**INTRODUCTION**

Elizabethkingia anophelis is a multi-drug resistant and pathogenic bacteria. We decided to investigate the Oxidative phosphorylation pathway in the Energy Metabolism pathway class that contains eight unique genes as found in PATRIC database (4). We went in and found this pathway and the group of the genes and downloaded them individually. We then took each unique gene and found its DNA sequence data and the genome for the surrounding genes in a spreadsheet that was provided to us. Finally, we compared transcription ratios of our genes when exposed to cefotax and imipenem in comparison to control samples. We found that exposure to cefotax results in a trend of up-regulation of ATP Synthase gene transcription. Exposure to cefotax resulted in a change in transcription levels across multiple genes in the oxidative phosphorylation pathway of E. anophelis. The gene encoding the beta subunit of ATP synthase was transcribed in significantly greater numbers (50% increase) when the culture was exposed to cefotax. The same gene was transcribed less when exposed to imipenem, though by not a significant level. For the gene encoding the epsilon subunit, transcription increased by 100% when exposed to cefotax and remained the same when exposed to imipenem. The gamma subunit gene transcription increased by 100% when exposed to cefotax and decreased by 50% when exposed to imipenem. Transcriptions for the alpha subunit did not change by significant values when the culture was exposed to either antibiotic. Transcriptions for the delta subunit did not change when the culture was exposed to cefotax, but interestingly increased by 10% when exposed to imipenem. Transcription levels were not altered significantly by exposure to either antibiotic. The RNA sequence of each individual gene and to see if the transcriptions to find out why. After finding the this information about the strains of ATP synthase, we used this to look at the transcription levels with a control, Cefotax, and Imipenem to see if they were altered, and then decided if there was a significant change from the fold change, to see if there were any similarities or differences between transcription levels when comparing the control sample to the treated samples.

**RESULTS**

The oxidative phosphorylation pathway is a central process in the cell, responsible for generating ATP from ADP and inorganic phosphate. Our research began with each member of the group looking at the unique genes of E. anophelis. We then moved on to look at the RNA sequence of each individual gene and to see if the transcriptions to find out why. After finding the this information about the strains of ATP synthase, we used this to look at the transcription levels with a control, Cefotax, and Imipenem to see if they were altered, and then decided if there was a significant change from the fold change, to see if there were any similarities or differences between transcription levels when comparing the control sample to the treated samples.

**DISCUSSION**

We looked at multiple genes in the oxidative phosphorylation pathway of E. anophelis, more precisely the alpha, beta, delta, gamma, epsilon, b, and c subunits, and looked at the changes in their transcription when exposed to cefotax and Imipenem. Exposure to cefotax, which breaks down and ruptures the cell wall breaking the bacteria (6), most of the genes have an increased transcription rate which we can hypothesize as an increase in ATP production for enzymes to repair the cell wall and keep the bacteria alive. Further research into this could give us a better explanation to why this happens. When the listed genes are exposed to imipenem, which is bactericidal to rapidly multiplying cells and affects the cell wall inhibiting cell multiplication and growth (7), most of the genes have a decreased transcription rate. With that information we can hypothesize that the cells not being able to grow or multiply would decrease energy production thus decreasing the production of ATP. Again, further research into this can better explain the reason this negative transcription happens. The genes that weren’t transcribed by much we deemed to be unaffected by the antibiotics and so they didn’t have to produce energy. In our research on the RAST database, we found the beta and epsilon genes to be separated from the rest of the genes that were right next to each other in the genome. This could be a process of evolution between the separate pieces but it could also be due to an error of the placement in the database. We could use this information to help further the studies of other researchers over the E. anophelis bacteria and bring up some ideas to complete the process that we started here.

**REFERENCES**