



# RNA Transcription in *E. anophelis*

GRP#13

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## ABSTRACT

In this study we were able to locate and analyze genes in the *E. anophelis*. After discovering our genes, we took a look at the pathways of the genes and briefly described them. Later, obtaining the DNA sequencing for our previously selected genes. Once we acquired the DNA sequences, we then took a look at the RNAseq data for the genes and thus directing us to analyze the surrounding genes.

## INTRODUCTION

*Elizabethkingia anophelis* is a Gram negative, non-spore forming bacteria arranged in singles and pairs of rod shaped cells. The cells appear as medium white, yellow, or grey colonies in cultures. *E. anophelis*' growth is optimal at 30-31 degrees Celsius and 37 degrees Celsius. *E. anophelis* is a non-motile bacteria. Oxygen is required as *iE. anophelis* is and obligate aerobe. It is positive in extracellular enzymes DNase, starch, and esculin. *E. anophelis* is negative in extracellular enzymes agar breakdown and starch. *E. anophelis* is positive in intracellular enzymes caalase, oxidase, indole, glucose, lactose, maltose, mannitol and trehalose. It is negative in intracellular enzymes urease, nitrate reductase, arabinose, raffinose, salicin, sucrose and xylose. It is resistant to over 20 antibiotics.

## MATERIALS AND METHODS

Once we navigated to the genomic database, we searched and selected any four genes coding for proteins and briefly described each individual gene. We also used the genomic database to find the DNA sequence for the genes. Then using BLAST to convert from the PATRIC database to RAST. Once the data had been converted, we were then able to analyze the statistics given on the spreadsheet to record the necessary data for the genes. After finding our genes and those surrounding, we acquired the Visual Region Information from the RAST database.

## RESULTS

### Pathway Name:

Fatty acid elongation

### GENES:

[1246994.3.peg.3466](#) - BcrR – Fold Change(Cefotax/Control) -1.0; Fold Change(Imipenem/Control) 2.0; Total mRNA 20; mRNA Control 5; mRNA Cefotax 5; mRNA Imipenem 10  
[1246994.3.peg.3494](#) - Oar Protein - Fold Change(Cefotax/Control) -1.0; Fold Change(Imipenem/Control) 1.1; Total mRNA 28; mRNA Control 9; mRNA Cefotax 9; mRNA Imipenem 10  
[1246994.3.peg.845](#) - Hypothetical Protein - Fold Change(Cefotax/Control) -1.8; Fold Change(Imipenem/Control) 1.1; Total mRNA 42; mRNA Control 16; mRNA Cefotax 9; mRNA Imipenem 17  
[1246994.3.peg.847](#) – Ribosome small subunit-stimulated GTPase EngC - Fold Change(Cefotax/Control) 1.7; Fold Change(Imipenem/Control) -1.9; Total mRNA 87; mRNA Control 27; mRNA Cefotax 46; mRNA Imipenem 14  
[1246994.5.peg.2619](#) - [3-ketoacyl-CoA thiolase Acetyl-CoA acetyltransferase](#) Fold Change (Cefotax/Control) 2.0; Fold Change (Imipenem/Control) -1.0; Total mRNA 4.0; mRNA Control 1; mRNA Cefotax 2; mRNA Imipenem 1  
[1246994.5.peg.2621](#) – [3-hydroxyacyl-CoA dehydrogenase](#) Fold Change (Cefotax/Control) -2.0; Fold Change (Imipenem/Control) -1.0; Total mRNA 5.0; mRNA Control 2; mRNA Cefotax 1; mRNA Imipenem 2  
[1246994.5.peg.2622](#) – [Enoyl-CoA hydratase](#) Fold Change (Cefotax/Control) -1.0; Fold Change (Imipenem/Control) 2.0; Total mRNA 4.0; mRNA Control 1; mRNA Cefotax 1; mRNA Imipenem 2  
[1246994.5.peg.1490](#) – [Enoyl-CoA hydratase](#) Fold Change (Cefotax/Control) 1.7; Fold Change (Imipenem/Control) -1.3; Total mRNA 1447.0; mRNA Control 415; mRNA Cefotax 715; mRNA Imipenem 317

## DISCUSSION

The reason for this research is to find out more about the *E. anophelis* genome. The majority of this data was collected by sending samples of *E. Anophelis* to a lab for analysis and once it was returned to us the results were sent to a supercomputer to be calculated into something we could understand. What we learned about the genes we researched was that most of them are seemingly unrelated to each other, other than the Acetyl-CoA acetyltransferase and the Enoyl-CoA hydratase and the later of the two hydrates the bond of the first gene. We also found that the gene Acetyl-CoA acetyltransferase reverses the formation of acetyl-CoA which involves nerve endings and synaptic reactions which could be seen as something that may cause symptoms in people infected with *E. anophelis* as it has something to do with the process that is the same as many poisons regarding the stop of production of acetyl-CoA.

## REFERENCES

- <http://rast.nmpdr.org/seedviewer.cgi?page=BrowseGenome&organism=1246994.5>
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- <http://darwin.biochem.okstate.edu/blast/blast1990.html>