School of Natural Sciences Presents: Ph.D. Thesis Defense

"Uncovering Deep Phylogenetic Signal in Plastid Genomes"

By: Travis J. Lawrence

PhD Candidate, Quantitative and Systems Biology , UC Merced

Advisor: David H. Ardell

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ABSTRACT:

I will show that a novel source of phylogenetic information from the plastid genome, the tRNA interaction network, coupled with machine-learning and distance-based methods, is capable of accurately reconstructing deep phylogenetic relationships. I will present three projects from my dissertation. First, I will present on the phylogenetic origin of plastids within the Cyanobacteria tree of life (CyanoToL). Previous studies have strongly supported contradictory conclusions, with plastids branching either early or late within the CyanoToL. I show that the structural features that determine the charging potential of a tRNA with its cognate amino acid, termed tRNA Class Informative Features (CIFs), differ for eight Cyanobacterial clades in a phylogenetically informative way that can be exploited using an Artificial Neural Network to classify genomes. I test hypotheses of the origin of plastids by classifying 440 plastids genomes. I found strong support for the origin of plastids among a late-branching clade of starch-producing marine/freshwater diazotrophic cyanobacteria. Furthermore, I show that previously used phylogenetic models are unable to accommodate systematic biases possibly explaining conflicting hypotheses. Second, I will present on using tRNA CIFs to determine the phylogenetic placement of gnetophytes, a small clade of plants, within the seed plant phylogeny. The location of gnetophytes has been contentious with phylogenomic studies supporting several relationships with cone-bearing seed plants (conifers). I use the Jensen-Shannon divergence to calculate a pairwise distance matrix between seed plant clades for plastid tRNA CIFs. Using standard distance-based phylogenetic algorithms I found support for gnetophytes as sister to conifers. Lastly, I describe the implementation of tsfm: tRNA structure function mapper, which provides methods for predicting tRNA CIFs.

BIOGRAPHY:

Travis grew up in Auburn, CA. He received his Baccalaureate of Science in Biology with a concentration in molecular biology in 2010 from California State University, Sacramento, where he become interested in evolutionary biology while researching polyploid speciation in plants under the supervision of Dr. Shannon L. Datwyler. He continued his research with Dr. Datwyler, where he used phylogenetic networks of nuclear genes to resolve the evolutionary relationships of a group of closely related polyploid plants in the genus Penstemon, receiving his Master of Science in Biology in 2013. He joined University of California, Merced in 2013 to pursue his PhD working with Dr. David H. Ardell on projects related to resolving deep evolutionary relationships. He plans to continue pursuing his research interests in plant ecology and evolution, and has accepted a post-doctoral position at Oak Ridge National Laboratory.