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Publications

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Genetic diversity and molecular phylogeny of *Planktothrix* (Oscillatoriales, cyanobacteria) strains from China

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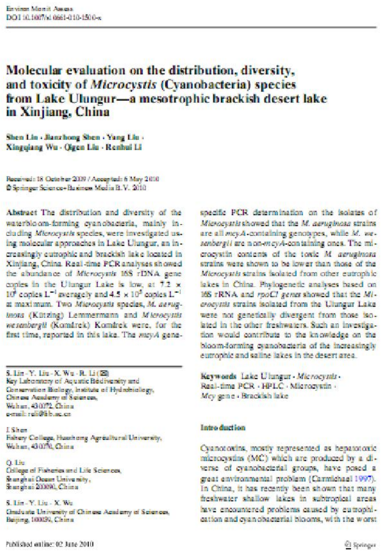
The genus *Planktothrix* Anagnostidis et Komárek 1988 represents an important, water-bloom forming cyanobacterial group, and it has been found to occur widely in heavy water blooms around China in recent years. In this study, genetic diversity and phylogeny of *Planktothrix* strains isolated from 16 Chinese waterbodies, based on 16S rRNA, *rbcLX* and *rpoC1* genes, were investigated. These *Planktothrix* strains, all green-colored, were morphologically divided into two groups as *P. agardhii* and *P. mougeotii*. However, phylogenetic analyses, based on the three gene regions, revealed that *Planktothrix* strains can generally form four clades, corresponding to *P. agardhii*, *P. pseudagardhii*, *P. mougeotii*, and *P.* cf. *agardhii* respectively, reflecting more diversity in the genus

Planktothrix than we expected. The clade of *P.* cf. *agardhii* found in this study was formed by 7 Chinese strains and representing a new evolutionary lineage of *Planktothrix*. The *Planktothrix* strains examined in this study have been identified as three insertion types within the intergenic spacer (IGS1) region between *rbcL* and *rbcX*. It was also revealed that *rbcLX* and *rpoC1* sequences in *Planktothrix* strains had lower haplotype but higher nucleotide diversities than 16S rRNA gene.

Lin S., Shen JZ, Liu Y, Wu XQ, Liu QG, 2011. **Molecular Evaluation on the Distribution, Diversity and Toxicity of *Microcystis* (Cyanobacteria) Species from Lake Ulungur -- an Increasingly Eutrophicated and Brackish Desert Lake in Xinjiang, China. *Environmental Monitoring and Assessment* (In Press).**



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Molecular evaluation on the distribution, diversity, and toxicity of *Microcystis* (Cyanobacteria) species from Lake Ulungur—a mesotrophic brackish desert lake in Xinjiang, China

Shen Lin · Jianzhong Shen · Yang Liu · Xingqiang Wu · Qigen Liu · Renhui Li

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Abstract The distribution and diversity of the waterbloom-forming cyanobacteria, mainly including *Microcystis* species, were investigated using molecular approaches in Lake Ulungur, an increasingly eutrophic and brackish lake located in Xinjiang, China. Real-time PCR analyses showed the abundance of *Microcystis* 16S rDNA gene copies in the Ulungur Lake is low, at 7.2 × 10^4 copies L^{-1} averagely and 4.5 × 10^5 copies L^{-1} at maximum. Two *Microcystis* species, *M. aeruginosa* (Kützing) Lemmermann and *Microcystis wesenbergii* (Komárek) Komárek were, for the first time, reported in this lake. The *mcyA* gene-specific PCR determination on the isolates of *Microcystis* showed that the *M. aeruginosa* strains are all *mcyA*-containing genotypes, while *M. wesenbergii* are non-*mcyA*-containing ones. The microcystin contents of the toxic *M. aeruginosa* strains were shown to be lower than those of the *Microcystis* strains isolated from other eutrophic lakes in China. Phylogenetic analyses based on 16S rRNA and *rpoC1 genes* showed that the *Microcystis* strains isolated from the Ulungur Lake were not genetically divergent from those isolated in the other freshwaters. Such an investigation would contribute to the knowledge on the bloom-forming cyanobacteria of the increasingly eutrophic and saline lakes in the desert area.

Keywords Lake Ulungur · *Microcystis* · Real-time PCR · HPLC · Microcystin · *Mcy* gene · Brackish lake

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Introduction

Cyanotoxins, mostly represented as hepatotoxic microcystins (MC) which are produced by a diverse of cyanobacterial groups, have posed a great environmental problem (Carmichael 1997). In China, it has recently been shown that many freshwater shallow lakes in subtropical areas have encountered problems caused by eutrophication and cyanobacterial blooms, with the worst

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The distribution and diversity of bloom forming cyanobacteria especially the genus *Microcystis* were investigated using molecular approaches in Lake Ulungur, an increasingly eutrophicated and brackish lake located in Xinjiang, China. Real-time PCR analyses showed the abundance of *Microcystis* 16S rRNA gene copies in the Ulungur Lake is low, at 7.2×10^4 copies L^{-1} averagely and 4.5×10^5 copies L^{-1} at maximum. Two morphological species *M. wesenbergii* and *M. aeruginosa* were first time reported in this lake. The *mcyA* gene- specific PCR determination on the isolates of *Microcystis* showed that the *M. aeruginosa* strains are all *mcyA* containing genotypes, while *M. wesenbergii* are non- *mcyA* containing ones. It was also shown that *Microcystis* strains in most regions of the lake are non-toxic. The microcystin contents of theses toxic strains were shown to be significant different and lower than those of the *Microcystis* strains isolated from other eutrophic lakes in China. Phylogenetical relationship based on 16S rRNA and *rpoC1* genes showed that the *Microcystis* strains isolated from the Ulungur Lake were not genetically divergent from those isolated in the other freshwaters. Such an investigation would contribute the knowledges on bloom-forming cyanobacteria in the increasingly eutrophicated and salinity lakes in the desert area.

林燊，彭欣，吴忠兴，李仁辉. 2008. 我国水华蓝藻的新类群——阿氏浮丝藻 (*Planktothrix agardhii*) 生理特性。 湖泊科学. 20(4): 437-44

Lin S, Peng X, Wu ZX, Li RH. 2008. Physiological characteristics of Planktothrix agardhii-A new taxa of b'oom cyanophyta in China. Journal of Lke Science. 20(4): 437-44. (in Chinese)

我国水华蓝藻的新类群——阿氏浮丝藻(*Planktothrix agardhii*)生理特性

Five strains of *Planktothrix* agardhii isolated from five regions around China were studied for their physiological characteristics, including growth rate, pigment composition, photosynthetic activity. The strain HAB1128 isolated from Guangzhou contained lower chlorophyll a(Chla), but higher C-PC content and higher C-PC ratio in total phycobiliprotein compared to other 4 strains. Results from electron transfer rate (ETR) showed that HAB1128 had higher photosynthetic ETR and the maximal ETR (ETRmax), which inferred that high-performance electron transfer chain retrieved the inadequacy of Chla of this strain, and lead to the neutral growth rate. On the contrary, HAB631 the strain isolated from East Lake (Wuhan), contained higher Chla content, but showed lower growth rate due to its weak electron transfer chain. No significant differences of physiological parameters were shown among three strains isolated from Beijing, Shanghai and Yunnan.

林燊 庄惠如 高汝承 陈荣 郑梦思, 2005, 激光辐照对不同饵料微藻生长的影响。 应用激光 25(25): 193-196

Lin S, Zhuang HR, Gao RC, Chen R, 2005. Growth Effect of Laser on Different Bait-Microalgae. Applied Laser. 25(25): 193-196 (in Chinese)

激光辐照对不同饵料微藻生长的影响

Growth Effect of Laser on Different Bait - Microalgae

Nd: YAG laser(wavelength 1.06µm, power 5w,radiation time 0.5-3min)and Ar+ (wavelength 488nm,power 70mv, radiation time 5-20min) laser were used to irradiate two kinds of bait-microalgae *Chaetoceros calcitrorns* and *Dicraterpia* sp. The proliferation and growth rates of irradiated cells were determined. The experimental result shows that the growth of Dicrateria sp was promoted after the irradiation of 1min Nd: YAG and 5min Ar+ laser. The irradiated cell proliferation was promoted by 42.9% and 48.1% in two day, but the improving effects faded away as time going by. The growth was inhibited af ter the irradiation of different radiation time in lag phase, but the growth of C. calcitrorns was promoted after the irradiation of 1min Nd: YAG and 10min Ar+ laser in exponential phase and generation. Among these, the growth rate was promoted by 27. 0 % af ter 1min Nd: YAG irradiation an d by 51.2 after 10min Ar+ laser irradiation. The different endurance and growth features were compared and analyzed among different lasers and parameters. The result proved conclusions from premises and reveal the prospect of appliance of lasers in bait-microalgae selection.

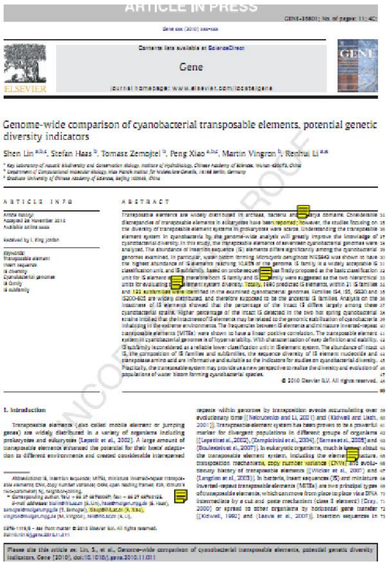
Wu ZX, Shi JQ, **Lin S** et al., Unraveling molecular diversity and phylogeny of Aphanizomenon (Nostocales, Cyanobacteria) strains isolated from China. Journal of Phycology. Online

Fifty three strains of the genus *Aphanizomenon* isolated from Chinese waters were employed to conduct morphological examination and sequencing of the 16S rRNA gene, rbcLX (Rubisco) and cpcBA-IGS gene regions. Based on morphological characteristics, the examined strains were divided into three morphotypes (*Aph. flos-aquae, Aph. gracile, and Aph. issatchenkoi*). Phylogenetic analysis based on 16S rRNA and *rbcXL* showed that *Aphanizomenon* strains could be divided into three main clades as Clade A of *Aph. flos-aquae*, Clade B of *Aph. gracile*, and Clade C of *Aph. issatchenkoi*, but two additional clades formed by Aph. ovalisporum and Aph. aphanizomenoides were found in the 16S rDNA based topology. All *Aph. issatchenkoi* strains were found to contain an additional 175 nucleotides from the 779 to 954nucleotide location in *rbcLX* region, compared with strains of *Aph. flos-aquae* and *Aph. gracile*. cpcBA-IGS based phylogenetic tree revealed that *Aph. issatchenkoi* strains were not discriminated from *Aph. flos-aquae* strains, however, a concatenated alignment of 16S rDNA, rbcXL and cpcBA-IGS led to the three distinct clades: *Aph. flos-aquae, Aph. gracile and Aph. issatchenkoi*, respectively. It is suggested that the taxonomic revision of *Aphanizomenon* and *Anabaena* genera is required to be performed by employing multilocus sequence analysis and polyphasic studies.

Key index words: Anabaena, Aphanizomenon, cpcBA-IGS, rbcXL, 16S rRNA

Lin S et al., 2010. Genome-wide comparison of cyanobacterial transposable elements, potential genetic diversity indicators. Gene, in press.

Transposable elements are widely distributed in archaea, bacteria and eukarya domains. Considerable discrepancies of transposable elements in eukaryotes have been reported; however, the studies focusing on the diversity of transposable element systems in prokaryotes were scarce. Understanding the transposable element system in cyanobacteria by the genome-wide analysis will greatly improve the knowledge of cyanobacterial diversity. In this study, the transposable elements of seventeen cyanobacterial genomes were analyzed. The abundance of insertion sequence (IS) elements differs significantly among the cyanobacterial genomes examined. In particular, water bloom forming Microcystis aeruginosa NIES843 was shown to have the highest abundance of IS elements reaching 10.85% of the genome. IS family is a widely acceptable IS classification unit, and IS subfamily, based on probe sequences, was firstly proposed as the basic classification unit for IS element system，therefore both IS family and IS subfamily were suggested as the two hierarchical units for evaluating the IS element system diversity. Totally, 1980 predicted IS elements, within 21 IS families and 132 subfamilies were identified in the examined cyanobacterial genomes. Families IS4, IS5, IS630 and IS200-605 are widely distributed, and therefore supposed to be the ancestral IS families. Analysis on the intactness of IS elements showed that the percentage of the intact IS differs largely among these cyanobacterial strains. Higher percentage of the intact IS detected in the two hot spring cyanobacterial strains implied that the intactness of IS elements may be related to the genomic stabilization of cyanobacteria inhabiting in the extreme environments. The frequencies between IS elements and miniature inverted-repeat transposable elements (MITEs) were shown to have a linear positive correlation. The transposable element system in cyanobacterial genomes is of hypervariabilty. With characterization of easy definition and stability, IS subfamily is considered as a reliable lower classification unit in IS element system. The abundance of intact IS, the composition of IS families and subfamilies, the sequence diversity of IS element nucleotide and transposase amino acid are informative and suitable as the indicators for studies on cyanobacterial diversity. Practically, the transposable system may provide us a new perspective to realize the diversity and evolution of populations of water bloom forming cyanobacterial species.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Genome-wide comparison of cyanobacterial transposable elements, potential genetic diversity indicators

Shen Lin, Stefan Haas, Tomasz Zemojtel, Peng Xiao, Martin Vingron, Renhui Li