A Diagnosis of ABC Transporters, ATP-binding proteins in *Elizabethkingia* anophelis R26

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ABSTRACT

Elizabethkingia anophelis originates from mosquitos and is commonly found in soil, river waters, and reservoirs. Elizabethkingia, itself, is a bacterium that has recently (March 2016) sprung an outbreak in Wisconsin, Michigan, and Illinois with a total of 65 cases (including 20 deaths). This has become the largest outbreak, and this bacteria is involved in the bloodstream of the host. We as a group or class are identifying selected genes within the genome, and we are trying to find and clarify different functions in hopes of adding to the research of Dr. Patricia Canaan.

INTRODUCTION

Our class, supervised by Dr. Canaan, is studying *Elizabethkingia anophelis*. Which is a bacteria that causes human disease.[3] This bacteria was first was traced back to the gut of mosquitoes.[4] The bacteria is resistant to multiple antibiotics.[3] Our study more focuses around the fact that the bacteria has multiple genes that code for ABC Transporter- ATP Binding Proteins.[1] It is believed that discovering why the bacteria codes multiple times for the same function can lead to a discovery of a way to combat the bacteria or at least understand the bacteria's reasoning for it. We lack the information as to understanding why, but by examining expression numbers we can determine how these genes potentially relate to the cells ability to cause disease in humans.[3].

MATERIALS AND METHODS

We navigated to the Rast database and logged into the database using the credentials that our teacher provided. We located our genes by searching for "ABC transporter ATP-binding proteins" in the function column of the database. That narrowed our search from 3,800 genes to 11 genes and from there we narrowed our search even more by choosing the five genes we thought to be the most interesting. Once we found our genes, we continued to use the Rast DB to compare and contrast the gene sequencing, the visual region information, and the transcription patterns.

						RE	SULTS
During this research assignment, we are unab to do any experimental activities to carry out any theories due to lack of information. We are only able to create theories, and evaluate possibilities of the genes in <i>Elizabethkingia</i> <i>anophelis</i> from the databases. We have discovered and chose 5 out of 11 genes within <i>E. Anophelis</i> that share the same functions[These include: • fig 1246994.5.peg.70 • fig 1246994.5.peg.347 • fig 1246994.5.peg.347						bleEach of these five gen function of being ABC binding proteins. ABC binding proteins are inv and export of a wide v ranging from all ions to The major function of A [1]nThe major function of A is to provide essential to by transporting substra- membrane Each individual	
 ng 1; fig 1; 	240994 246994	.5.peg./	2982 8603				was compared
	Transcripts under Control Conditions	Transcripts grown with Cefotax	Transcripts grown with Imipenem	Total Transcripts overall 3 conditions	Fold Change in transcription in <u>Cefotax</u> compared to	Fold Change in transcription in Imipenem compared to	changes or lack of genes are not ali
Gene 70	1	2	1	4	Control 2.0	Control -1.0	when referring
Gene 296	17	9	36	62	-1.9	2.1	number) of tra
Gene 347	92	78	75	245	-1.2	-1.2	specific gene
							function for E
Gene 2982	3	6	3	12	2.0	-1.0	anophelis R26
Gene 3603	9	13	13	35	1.4	1.4	expression of the second s
Fach	of that	rongorik	and game		agos tal	10.110	identified by th
something specific and different for each of the							BLASTDB. Th
	C I	cho	sen gen	es.			comparisons are
Gene 70 was surrounded by hypothetical proteins,							in the t
utative membrane protein. For this significance, it is							• ng 1246994.5.peg./0
more 1	han lik	ely regu	ilated by	y the tra	anscript	ional	E. anophelis R2
Gene 206 was surrounded by hymothetical proteins							• fig 1246994.5.peg.296
Hydroxymethylglutaryl-CoA reductase, and							anophelis R2
COG2363.							• fig 1246994.5.peg.347
Gene 347 was surrounded by hypothetical proteins							
considered non active for the bacteria.							
Gene 2982 was surrounded by a Sensor histidine							• fig 1246994.5.peg.2982
kinase, a response regulator, Probable RND efflux							anophelis R2
ABC Transporter, permease protein							• fig 1246994.5.peg.3603
Gene 3603 was surrounded by a TonB-dependent							
siderophore receptor and hypothetical proteins.[1]							E. anophelis K2 ///

nes share a common C Transporter ATP-C Transporter ATPvolved in the import variety of substrates to macromolecules. ABC import systems nutrients to bacteria ates through the cell e[1][3]

gene transcript We as a group iny significant of changes. These ike in many ways to their level (or anscripts. Each 's identity and Elizabethkingia is shown in the he transcripts, if e RASTDB and he results of the shown to the left table.[2]



DISCUSSION

When examining the data from the Copy of E.anoR26_RNAseqData_FoldChanges excel sheet, there is no significant change in expression between the five ABC Transporter ATP-binding protein genes within Elizabethkingia anophelis. This means if the genes are expressed at all then they are expressed very little. Multiple factors may be responsible for this type of this response. For example, due to the redundancy in function between the genes, Elizabethkingia anophelis may express all the genes however they may not be "fully" expressed. This would mean that Elizabethkingia anophelis is producing a specific ABC transporter for ATPbinding proteins, however; because they all have similar functions, each ABC transporter can be used for a wide range of functions. In addition to this, there is posable explanation for this reaction in expression. Which is that all five ABC transporters, although unlikely due to the redundancy of the function, may be housekeeping genes. This would mean that all five ABC transporters would be expressed at all times, no matter the circumstances. This could be due to the functioning nature of ABC transporters. ABC transporters are used in active transport of a compound or a class of compounds over the membrane of the bacteria, which would be fundamental to Elizabethkingia anophelis due to the environment that it lives in. Elizabethkingia anophelis is found in the gut of mosquitos, and, as the result, Elizabethkingia anophelis would need a specific set of ABC transporters to allow it to move compounds in and out of its membrane. In addition to this one distinct finding between the five genes is that gene fig|1246994.5.peg.296 is commonly found in many other bacteria related species as well.

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