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Perspective of cyanobacterial harmful algal bloom (*HAB*) mitigation: *Microcystis* toxin degradation by bacterial consortia

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Microcystis thrive in eutrophic water bodies laden with toxins and metabolites that adversely affect the water quality. In the present study, attempts have been made to demonstrate inhibition of *Microcystis* growth and degradation of its toxin (microcystin) by three algalytic bacterial isolates, *viz.*; *Rhizobium* sp. (MF185100), *Methylobacterium zatmanii* (MF185099), *Sandaracinobactor sibiricus* (MF185098). *Microcystis aeruginosa* was collected from eutrophic lake of Central India and purified by sequential antibiotic (ampicillin, kanamycin and imipenem) treatment. Purified Microcystis culture was subjected to bacterial interactions for understanding algalytic activity. It was observed that interaction of consortia of three isolated bacteria as mentioned above showed 95% *Microcystis* lysis in BG-II media as analyzed spectrophotometrically (OD678 nm). The 16S rDNA sequence analysis of consortia members showed their phylogenetic relationship with reported algicidal Rhizobiaceae and Dermabacteraceae. Interestingly, one consortia member *viz.* *Rhizobium* sp. (MF185100) was capable of utilizing *Microcystis* toxin as sole carbon source for its growth. Interaction studies of *Microcystis* and algalytic bacteria revealed gradual decrease (>95% degradation in 25 days) in microcystin toxin concentration as revealed through HPLC analysis. The present study, thus proposes using algicidal bacteria for sustainable mitigation of Microcystis found trapped in cyanobacterial harmful algal bloom (HAB).

Keywords: 16S rDNA, Cyanotoxicity, Microcystin, *Microcystis aeruginosa*