Do summer cyanobacterial blooms negatively affect prey and commercial fish recruitment in the great lakes?

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ABSTRACT:

Harmful algal blooms dominated by cyanobacteria (cHABs) have emerged as a critically important problem in the Great Lakes, which may threaten both human health and fisheries production. While the composition of cHABs varies among ecosystems, the cyanobacterium *Microcystis aeruginosa* (Ma) causes much of the problem in the Great Lakes, as well as elsewhere in the world. Some strains of Ma produce toxins (microcystins; MCs) while others don't. We hypothesized that both of MC+ and MC- categories could harm the production and health of summer-spawning fishes by interfering with hormonal functions that alter reproductive processes. We assessed: 1) effects of summer cHABs on hormones in reproductive adults, their gonads in field-collected yellow perch (YP; *Perca flavescens*); 2) reproductive injury targets and biomarkers in YP embryos, and larvae exposed to *Microcystis aeruginosa* exudates (MaE) in the lab; 3) impair viability and reproductive gene expression in fish cell lines; and 4) estrogenic potential chemicals in MaE by metabolomics, machine learning and E-screen assay. We found that: 1) YP sampled from northwestern basin of Lake Erie bloom-affected sites were significantly smaller than those of clear water sites. Female perch from bloom-affected sites also exhibited reduced concentrations of the reproductive regulatory hormone gonadotropin-releasing hormone (GnRH) and reduced gonadosomatic indices. However, site-specific differences other than bloom presence were likely responsible for the differences in body size and physiological parameters observed in sampled YP from southwestern basin of Lake Erie; 2) MaE decreased YP embryonic fertilization rates, increased mortalities and heart rates, while larval length was altered by MaE as well. MC+ and MC- strains had different effects; 3) exudates of the nonmicrocystin(MC)-producing strain significantly reduced viability in cell lines and induced significant cellular stress and/or injury in six of the eight cell lines, and significantly altered expression of developmental and sex steroidogenic genes; 4) six compounds from MaE (daidzin, biochanin A, phenylethylamine, rhein, o-Cresol, and arbutin) were identified as estrogenic potential chemicals.