**Novel toxin-antitoxin system in *Synechococcus*: A resilience mechanism in response to environmental stresses**

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The Chesapeake Bay estuary system is listed by the U.S. Environmental Protection Agency as an “impaired waterbody”. It suffers from excess nutrient inputs of nitrogen and phosphorus as well as poor water clarity related to high sediment loads. Often this eutrophication leads to large cyanobacterial blooms, which often are part of a specific clade of *Synechococcus*. Understanding how these *Synechococcus* consistently out competes other cyanobacteria can be answered by exploring gene content and functional molecular biology. Bacterial toxin-antitoxin (TA) systems are known genetic elements composed of a toxin gene and its cognate antitoxin with the ability to regulate growth. TA systems have not been found in marine *Synechococcus and Prochlorococcus*. Here we report the finding of TA systems in *Synechococcus* CB0101, and their response to four different stressors; nitrogen and phosphate starvation, zinc toxicity, and phage infection. This study is the first to identify and describe that chromosomal toxin-antitoxin systems are not only present in marine *Synechococcus,* but also differentially expressed under stressful conditions. Eight pairs of TA systems consisting of type I (1), II (6), and III (1) were identified in CB0101. We demonstrated that the *relE/relB* TA pair were active and arrested translation when CB0101 is under stress, but the arrest is reversible when the stress event was removed. Consequently, TA systems in CB0101 have a potential to regulate cell growth and translation to better aid in responding to rapidly changing environments. The presence of such systems could be important for other marine picocyanobacteria and will promote future studies on the diversity, evolution and ecological significance of TA systems.