

Phytoplankton Demethylation: An Unexplored Pathway of Methylmercury Detoxification

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Phytoplankton represents a large group of phototrophic microscopic organisms in freshwater and seawater and serve as a key entry point for the trophic transfer and bioaccumulation of the neurotoxin methylmercury (MeHg) in aquatic food webs. However, whether phytoplankton could degrade and metabolize MeHg is unknown, despite early recognition that algal blooms lead to decreased levels of MeHg in fish. The present study was aimed at determining: (1) whether or not certain phytoplankton species are capable of degrading MeHg, either in the dark or under sunlit conditions; and (2) whether the degradation occurs *in vivo*, and what are the potential mechanisms responsible for MeHg degradation. We provide experimental evidence indicating a novel pathway of MeHg degradation by freshwater and marine phytoplankton independent of light. The freshwater alga *Chlorella vulgaris*, the marine diatom *Chaetoceros gracilis*, and the cyanobacteria *Microcystis sp.* and *Synechocystis sp.* (also known as blue-green algae) converted 50–95% of MeHg (25 nM) to inorganic Hg intracellularly over 5 days in the dark. The dominant degradation products were elemental Hg(0) and/or Hg(II), although phytoplankton genomes do not contain the canonical *mer*-mediated demethylation pathway. Given the increasing incidence of algal blooms in lakes and marine systems globally, these findings suggest a hitherto unknown yet potentially widespread biological pathway of MeHg degradation and the important role phytoplankton may play in detoxifying MeHg in the environment.