**OSU Professors and Students are first to have a Bacterium’s Genome Sequenced**

 Being the first to discover something in the science field is always an amazing feat no matter how small, literally! Professors and students at Oklahoma State University recently had the genome of *Chryseobacterium* sp. Hurlbut01 sequenced. This was the first time this particular strain of bacteria had been isolated and had its genome sequenced. If you are not familiar with cell and molecular biology, you might be asking yourself, “What is genome sequencing?” First, a genome is an organism’s complete set of DNA. It includes the genes, the noncoding DNA, and the genetic material of the mitochondria. Genome sequencing is the process of determining the entire DNA sequence found in an organism’s genome. In other words, it’s used to figure out the order of nucleotides in an organism’s entire set of DNA, also known as the genetic code.

I recently sat down and talked to Dr. Elshahed, one of authors on this published research titled “Draft Genome Sequence of the Environmental Isolate *Chryseobacterium* sp. Hurlbut01.” Dr. Elshahed told me that he has been a professor at Oklahoma State University for 11 years and currently teaches two microbiology classes, one for undergraduate students and one for graduate students. His work is focused on two main research areas: environmental genomics of novel yet uncultured microbial phyla and the metabolism, genomics, diversity, the biotechnological potential of anaerobic gut fungi. When I asked him if that was really the first time that strain of bacteria had been isolated and sequenced, he confirmed. However, even though the bacteria had been isolated from a light switch surface in Stillwater, Oklahoma, its genome was not sequenced at Oklahoma State University. Dr. Elshahed explained that it was sent to the University of Georgia Genomics Facility to be sequenced due to price reasons at the time, even though OSU had the technology and resources to do it.

There are a currently a couple different ways to have an organism’s genome sequenced. When I asked Dr. Elshahed which method was used for the *Chryseobacterium* strain he said it was sequenced using the Illumina platform. I myself have looked into and learned about the newest and developing method of DNA sequencing that uses nanopores. So naturally I asked him his thoughts on nanopore DNA sequencing and why this method wasn’t used on the organism. He explained that nanopore DNA sequencing has drawback unlike Illumina; Illumina is cheaper, more reliable, and more accurate. Dr. Elshahed said, “Right now the nanopore technology is like the expensive electric car…it shows all this great potential but it still needs to be perfected before it can become effectively commercialized.”

Once the University of Georgia had sent back the sequenced genome to Stillwater, it was analyzed for the first time ever. A 16S rRNA gene sequence comparison was used to identify different strains with sequenced genomes that are most closely related to *Chryseobacterium* sp. Hurlbut01. The reason why the 16S rRNA gene sequence is used for phylogenetic studies is because it is extremely conserved between different species of bacteria. After the comparison, they discovered that a number of *Chryseobacterium* sp. Hurlbut01 genes didn’t have any substantial similarities to the closest 16S rRNA relative genomes. Furthermore, 233 genes were identified to be unique to the Hurlbut01 strain after comparison of its genome to all available *Chryseobacterium* genomes. These results show the extreme level of intralineage diversity within members of this genus, even though there’s a high level of 16S rRNA gene sequence similarity.

**References**

M. Couger, et al. (2015). Draft Genome Sequence of the Environmental Isolate *Chryseobacterium* sp. Hurlbut01.