Citrus Greening Disease: Comparative Genomics of 
*Liberibacter asiaticus* and *Sinorhizobium meliloti*

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**Abstract:**

Alongside Dr. David Kuykendall, Microbiologist at the USDA-ARS located in Beltsville, Maryland, I was tasked with working on a comparative genomics project pertaining to a microbe (*Candidatus Liberibacter asiaticus*) which is known to cause Citrus Greening disease in citrus plants. Dr. Kuykendall is currently doing a comparative genomic project, which will help us to better understand this microbe in efforts to develop an appropriate treatment and mechanism to protect the citrus plants, since we agriculturally rely on them. My job, as a student intern, is to assist Dr. Kuykendall by utilizing bioinformatics as well as wet-lab experiments (including running DNA gels and PCR tests) to determine the similarities between this microbe and a known rhizobium (that we already know how to treat against citrus plant). Although this research is ongoing, we have already found major regions of synteny (or similarities) between the *Liberibacter* and *Sinorhizobium* (the microbe we are utilizing for comparison). These similarities may give further insight in the appropriate measures of treatment required for this disease.

**Introduction:**

There is currently a microbe called *Candidatus Liberibacter asiaticus* which causes Citrus Greening disease in plants. This disease greatly impacts the citrus fruit industry, in that it greatly reduces production (in Asia, Africa, Brazil, Arabian Peninsula, and America) kills the trees, and makes the fruit less marketable. Moreover, trees that are infected by this microbe die within a few short years as there is currently no known cure. *Candidatus Liberibacter asiaticus* is a citrus plant specific microbe, meaning that it only attacks citrus plants and is not harmful to humans or animals.

**Microsynteny:**

Below is an example of the utilization of NIH’s NCBI gene database to determine what regions of the chromosomes of *Liberibacter* are microsyntenous (or have at least 3 genes in the same order) with *Sinorhizobium*. Both figures come directly from the NCBI database.

**Results:**

As it stand, we have only done preliminary comparative genomics and as such tangible results are minor.

- From comparing genomic sequences of the *Liberibacter* and *Sinorhizobium*, we have found a total of 72 microsyntenous regions.
- The longest region of similarity was 30 genes long and coded for flagellar components of the cell.
- The regions ranged from 3 genes to 30 genes with a total gene distance of 60043.
- There was a high rate of conservation of ribosomal proteins.

**Discussion:**

The current findings have helped the research team better understand the genomic structure of *Candidatus Liberibacter asiaticus*. One such finding was in the discovery of a 30 gene mycrosyntenous region in which all of the genes from *Sinorhizobium* were conserved in the *Liberibacter* (not only in order, but the function was the same as well.) All of the genes in this particular region coded for flagellum, in one way or another. This is evidence that the mechanism that *Sinorhizobium* utilizes to make a flagellum and also to make it work is also utilized by the *Liberibacter*. Other major conservation was found in the ribosomal proteins of both microbes. The vast majority of the conserved genes that were found belonged to this group. While comparing the genomes of the two microbes, we also found that some of the genes found in the *Liberibacter* were lost in the *Sinorhizobium* and vice versa. This is an indication that at some point during the evolution of these microbes it became less advantageous or useful for certain genes to persist.

**Further Implications:**

This project is ongoing. The next phase of the research is to perform PCR (Polymerase Chain Reaction) on the samples of *Liberibacter asiaticus* and *Sinorhizobium meliloti* to amplify the sections of DNA that we have thus far indicated as microsyntenous. This will allow us to see exactly how similar the two microbes are and thus allow researchers to deduce a way to treat citrus plants that are become infected.

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