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Systemic, early-season *Microcystis* blooms in western Lake Erie and two of its major agricultural tributaries (Maumee and Sandusky rivers)

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ABSTRACT

Recurrent, massive cyanobacterial blooms composed mainly of the genus *Microcystis* indicate a broad-scale re-eutrophication of Lake Erie. In the past, ameliorating eutrophication relied on intentionally decreasing point-source tributary nutrient, especially phosphorus, loads to the lake. However, recent research has shown that tributaries load not only nutrients but also bloom-levels of phytoplankton, including *Microcystis*. We built on this previous work by sampling earlier in the year and in much smaller tributaries in both the Maumee and Sandusky systems. We found *Microcystis* wet biomasses in these tributaries averaged 3.16 mg/L (±0.59 mg/L, one standard error of the mean) in 2009 and 3.42 mg/L (±0.55 mg/L) in 2010. Importantly, we found *Microcystis* in small ditches in March, much earlier than previously observed. *Microcystis* biomass did not directly correspond to measured phosphorus, chlorophyll, or phycocyanin concentrations likely reflecting complexities associated with lagged physiological responses and/or non-linear growth relationships. Consequently, our findings emphasize that *Microcystis* blooms form a more broad-scale problem than previously documented, occurring far upstream much earlier in the year.

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Introduction

Lake Erie continues to undergo re-eutrophication (Allinger and Reavie, 2013) as evidenced by recurrent massive cyanobacterial blooms (Michalak et al., 2013; Stumpf et al., 2012), particularly of *Microcystis* spp. (Bridgeman et al., 2013; Stumpf et al., 2012), after a period of documented lower phytoplankton abundances (Conroy et al., 2005, 2008b). Finding ways to ameliorate these blooms in Lake Erie has historically relied on the classic model of bloom facilitation in lakes (sensu Carpenter et al., 1998) where stream-derived nutrients drive within-lake phytoplankton growth. Overall, this model has widely informed nutrient reduction programs with great success (DePinto et al., 1986). Lake Erie recovering from its one-time status as a "Dead Lake," in particular, has made it the poster child for eutrophication remediation through point and non-point source nutrient reduction (Koonce et al., 1996; Makarewicz and Bertram, 1991). So why does re-eutrophication, as evidenced by an increased cyanobacterial biomass starting in the mid-1990s (Kane et al. in this issue; Conroy et al., 2005, 2008b), continue in Lake Erie?

Herein, we build on previous documentation of viable stream algal and cyanobacterial assemblages (Conroy, 2007; Bridgeman et al., 2012) by expanding our sampling in time and space, commencing sampling as early as late March at sites ranging from low-order streams to offshore Lake Erie. We specifically ask two straight-forward questions: *Where* and *When* do *Microcystis* blooms start? Answers to these simple questions have critical implications for attempts to remediate recently observed massive blooms in Lake Erie (Michalak et al., 2013). For example, Bridgeman et al. (2013) showed that the *Microcystis* blooms in the lake in 2011 were 2.4 times more intense (i.e., larger biovolume) than the second highest bloom (2008), and 29 times the smallest bloom (2002). If these *Microcystis* blooms commence far upstream early in the year versus farther downstream in main-stem tributaries or in near- and offshore areas of Lake Erie in late summer, then implementation of nutrient best management practices will need to be modified accordingly in time and space. Further, the problem of upstream, early-season blooms contrasts distinctly with offshore, late-summer blooms, essentially making a regional, broad-scale problem a local issue.

Methods

We sought to identify the initiation of *Microcystis* blooms both spatially and temporally in the Maumee and Sandusky systems (river, bay, and nearshore Lake Erie portions). Previous studies documented the presence of cyanobacteria in the main stems of the Maumee

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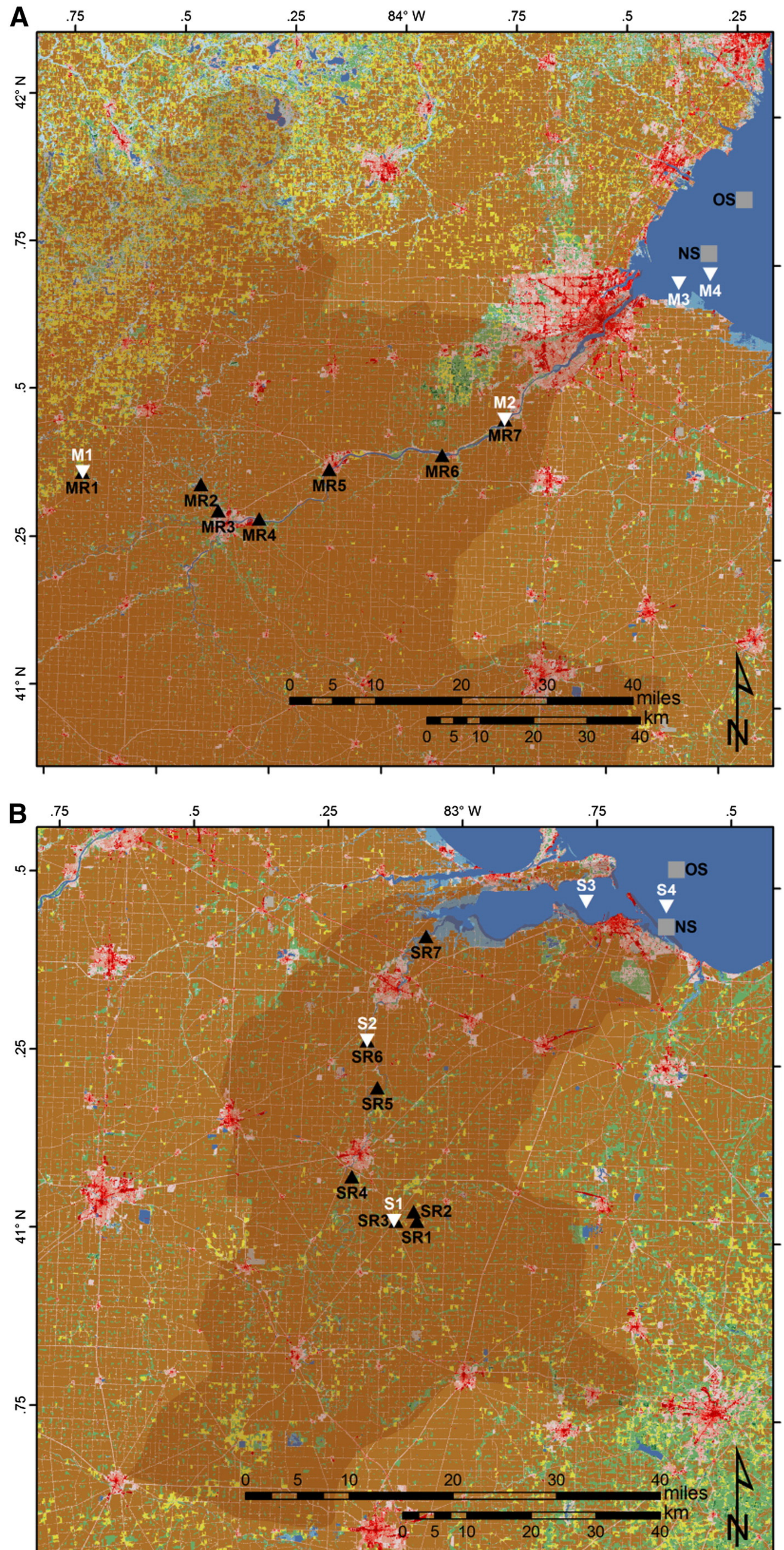

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