Edward Bird

Dr. Youssef’s research on the Novel Phylum Candidatus Krumholzibacterium zodletonense

 I will be writing about Dr. Youssef new discovery of the novel bacterial phylum Candidatus Krumholzibacterium zodletonense. This bacterium was found in a natural spring in south-west Oklahoma, which was rich in sulfur and anoxic sulfide. This paper was published in the journal Systematic and Applied Microbiology in January of 2019. This bacterium actually started as a graduate class example, and practice metagenome. The class ran many different bioinformatical analyses and then discovered that it was a candidate for a new phylum. The group, along with Dr. Youssef and Dr. Mostafa wrote the paper after the class had finished in the fall of 2018.

 The reason this bacterium had to be captured, and sequenced from the spring is because it is not possible to grow it under laboratory conditions. Also through this method, of environmental metagenomics sampling, many other bacteria could be sequenced at the same time, giving more possibilities for unique and interesting bacteria to be studied. The reason these unique bacteria need to be studied is they are a source of novel biochemical pathways, and many different forms of antibiotic producing bacteria have been found using this method. While these techniques are lowering in cost today, they are still technically difficult, and require many computerized analyses.

Bioinformatical analyses rely on the use of highly complex algorithms to predict where the shorter fragments of DNA connect together, what DNA is associated with other DNA, and how to match DNA fragments to each other. These are just some of the more basic procedures of genomic annotation, but are used here in this analysis. For this project the raw data was first assembled into a MAG, and the binning of the contigs was then conducted to create an individual assembly for the organism. An assembly is basically the genome of the organism, but cut up into short fragments due to how sequencing is conducted. Using the assembly it was then possible to predict genes, as bacteria do not have introns. These predicted genes were then compared to a database of existing phylum to see there it fit, using a combination of 120 single markers. This is where it was found that this organism did not fit in genetically with any of the other phylum. At this point more analyses were conducted to determine functions of the bacteria

Once again the predicted genes were used to predict the function of the bacteria. This was done as most bacteria’s common genes are similar, like those used in certain biochemical pathways. In this way, comparing its genetic composition to other known genes, it was possible to predict many things of this novel phylum. It was predicted that is was a slow growing, gram negative rod, with a type IV pillis. It was also predicted to be anoxic heterotrophic, and fermentative. Many other statistics were produced, and many of features of this bacterium were predicted, letting us know virtually everything about this bacterium without ever being able to have it in the laboratory. Research into previously unknown bacterium is important for the discovery of new medicines, or even biochemical pathways that may be useful to the industrial sector.