EEOB563 Final Project Outline

Background

*Pseudomonas syringae* pv. *syringae* B728a contains photosensory proteins that allow this bacterium to respond to light. The light response plays a role in *P. syringae’s* swarming motility, ability to colonize the host (the common grean bean), and virulence. My dissertation research focuses on identifying downstream components in the photosensory pathway of this organism. Using RNAseq analysis we discovered that KaiC, a gene that is associated with Circadian rhythm cycles, is highly regulated by one of the photosensory proteins (BphP1). It is likely that the photosensory pathway is intrinsically linked with the Circadian rhythm of *Pseudomonas syringae* and therefore it is important that I understand the origin and function of the *kaiC* gene better. Usually *kaiC* is in an operon k*aiABC*, but B728a only contains the *kaiC* gene. For the final project I would like to do a phylogenetic analysis of the *kaiC* gene from multiple species and strains of bacteria that contain both complete *kai* operons and partial (*kaiC* only) operons.

Hypotheses

If the *kaiC* gene from B728a clusters near a particular grouping of bacteria it will give me valuable information to the function of the gene in B728a. For example, if *kaiC* from *Pseudomonas syringae* clusters near plant associated bacteria it probably serves a different purpose than the *kaiC* that is present in cyanobacteria which are largely photosynthetic. I may also learn information regarding possible horizontal transfer of *kaiC* into B728a by identifying closely related species.

Data

A new dataset will be formed using genebank and compiling a list of organisms that contain the *kai* operon as well as stand-alone *kaiC* genes.

Proposed methods

*kaiC* genes will be aligned using Mafft –auto. The file will be converted into a nexus format and I will use Bayesian analysis to identify phylogeny.