

# ABSTRACT BOOK

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# ONE, NO ONE AND ONE HUNDRED THOUSAND *PLANKTOTHRIX* SPECIES: IS LATERAL GENE TRANSFER A NEGLECTED SOURCE OF GENETIC DIVERSITY?

**Domenico D'Alelio, Andrea Gandolfi, Nico Salmasso**

IASMA Research and Innovation Centre, Fondazione Edmund Mach, Environment and Natural Resources Area, Via E. Mach 1, I-38010 S. Michele a/Adige (Trento), Italy. E-mail: domenico.dalelio@iasma.it

The systematics of the genus *Planktothrix* (cyanobacteria) basically relies on phenotypic and ecological traits. In fact, attempts towards the definition of species by means of morphological, genetic and biochemical analyses are scanty and have been carried out using few sympatric strains which probably under-represent the actual diversity. On the other hand, the idea that the whole genus could be monospecific is still supported. We isolated about 300 strains of *Planktothrix* from eight lakes in Northern Italy and analyzed their morphology and genetics (i.e. for *rpoC1* and *rbcLX* coding-genes). The *rpoC1* gene was highly polymorphic, with about 30 single nucleotide polymorphisms, resulting in an overall diversity of ~6%; differences in *rbcLX* were less abundant. The strains clustered into two main genotype-groups: one was associated to the "species" *P. rubescens*, whose red-water blooms are reported in meso/oligotrophic lakes; the other included sequences recombinant between *P. rubescens* and *P. agardhii*, the latter being a green-water bloom "species" reported in eutrophic lakes. Furthermore, even sequences published on GenBank by previous authors and referring to strains putatively identified as either *P. rubescens* or *P. agardhii* clustered in the "recombinant clade". Our study, still in progress, points out the fact that recombination, probably as lateral gene transfer, could potentially limit the formation of stable species within the genus *Planktothrix*; a potential consequence of this phenomenon might be that different scientists could attain distinct ideas of a single biological entity, depending on the nature of each observer's observation (i.e. a sort of "Pirandellian syndrome").

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# COMPREHENSIVE TRANSCRIPTOME ANALYSIS OF *ALEXANDRIUM TAMARENSE* REVEALS INDEPENDENT ORIGIN OF SAXITOXIN SYNTHESIS IN CYANOBACTERIA AND DINOFLAGELLATES

**Jeremiah D. Hackett<sup>1</sup>, Jennifer H. Wisecaver<sup>1</sup>, Dave M. Kulis<sup>2</sup>, Donald M. Anderson<sup>2</sup>, Debashish Bhattacharya<sup>3</sup>, F. Gerald Plumley<sup>4</sup>, Deana L. Erdner<sup>5</sup>**

<sup>1</sup> Department of Ecology and Evolutionary Biology, University of Arizona, P.O. Box 210088, Tucson, AZ 85721, USA. E-mail: hackettj@email.arizona.edu.

<sup>2</sup> Biology Department Woods Hole Oceanographic Institution, Woods Hole, MA 02543, USA

<sup>3</sup> Department of Ecology, Evolution, and Natural Resources, Institute of Marine and Coastal Sciences, Rutgers University, New Brunswick, NJ 08901, USA

<sup>4</sup> Bermuda Institute of Ocean Sciences, St. George's GE01, Bermuda

<sup>5</sup> Department of Marine Science, University of Texas, 750 Channel View Dr., Port Aransas, TX 78373, USA

We assembled a comprehensive transcriptome dataset for the saxitoxin-producing dinoflagellate *Alexandrium tamarense* combining over 10 gigabases of expressed sequence tag, 454 and Illumina pyrosequencing data. The resulting assembly comprises 112,383 contigs with an average coverage of 100X, from which 56,578 proteins were predicted. We also generated 454 transcriptome data for three additional toxic dinoflagellates: *A. tamarense* SPE10-03, *Pyrodinium bahamense*, and *Gymnodinium catenatum*. Searching these data, we identified 274 potential homologs of 14 cyanobacterial saxitoxin genes including all of the genes directly involved in toxin synthesis. We used these candidate proteins in phylogenetic analyses to determine their evolutionary history. Four dinoflagellate candidate proteins group closely with cyanobacterial saxitoxin genes in phylogenetic analyses and are likely the homologs of *sxtA*, *sxtB* and *sxtG* in dinoflagellates. *SxtA* is split into two proteins in the dinoflagellates with *sxtA1* corresponding to the N-terminal portion with methyltransferase and acyl carrier protein domains and *sxtA2* corresponding to the C-terminal portion with the aminotransferase domain. Phylogenetic analyses of *sxtA*, *sxtB* and *sxtG* homologs suggest that they were acquired independently in cyanobacteria and dinoflagellates from similar bacterial sources. The *A. tamarense* transcriptome does not contain phylogenetically related homologs for the remaining saxitoxin genes. However, we identified candidate functional homologs for all of the remaining saxitoxin synthesis genes that were acquired from a variety of sources. These results indicate that the saxitoxin synthesis pathways in cyanobacteria and dinoflagellates were assembled independently using genes with similar functions, but from phylogenetically unrelated sources.