

International Conference and Expo on

Water Microbiology & Novel Technologies

July 18-19, 2016 Chicago, USA



Jingrang Lu

US Environmental Protection Agency, USA

qPCR and RT-qPCR of harmful cyanobacteria at Lake Harsha, Ohio, during summer

Cyanobacteria blooms have increased in recent years and are becoming a greater public concern due to their potential ecological and health impacts. Detection of toxic cyanobacteria using qPCR and RT-qPCR allows for the rapid identification of blooms by combining specificity and sensitivity with speed and high sample processing capability. Toxic cyanobacteria from the water samples of five sites in Lake Harsha, which is used for local recreational activities and as a source of drinking water, were detected using a panel of qPCR assays for most of toxin-producers (HEP and CD1) or only toxic *Microcystis* spp. (*mcyG* and *mcyA-MS*) targeting the toxin-producing genes of *mcyA*, *mcyE*, *ndaF* and *mcyG*. Overall performance of the four assays were highly correlated with each other for DNA along weekly and daily samples, indicating similar level of copy numbers and amplification efficiency of the targeted genes. The quantity of total toxic cyanobacteria reached $>10^8$ cell L⁻¹ in early June and remained at high density until the end of July. During this period, the signals of qPCR between HEP and *mcyG* or *mcyA-MS* were in agreement and demonstrated that *Microcystis* spp. dominated the toxin producers. Before this period, the lower amount of toxic cyanobacteria reflected by HEP and CD1, were non- *Microcystis* spp., while after this period approximately only half of *Microcystis* spp. accounted for the total toxin producers. RT-qPCR results showed the same trend as qPCR but with higher variations in assays for *Microcystis* spp., indicating potential toxins were produced mainly by *Microcystis* spp. Generally much lower signals of qPCR and RT-qPCR were detected from deep water than surface water suggesting that the majority of toxins were generated from surface water. Further analysis will be performed with microscopic and physiochemical data and toxin measurement to determine future development of molecular tools and its application to monitoring toxic cyanobacteria.

Biography

Jingrang Lu is a Biologist at the US Environmental Protection Agency in Cincinnati, USA. His research work focuses on the molecular method development and detection of pathogenic bacteria in water using transcriptomic, metagenomic and genomic analysis and host animal model and to assess water quality and pathogenic risks. He holds a PhD in Microbial Ecology and MS in Zoology. He has over 60 peer reviewed publications to his credit. His main interests are to apply molecular approaches to applied environmental microbiology and public health researches.

lu.jingrang@epa.gov

Notes: