.peg.155 | ATP Synthase alpha chain | 126 | 146 | 117 | 389 | +1.2 | -1.1 |
| fig 1246994.5.peg.156 | ATP Synthase delta chain | 105 | 106 | 232 | 443 | +1.0 | +2.2 |
| fig 1246994.5.peg.157 | ATP Synthase F0 Subunit B | 36 | 47 | 23 | 106 | +1.3 | -1.6 |
| fig 1246994.5.peg.158 | ATP Synthase F0 Subunit C | 110 | 125 | 97 | 332 | +1.1 | -1.1 |
| fig 1246994.5.peg.159 | ATP Synthase F0 Subunit A | 182 | 281 | 102 | 565 | +1.5 | -1.8 |

Table 1. The gene expression of each researched gene under the presence of a control, Cefotax antibiotic and Imipenem antibiotic. Genes that were expressed significantly higher are highlighted in yellow.

DISCUSSION

While all of the researched genes were involved in a subunit of the ATP synthase reaction, the ATP synthase beta chain (Figure 1) was not located near the other ATP synthase subunits (Figure 2). However the ATP synthase beta chain gene did not express itself significantly higher under the presence of Cefotax or Imipenem antibiotics, thus location was concluded to be unimportant.

The ATP synthase gamma chain did significantly increase expression under the presence of the Cefotax antibiotic (Table 1). This could indicate that the regulation function of this subunit was harmed in the presence of this antibiotic and higher amounts were needed.

The ATP synthase delta chain significantly increased under the presence of the Imipenem antibiotic (Table 1). The function of this subunit is to attach the alpha and beta subunits to the peripheral stalk and is crucial to prevent these subunits from rotating⁵. Thus if gene expression is increased it could indicate that this connection between the peripheral stalk and alpha/beta subunits might have been harmed in the presence of the Imipenem antibiotic.

While each subunit has its own function in the ATP synthase reaction, each comes together to serve a specific function. For example, if the delta chain is harmed under the Imipenem it could allow the alpha and beta units to rotate which would upset the entire reaction and severely harm the bacteria's ability to create ATP or energy. If this process is harmed it could possibly reveal a way to kill the bacteria and reveal a cure.

REFERENCES

¹ Alex Berezow. 2016. Elizabethkingia: Is This Mysterious Disease Coming from Hospitals? Retrieved October 25, 2016 ²Elizabethkingia anophelis: The Upper Midwest Scourge. n.d. Retrieved October 25, 2016 ³ DI TPIC Distribution of the Statement of the State

³ PATRIC Database:

https://www.patricbrc.org/portal/portal/patric/CompPathwayTable?cTy pe=genome&cld=1246994.3&algorithm=PATRIC&ec_number= 4RAST Database: http://rast.nmpdr.org/rast.cgi?page=Jobs 5Jonathan M. May, Permalink. 2013. ATP Synthase, an Energy-Generating Rotary Motor Engine. Retrieved November 01, 2016