Kennedie Helton, Lindsie Bortka, Caroline Price, Nikki Prince, & Dr. Patricia Canaan

ABSTRACT

Elizabethkinga anophelis is one strain in the *Elizabethkinga* species. This strain is found in the gut of mosquitos and causes human disease. We have researched five genes in the pathway of Osmoregulation, which controls the amount of water allowed in and out of the cell, in *Elizabethkinga anophelis* R26. While researching these genes, we have concluded that the genes in Osmoregulation in *Elizabethkinga* anophelis R26 have a significant change in the presence of Imipenem the majority of the time. The genes in Osmoregulation are all concluded not to be a part of an operon. Therefore, all of these genes work independently to perform the subfunction of Osmoregulation. This is vital to the cell becuase it helps to prevent the cell from becoming too hypotonic and too hypertonic and helps to keep it in a stable isotonic state

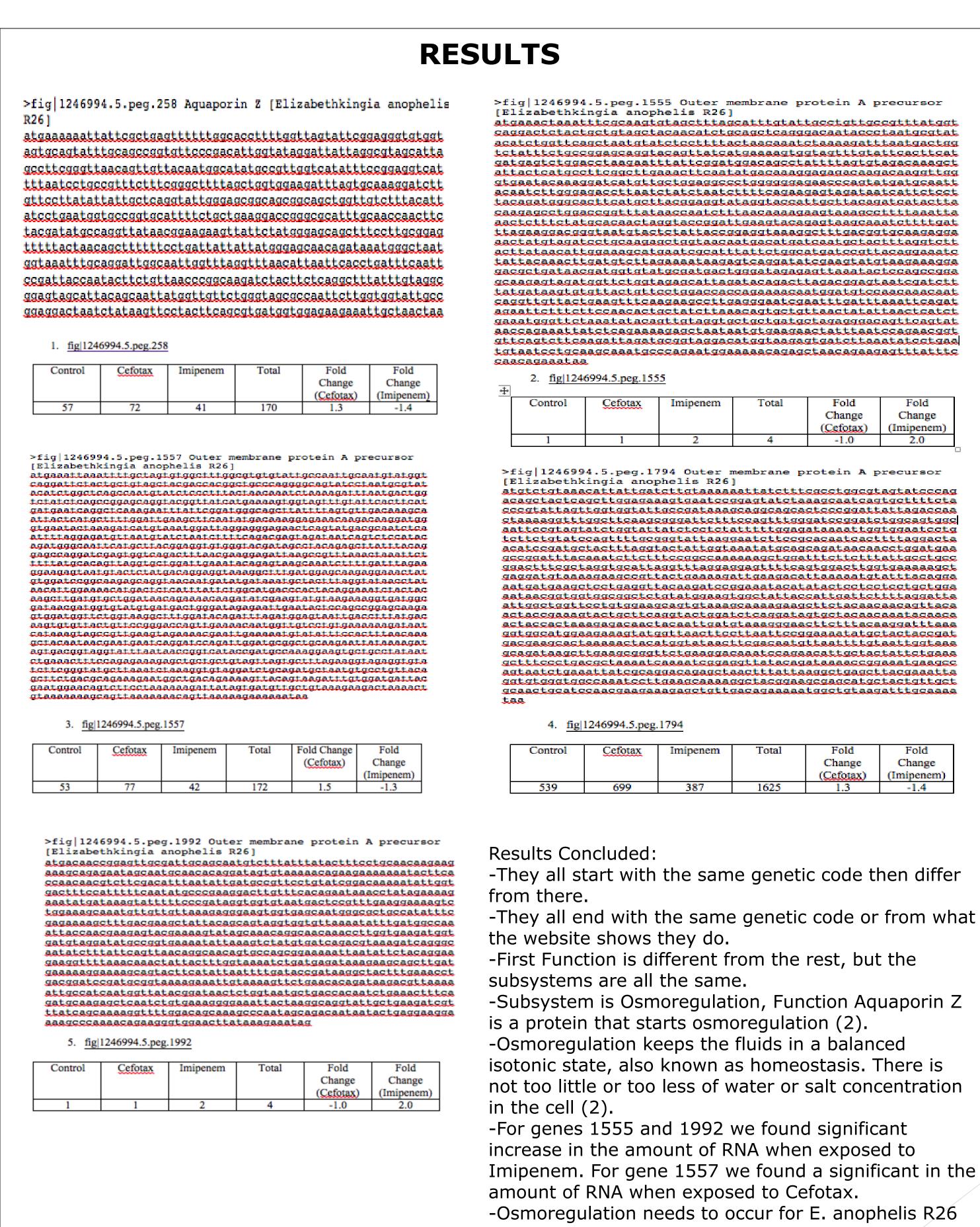
INTRODUCTION

Elizabethkingia anophelis is apart of the Elizabethkingia species. *E. anophelis* is a Gram-negative bacteria. *E. anophelis* is a dominant bacterial species found in the gut ecosystem of the malaria vector mosquito Anopheles gambiae. E. anophelis is a known human pathogen with cases reported worldwide, the most recent being Wisconsin. In multiple clinical cases, multidrug resistance was reported and the isolates were resistant against a wide variety of antibiotics. Studies also show that *E. anophelis* is an emerging bacterial pathogen for hospital environments, and its transmission route remains unknown (1). Bacteria can rapidly change their gene expression. We were trying to determine if there was a signifignt change in expression of 5 genes with the common sub-function Osmoregulation in the presence of Cefotax and Imipenem.

MATERIALS AND METHODS

In the course of our research, we used the RAST database to navigate the *Elizabethkingia anophelis* genome in order to try and link the various genes that handle osmoregulation within the cells of *Elizabethkingia* anophelis. After logging onto the RAST database, we navigated to the complete list genes within *Elizabethkingia* anophelis and searched for the subsystem "Osmoregulation" in order to identify the genes involved in this process. We found five genes that control osmoregulation, and used the RAST database to identify the specific functions of the five genes. Four of them have their function identified as "outer membrane protein A precursor" while the fifth is "glycerol uptake facilitator protein". We recorded these genes, their names, their DNA sequences, the genes that surround them, and their transcription sequence in our lab notebooks, then used what we found to make a conclusion.

Osmoregulation: *Elizabethkingia anophelis* Are You in or Out?



mbrane pi	rotein A p	recursor
atttgtati agetcagg gacageta gacageta tgacageta tgacageta tgacageta aggtaccai aggtaccai aggtaccai attetggca tgacagatai ggatagaga tacagatai ggatagaga tacagatai ggatagaga tgacagetai ggatagaga tgacagetai ggatagaga tgacagetai ggatagaga tgacagetai ggatagaga tgacagaga	accepting accept	catttataat taatgogtat taatgogtat taatgogtag ttooottoot agacaaaggt agacaaaggt tgatgogat tgatgogat toottttgat tgoaagagga tttaggtott acaggaaatc taagaaagga tcoaggogga atcoagcogga aatcgatott aagaaagga tooagcogga aatcgatott aagaaacgat taagtogatot taagtogatot agttoogga atatootgatot agttoogga atatootgatot agttoogga atatootgatot
Total 4	Fold Change (<u>Cefotax</u>) -1.0	Fold Change (Imipenem) 2.0
embrane protein A precursor		
aggcagca cagtttgg ttttggag atcttcag agctgga aggtttcag tgaagaca gatttcag tgaagaca tgaaggaag tcaggata taattceg aaagggaag taattceg aatccaga taattceg	ctoccggatt atacaggatc atacaggatc cagatacca ttottottt stggacttgg ttacacatgt atactoctcc cattgattot ctottacaac gtgctacaac stgctacaac stgctacaac stacttgttaca gaaaatatgc ttaattttgt acattgctac	tgetttteta attagaceaa tggeagtgge tggaateetg ttaggaeta eetggatgaa attgeetgee tgaaaaaget atttaeagga teetgetgga teetgetgga tttaggatta aasagatttaea taetaeegat aattggtaaa tattetgaaaa tattetgaaa tattetgaaa tatteggtaaa tattetgaaa tatteggtaaa tatteggtaaa tatteggtaaa tatteggtaaa
Total	Fold Change (Cefotax) 1.3	Fold Change (Imipenem) -1.4
e genetic code then differ genetic code or from what om the rest, but the on, Function Aquaporin Z regulation (2). luids in a balanced		
homeostasis. There is		

to survive in the presents of antibiotics.

DISCUSSION

Elizibethkingia anophelis is a bacteria that confounds everyone at this time. No one knows much about this bacteria and what it does and can do. By researching genes and pathways in this bacteria we have found a pathway that is vital to *Elizabethkingia* anophelis for it's survival. Osmoregulation helps it stay in a balanced osmotic environment. Without osmoregulation this bacteria could go into a hypotonic state and possibly explode. This bacteria could also go into a hypertonic state and dry out and die. Because of osmoregulation the bacteria can stay in a balanced isotonic state. There are multiple genes in *Elizabethkingia* that work in osmoregulation, yet all of these genes work separately not as an operon. This can mean that this bacteria has multiple backups to work to help it survive instead of depending on multiple to work together as a group. This means that *Elizabethkingia anophelis* cannot easily have a buildup of fluids that drowns the salt concentrations and cannot easily have a high salt concentration and little water to dehydrate it. All of the osmoregulation genes work to keep the bacteria balanced and they each also have different significant changes to different types of antibiotics, or none at all, making it hard to destroy all these genes.

REFERENCES

- 1. "Elizabethkingia Anophelis MicrobeWiki." Microbe Wiki. N.p., n.d. Web. 1 Nov. 2016.
- 2. European Bioinformatics InstituteProtein Information ResourceSIB Swiss Institute of Bioinformatics. "Imidazoleglycerol-phosphate Dehydratase." HisB. N.p., 2016. Web. 01 Nov. 2016.

