

Drop It Like It's Shock

Dr. Patricia Canaan, Jarrett Green, Kelly Wade, Joe Zucconi

ABSTRACT

To learn more about the bacterium, *Elizabethkingia anophelis*, we researched a pathway of five heat shock proteins and gathered information to aid Dr. Canaan in her research. After researching these proteins using the RAST and BLAST databases provided, we found that these proteins can be caused by stress and can oversee the correct folding and packaging of proteins. We also found that these proteins were transcribed in all three growth conditions which means they contribute to the process of making mRNA. Our research concludes the transcription of these five heat shock proteins.

INTRODUCTION

Elizabethkingia anophelis is a gram-negative, rod-shaped bacterium which as resulted in a multistate outbreak of mainly bloodstream infections in the states of Wisconsin, Michigan, and Illinois (1). Affecting primarily those individuals over 65 years of age with at least one serious underlying health conditions, the states long with the Centers for Disease Control and Prevention are attempting to isolate the source(s) and contain the outbreak before further spread occurs. (1). We are researching this topic to aid Dr. Canaan in her research to learn more about it and eventually find cure.

MATERIALS AND METHODS

We found our genes using the link on Brightspace that navigated the RASTdb. Under function, we searched heat shock, and five similar proteins popped up. We chose to research heat shock proteins purely based off of scientific interest. We then recorded basic information for each gene. We then navigated to the BLAST website using the link listed on Brightspace. Then, we typed in peg.223, peg.344, peg.345, peg.1796, and peg.2314 into the search engine. This allowed us to figure out the FASTA sequence for each gene, which then in turn revealed whether or not each gene was transcribed or not. We used the E.anor26_RNAseqData_FoldChanges table to determine if there were any significant changes in three different growth conditions of the control group, Cefotax, and Imipenem. A significant change is where the fold change is greater than or equal to 1.5 or less than or equal to -1.5.

RESULTS

According to en.wikipedia.org, heat shock proteins are now known to also be expressed during other stresses including exposure to col, UV light, and during wound healing or tissue remodeling (3). Many members of this group perform chaperone function by stabilizing new proteins to ensure correct folding or by helping to refold proteins that were damaged by the cell stress (3). Production of high levels of heat shock proteins can also be triggered by exposure to different kinds of environmental stress conditions, such as infection, inflammation, exercise, exposure of the cell to toxins. (3).

The two genes that surround peg.223 are peg.224 which is a hypothetical protein and tRNA. Surrounding peg.344 is peg.345, another heat shock protein and peg.343 which is Zinc dependent aminopeptidase protein. Next to peg.345 are peg.344 (a heat shock protein) and peg.347, an ABC transporter ATP-binding protein. Surrounding peg.1796 is peg.1795, a Manganese transport protein and peg.1798 (a hypothetical protein). Next to peg.2314, is peg.2313, a Aconitate hydratase and peg.2315 (a hypothetical protein).

DISCUSSION

All of the heat shock proteins are caused by stressful situations. The second gene is also known as heat shock protein 10. It is a co-chaperone to heat shock protein 60 and they work together. They aid in overseeing the correct folding and packaging of proteins so that they function correctly (2). All are either co-chaperones or part of the chaperone family, and aid in the folding and over watching of correct protein packaging.

All of our genes were transcribed which means that their DNA is in the process of converting to mRNA (5).

This process goes through the following steps:

- RNA polymerase, together with one or more general transcription factors, binds to promoter DNA.
- RNA polymerase creates a transcription bubble, which separates the two strands of the DNA helix. This is done by breaking the hydrogen bonds between complementary DNA nucleotides.
- RNA polymerase adds RNA nucleotides (which are complementary to the nucleotides of one DNA strand).
- RNA sugar-phosphate backbone forms with assistance from RNA polymerase to form an RNA strand.
- Hydrogen bonds of the RNA-DNA helix break, freeing the newly synthesized RNA strand.

If the cell has a nucleus, the RNA may be further processed. This may include polyadenylation, capping, and splicing.

The RNA may remain in the nucleus or exit to the cytoplasm through the nuclear pore complex (5).

REFERENCES

1. Downey, Pamela. "Elizabethkingia Anophelis: The Upper Midwest Scourge." *CEUfast*. N.p., n.d. Web. 1 Nov. 2016.
2. "GroES." *Wikipedia*. Wikimedia Foundation, n.d. Web. 27 Oct. 2016.
3. "Heat Shock Protein." *Wikipedia*. Wikimedia Foundation, n.d. Web. 27 Oct. 2016.
4. "Seed Viewer - Browse Genome." *Seed Viewer - Browse Genome*. N.p., n.d. Web. 01 Nov. 2016.
5. "Transcription (genetics)." *Wikipedia*. Wikimedia Foundation, n.d. Web. 01 Nov. 2016.

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Feature ID	Type	Contig	Start	Stop	Length (bp)	Function	Subsystems	Region
figl1246994.5.peg.223	CDS	gii442560384 gb ANIW01000066.1	235986	235537	450	Ribosome-associated heat shock protein implicated in the recycling of the 50S subunit (S4 paralog)	Cell division-ribosomal stress proteins cluster, DNA replication cluster 1, Heat shock dnaK gene cluster extended	show
figl1246994.5.peg.344	CDS	gii442560384 gb ANIW01000066.1	374925	375203	279	Heat shock protein 60 family co-chaperone GroES	GroEL GroES	show
figl1246994.5.peg.345	CDS	gii442560384 gb ANIW01000066.1	375320	376945	1626	Heat shock protein 60 family chaperone GroEL	GroEL GroES	show
figl1246994.5.peg.1796	CDS	gii442562097 gb ANIW01000060.1	52593	53129	537	Heat shock protein GrpE	GroEL GroES, Heat shock dnaK gene cluster extended, Protein chaperones	show
figl1246994.5.peg.2314	CDS	gii442562633 gb ANIW01000057.1	7430	6963	468	Small heat shock protein	- none -	show