

Abstract

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Title

Individual-based modelling of the vertical distribution of *Microcystis aeruginosa* blooms in a shallow lake

Description

We developed an individual-based model (IBM) to simulate the vertical position of the cyanobacterium *Microcystis aeruginosa* in a shallow lake. *Microcystis aeruginosa* can produce toxins and adversely impacts water quality, human and animal health. Key physical and physiological processes controlling the growth and size of *Microcystis aeruginosa* colonies were incorporated into the IBM coupled which included a 3D hydrodynamic model. Hydrodynamic modeling was performed by considering wind stress, heat exchange with the atmosphere, bottom friction, inflows, and net precipitation. The model was applied to the Forest Lake in South-East Queensland, Australia, in summer of 2020. During this period, cell counts of *M. aeruginosa* exceeded 3×10^5 cells mL⁻¹. Model results showed that when the lake was mixed, the percentage of small-size colonies was very high as a result of colony disaggregation; whereas the development of strong stratification suppressed vertical mixing and increased the percentage of large-size colonies. The simulations supported the hypothesis that aggregation of colonies at low turbulence levels is important for cyanobacterial bloom development because colony aggregation leads to the formation of larger colonies with a higher floating velocity that can dis-entrain from turbulent mixing and hence accumulate at the surface. Capturing variations in colony size is shown to yield a more accurate forecast of cyanobacterial bloom development and should be included in modelling dynamics of colony-forming cyanobacteria.