We Are Not That Important

GRP# 11

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ABSTRACT

Elizabethkingia anophelis, a bacteria commonly found in the belly of mosquitoes, has recently been causing sickness and death in humans (1). The purpose of this experiment was to determine how different antibiotics affected the transcription of certain genes in *E. anophelis* R26. We chose five genes that corresponded to the amino sugar and nucleotide sugar metabolism pathway. Those five genes, DNA Primase, Beta-hexosamine, Multiple polyol-specific dehydrogenase, Fructokinase, and Mannose-1-phosphate guanylyltransferase, were transcribed a total of 97 times, with minimal variance under each condition. We can conclude that the five genes we were interested in, were not vital to *Elizabethkingia anophelis.*

INTRODUCTION

Elizabethkingia is a type of bacteria normally found in the environment like in soils, rivers, and reservoirs. This bacteria rarely makes people sick, but there have been a few localized outbreaks in the U.S. that are normally in healthcare environments. It has been known to cause meningitis or bloodstream and respiratory infections in people with weak immune systems (1). We have been studying the *Elizabethkingia anophelis*. Our group chose the amino sugar and nucleotide sugar metabolism pathway. The amino sugar and nucleotide sugar metabolism pathway codes for genes that assist in the catabolism (breakdown) and anabolism (synthesis/creation) of amino sugars and nucleotide sugars (2). The five genes we chose from this pathway are DNA primase, Beta-hexosaminidase, Multiple polyol-specific dehydrogenase, Fructokinase, and Mannose-1-phosphate guanylyltransferase.

MATERIALS AND METHODS

Digital Databases
•Patric Database (3)
•RAST Database (4)
•BLAST (5)
•Digital Lab Notebook

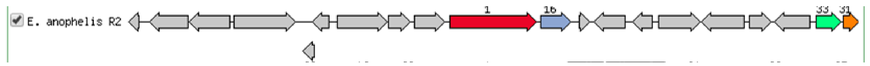
1.We chose five gene in the amino sugar and nucleotide sugar metabolism for *Elizabethkingia anophelis* R26.
2.We then recorded the number of transcriptions for each of the five genes under each of the three conditions *E. anophelis* was grown.
3.We determined the level of significance for each of the genes and their numbers of transcriptions.

RESULTS

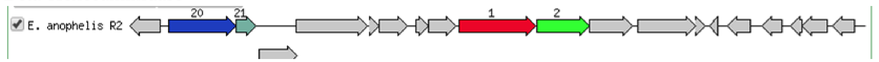
Gene Names	Control Condition	Cefotax	Imipenem	Total Number	Cefotax-Control	Imipenem-Control
DNA Primase	5	7	5	17	1.4	-1.0
Multiple Polyol–Specific Dehydrogenase	2	1	4	7	-2.0	2.0
Fructokinase	8	7	11	26	-1.1	1.4
Mannose-1-Phosphate Guanylyltransferase	5	2	6	13	-2.5	1.2
Beta-Hexosaminidase	10	8	16	34	-1.3	1.6

The five genes of interest were transcribed a total of 97 times out of all three conditions. DNA Primase was transcribed 17 times in total. While multiple polyol–specific dehydrogenase and mannose-1-phosphate guanylyltransferase were both transcribed even less. Fructokinase with 26 total transcriptions and beta-hexosaminidase with 34 total transcriptions, although had more transcriptions than the other three genes, still did not have enough data to make any conclusions about *E. anophelis* R26.

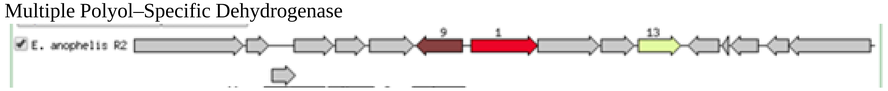
DNA Primase



Beta-Hexosaminidase

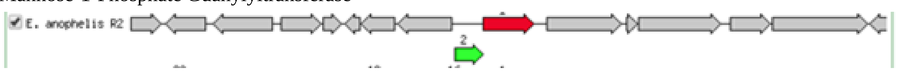


Multiple Polyol–Specific Dehydrogenase



Fructokinase

Mannose-1-Phosphate Guanylyltransferase



Using the RAST database we were able to compare the genes surrounding each of the genes of interest and determine the possible reasons for such low transcriptions rates.

DISCUSSION

The purpose of this experimenting on *Elizabethkingia anophelis* R26 was to discover how the bacteria was affected in different environments; normal conditions, cefotax, and imipenem. The goal was to determine what genes were turned off or turned up by the bacteria in each of the conditions. This was done by, allowing *E. anophelis* R26 to grow in the three different conditions. Then the bacteria was collected and the number of transcriptions for each of the genes was recorded. With the amount of transcriptions for each of the genes we were able to determine how each condition affected the genes transcribed and how many times each of those genes were transcribed. From the roughly 3800 genes, we chose five gene that corresponded to the amino sugar and nucleotide sugar metabolism pathway in *E. anophelis* R26. Our five genes--DNA Primase, Beta-hexosamine, Multiple polyol-specific dehydrogenase, Fructokinase, and Mannose-1-phosphate guanylyltransferase--were barely transcribed in all three of the environmental conditions. With roughly 124 million total RNA reads, the five genes of interest were only transcribed a total of 97 times. With this information we can determine the five genes of interest were not necessary in the catabolism of the antibiotics, imipenem and cefotax. However the severely low number of transcriptions can be attributed to the genes not being needed in the bacteria. The genes of interest may not important to the everyday function of the cell, which would explain low transcription numbers. There is also a possibility that *E. anophelis* R26 does not actually have these genes, and the databases incorrectly predicted these genes. With this data we can not truly determine whether *E. anophelis* R26 was affected by the different conditions based on the genes we chose.

REFERENCES

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