# Significant Strands in E. Anophelis R26

24

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## INTRODUCTION

Elizabethkingia Anophelis R26 is a bacteria that causes human disease; it was originally isolated in the gut of mosquitoes(3). It is resistant to many different antibiotics including most betalactames. Beta lactames are antibiotics starting with penicillin and then all the generations of penicillin there after. Before this experiment was started Dr. Canaan and her lab team had sent in data containing information on how Elizabethkingia Anophelis R26 was affected by the beta lactames Cefotax and Imipenem (3). The interpretations of the data were received while group 24 was conducting research. The data received back showed the rates at which RNA was being transcribed by Elizabethkingia Anophelis R26 while it was under normal conditions and under the affects of Cefotax and Imipenem. Before this data had been obtained, group 24 had been looking at a set of five genes that they thought could be working together. These genes were 1548 which is a bifunctional protein: zinc-containing alcohol dehydrogenase; 1550 which is a ATP Dependent DNA Helicase RecQ; 1553 which is a cell division trigger factor;1554 which is a Methionyl-tRNA formyltransferase; and 1555 which is a outer membrane protein A precursor (2). Using the data obtained from Dr. Canaan's research, group 24 was able to see exactly how each of the genes being investigated were being transcribed in the different environments.

## MATERIALS AND METHODS

Using the RAST db, the group searched for a cluster of genes that were interesting on the genome browser (2). Once the group determined a cluster of genes, the group used Google and Wikipedia to discover more information about the genes and record their functions. After recording the results, the group was given a table which consisted of the fold changes observed for Elizabethkingia Anophelis R26 while it was grown under control conditions, then with Cefotax, and Imipenem. The group searched and recorded the number of transcripts observed grown under control conditions, Cefotax, and Imipenem as well as the total number of transcripts observed in all conditions and the fold change in transcription in Cefotax compared to the control and Imipenem compared to the control for each of the genes in the group (3). Significant changes in the abundance of transcripts within the conditions were also noted in the results. The group returned to the RAST db and located the genes by searching. With each gene, the gene name was selected which led to a new page that contained an image for the Visual Region Information, where the image was captured through a screenshot and was cropped to display the region of interest.

## SUMMARY OF RESULTS

Gene 1548 showed a significant difference when Impenem was present but not when Cefotax was present. Gene 1550 did not show any significant results in the presence of Cefotax or Impenem. Gene 1553 and 1555 showed significant fold changes when exposed to Impenem, but not to Cefotax. Gene 1554 had the opposite reaction when it showed significant fold change when exposed to Cefotax compared to Impenem. The table shows that four of the five genes that we looked at had a significant fold changes.

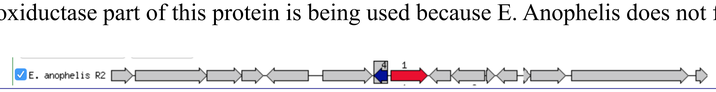
Table 1 (3)

| Genes | Total | Control | Cefotax | Impenem | Fold changes with Cefotax | Fold changes with Impenem |
|---|---|---|---|---|---|---|
| 1548 | 79 | 21 | 27 | 31 | 1.3 | 1.5 |
| 1550 | 3 | 1 | 1 | 1 | -1.0 | -1.0 |
| 1553 | 4 | 1 | 1 | 2 | -1.0 | 2.0 |
| 1554 | 4 | 1 | 2 | 1 | 2.0 | -1.0 |
| 1555 | 4 | 1 | 1 | 2 | -1.0 | 2.0 |

## RESULTS

**Gene 1548: Bifunctional Protein-Zinc-containing alcohol dehydrogenase**

This protein has two functions. It is an alcohol dehydrogenase and a Quinone oxidoreductase (2). In bacteria an alcohol dehydrogenase acts as a catalyst in fermentation (8). It allows the bacteria to thrive because, because it has a constant supply of NAD+. The second part of this protein the Quinone oxidoreductase keeps the bacteria in a constant supply of NADP+ and semiquinone (9). In Elizabethkingia Anophelis R26 it is more likely that the oxiductase part of this protein is being used because E. Anophelis does not ferment.

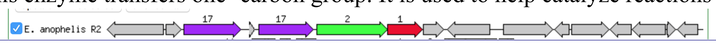



**Gene 1550: Cell division trigger factor**

It manages the creation and destination of the Z ring, a structure that marks where the cell will divide. This strand is crucial as the formation of the Z ring determines the site of division as well as the moment the cell divides (6).

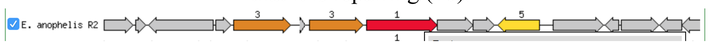

**Gene 1553: Methionyl-tRNA formyltransferase**

This enzyme transfers one- carbon group. It is used to help catalyze reactions (5).



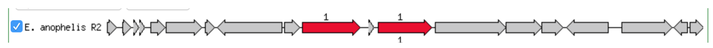

**Gene 1554: ATP Dependent DNA Helicase RecQ**

It is involved in a recombination pathway, which is a genetic recombination that brings identical molecules together of DNA (7). It is an enzyme involved and in various types of DNA repair. This protein has been known to also be involved in genetic disorders because if its ability to mismatch genes that it is repairing (10).




**Gene 1555: Outer membrane protein A precursor or OmpA**

It is used to code major outer membrane protein. OmpA has lots of different mutations. OmpA can be utilized in many different ways by different proteins. In some cases it is used as a processing protein. It guides other proteins where they need to be (1,4).




## ABSTRACT

Our group was interested in looking at proteins in Elizabethkingia Anophelis R26. We found a set of five genes that we thought worked together to create cell division. In order to find these genes we used the Rast Database (2). Once we had located the genes of interest we looked at the table of fold changes provided by Dr. Canaan to see if they were actually being transcribed (3). The table showed that four of the five genes we were investigating had significant fold changes. We concluded that because of the number of transcriptions that the only gene that really had significant fold changes was that of gene 1548. Further studies would need to be conducted to verify whether or not the set of five genes are actually involved in cell division or not.

## DISCUSSION

After searching the fold changes, all genes except for 1548 are insignificant as the total fold changes were never greater than four. Since these changes are not greater than four, there is not enough data to prove whether it was a significant change, thus ruling the data insignificant. At first, the cluster of genes seemed to be related to each other through cell division. We believed these five proteins all played a part in the creation of new cells. The bio functional protein containing zinc gives the cell that is about to split energy. The cell division trigger uses that energy to create a division in a cell. After that the Met-t RNA formyltransferase translate initial bacterial factors. DNA Helicase RecQ comes along and repairs the DNA of the new cell. Finally OmpA helps to build up the outer wall of the cell and make it durable. However, the process of cell division is more complicated than we thought. Further studies would need to be conducted to verify if the genes that we have located are in fact involved in cell division.

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