

IMET Dissertation Defense

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Toxin-Antitoxin Systems and Other Stress Response Elements in Picocyanobacteria and their Ecological Implications

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Picocyanobacteria (mainly *Synechococcus* and *Prochlorococcus*) contribute significantly to ocean's primary production. Unlike *Prochlorococcus*, which is mainly constrained to warm and oligotrophic ocean, *Synechococcus* has a ubiquitous distribution. *Synechococcus* is present in freshwater, estuarine, coastal, and open ocean habitats. They have also been found in polar regions and hot springs. Endemic to the hot and the cold, the saline and the fresh, and every condition in between, *Synechococcus* appears to have the capability to adapt and tolerate nearly any environment and climate. This ability to conform to any aquatic environment is possible through their genome plasticity, a character that is not present in the *Prochlorococcus*. Due to the differential distribution of the genera, *Synechococcus* is considered a generalist and *Prochlorococcus* is considered a specialist in ecological theory. More than 400 picocyanobacterial genomes have now been sequenced, and this large genomic resource enables comprehensive genome mining and comparison. One possibility is to study the prevalence of Toxin-Antitoxin (TA) systems in picocyanobacterial genomes. TA systems are present in nearly all bacteria and archaea and are involved in cell growth regulation in response to environmental stresses. However, little is known about the presence and complexity of TA systems in picocyanobacteria. By querying 72 complete genomes of freshwater, estuarine, coastal and ocean picocyanobacteria, Type II TA systems (the most well studied TA family) were predicted in 27 of 33 (81%) *Synechococcus* strains, but none of 38 *Prochlorococcus* strains contain TA genes. The number of TA pairs varies from 0 to 80 in *Synechococcus* strains, with a trend for more type II TA systems being predicted in larger genomes. A linear correlation between the genome size and the number of putative TA systems in both coastal and freshwater *Synechococcus* was established. In general, open ocean *Synechococcus* contain no or few TA systems, while coastal and freshwater *Synechococcus* contain more TA systems. The type II TA systems inhibit microbial translation via ribonucleases and allow cells to enter the "dormant" stage in adverse environments. Inheritance of more TA genes in freshwater and coastal *Synechococcus* could confer a recoverable persister state which would be an important mechanism to survive in variable environments. Different genotypes of *Synechococcus* are present in the Chesapeake Bay in winter and summer. Winter isolates of *Synechococcus* have shown high tolerance to cold conditions and other stressors. To explore their potential genetic capability, complete genomes of five representative winter *Synechococcus* strains CBW1002, CBW1004, CBW1006, CBW1107, and CBW1108 were fully sequenced. These five winter strains share many homologs that are unique to them and not shared with pelagic *Synechococcus*. Their genomes are enriched with particular desaturases, chaperones, and transposases which are not found in other distantly related *Synechococcus*. These shared genomic features between the winter strains imply that maintaining membrane fluidity, protein stability, and genomic plasticity are important to cold adaptation of *Synechococcus*. The winter strains also contain genes that are not traditionally considered with the canonical bacterial cold shock response. They contain a particularly high abundance of Type II TA pairs with complex association networks. They feature promiscuous toxins which support the mix and match hypothesis as well as some more monogamous toxins which tend to pair with their traditionally named antitoxin. Expression of certain TA transcripts in response to environmental stress has been observed in the model strain CB0101, and the activity of one TA pair in CB0101 for growth arrest has been experimentally confirmed via transformation into *E. coli*. My thesis work has identified interesting genetic systems related to niche partitioning of picocyanobacteria, particularly among the Chesapeake Bay *Synechococcus*. Future studies are paramount to understand the functional role of TA systems, desaturases, chaperones, and transposases of picocyanobacteria under various environmental stressors.

Host:
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