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Re-eutrophication of Lake Erie: Correlations between tributary nutrient loads and phytoplankton biomass

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ABSTRACT

Both abiotic and biotic explanations have been proposed to explain recent recurrent nuisance/harmful algal blooms in the western basin and central basin of Lake Erie. We used two long-term (>10 years) datasets to test (1) whether Lake Erie total phytoplankton biomass and cyanobacterial biomass changed over time and (2) whether phytoplankton abundance was influenced by soluble reactive phosphorus or nitrate loading from agriculturally-dominated tributaries (Maumee and Sandusky rivers). We found that whereas total phytoplankton biomass decreased in Lake Erie's western basin from 1970 to 1987, it increased starting in the mid-1990s. Total phytoplankton and cyanobacterial seasonal (May–October) arithmetic mean wet-weight biomasses each significantly increased with increased water-year total soluble reactive phosphorus load from the Maumee River and the sum of soluble reactive phosphorus load from the Maumee and Sandusky rivers, but not for the Sandusky River alone during 1996–2006. During this same time period, neither total phytoplankton nor cyanobacterial biomass was correlated with nitrate load. Consequently, recently increased tributary soluble reactive phosphorus loads from the Maumee River likely contributed greatly to increased western basin and (central basin) cyanobacterial biomass and more frequent occurrence of harmful algal blooms. Managers thus must incorporate the form of and source location from which nutrients are delivered to lakes into their management plans, rather than solely considering total (both in terms of form and amount) nutrient load to the whole lake. Further, future studies need to address the relative contributions of not only external loads, but also sources of internal loading.

Introduction

The increased severity in the distribution and frequency of hypoxia (Diaz, 2001; Rabalais et al., 2010) and the increase in algal biomass (especially in Harmful Algal Blooms (HABs)) (Paerl et al., 2011) indicate that many aquatic ecosystems, on a global scale, are becoming more eutrophic (Dobiesz et al., 2010; Rabalais et al., 2009). Both point source and non-point nutrient pollution have historically caused eutrophication. However, while it appears that point-source pollution in many areas (e.g., Laurentian Great Lakes) has decreased (DePinto et al., 1986; Dolan and Chapra, 2012), non-point source nutrient loading has increased in many areas (e.g., Gulf of Mexico) and could increase into the future (Donner and Scavia, 2007; Rabalais et al., 2010). The increase in nutrient loading is leading to current eutrophication in freshwater, estuarine, and coastal marine ecosystems, but there is controversy over whether phosphorus should be the sole focus to remediate eutrophication issues (Schindler et al., 2008), or whether P and N must both be controlled (Conley et al., 2009; Paerl, 2009). Further there is abundant evidence that freshwater (Keatley et al., 2011), estuarine (Paerl et al., 2011), and coastal marine ecosystems (Rabalais et al., 2009) are all currently undergoing eutrophication.

Lake Erie is currently displaying a pattern of re-eutrophication. The success of the Great Lakes Water Quality Agreement and subsequent control of point-source nutrient pollution that led to declines in algal blooms and (possibly) low oxygen events in Lake Erie by the 1980s is well documented (DePinto et al., 1986; Makarewicz and Bertram, 1991). However, the improvements in the eutrophication indicators that led to the declared "restoration" of Lake Erie by the early 1990s (e.g., Ludsin et al., 2001) have reversed, or our understanding of nutrient-algal relationships has become less clear (Matisoff and Ciborowski, 2005). Large blooms of toxic or potentially toxic cyanobacterial HABs (Bridgeman and Penamon, 2010; Budd et al., 2002; Michalak et al., 2013; Millie et al., 2009; Ouellette et al., 2006) and the nuisance green alga *Cladophora* (Higgins et al., 2005; Stewart and Lowe, 2008) have returned to Lake Erie and dissolved oxygen depletion

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and hypoxia/anoxia in the central basin continue to be problematic (Burns et al., 2005; Conroy et al., 2011; Zhou et al., 2013).

The original management actions that led to a reversal of eutrophication in Lake Erie were based on total phosphorus loading–chlorophyll *a* relationships (Vollenweider, 1976) and produced a reduction of point-source nutrient loading to the lake. Recently, however, in-lake concentrations of soluble reactive phosphorus (Charlton and Milne, 2004) and overall phytoplankton biomass (often dominated by the HAB genus *Microcystis*) have increased (Conroy et al., 2005b), while total phosphorus loading to the lake has remained below the 11 kilotonne level mandated by the Great Lakes Water Quality Agreement (Dolan, 1993; Dolan and McGunagle, 2005). However, agricultural non-point sources of soluble reactive phosphorus have increased and contribute a larger proportion of total phosphorus loads to Lake Erie (Joosse and Baker, 2011; Richards et al., 2010). Further, nitrogen has been identified as potentially capable of limiting growth of freshwater cyanobacterial blooms and has been suggested as a nutrient that management should control to reduce eutrophication of inland waters (Lewis et al., 2011; Paerl et al., 2011). Evidence has been found for Lake Erie that, at times, nitrogen can limit cyanobacterial growth (Chaffin et al., 2013) and thus the role that nitrogen loading has on Lake Erie's re-eutrophication needs to be explored further.

To determine the interaction between external nutrient loads and primary producer abundance in Lake Erie (WB and CB), we used two long-term datasets to test (1) whether total phytoplankton biomass (PPL) and cyanobacterial biomass (Cyano) were indeed increasing in Lake Erie and (2) whether phytoplankton biomass was correlated with soluble reactive phosphorus (SRP) and nitrate (NO_3) loadings from agriculturally-dominated tributaries (i.e., the Maumee and Sandusky rivers).

Methods

Long-term phytoplankton biomass and nutrient loading datasets

All of the data used in these analyses have been described fully previously with respect to field sampling locations and methods as well as laboratory analytical techniques (Conroy et al., 2005b; Richards et al., 2009). For our current analyses, phytoplankton biomass data from the western basin (WB) and central basin (CB) of Lake Erie were used because these basins receive the largest nutrient loads due to their proximity to major tributaries with high agricultural land use (Richards et al., 2010). Plankton sampling sites can be found in Conroy et al. (2005b) and locations of the nutrient sampling sites on the Maumee and Sandusky Rivers can be found in Conroy et al. (in this issue). Typical annual flows for the Maumee River are 1.50 km^3 and 0.33 km^3 for the Sandusky River (Richards et al., 2010) and thus the Maumee River typically contributes about 25% of the runoff to Lake Erie (Bolsenga and Herdendorf, 1993), with the Sandusky River contributing approximately 5%. Further, the Sandusky River typically loads 24% of the SRP loaded annually by the Maumee River (Michalak et al., 2013, Supporting Information). All phytoplankton biomass data are reported as seasonal (May–October) averages (either arithmetic or geometric means) or medians (Conroy et al., 2005b). Condensed methodologies for phytoplankton biomass (Kane, 2004) and nutrient loading (Richards et al., 2009) data can be found below.

Phytoplankton biomass determination

Phytoplankton water samples were obtained with an integrated water sampler (2.5 cm diameter tube) from the surface to twice the Secchi depth. Collected water was poured into a clean plastic bucket from which a 250 mL sample was taken. Each sample was preserved in a Mason jar with Lugol's solution, using approximately 1 mL of Lugol's for every 100 mL of sample. All samples were then transported to The Ohio State University, transferred into a graduated cylinder, and allowed to settle for 3 days. Each sample was then concentrated down to 30 mL by siphoning off liquid from the top and transferring the remaining sample to a 37 mL vial. Subsamples of approximately 3–5 mL were obtained from the concentrated samples and placed into an Utermöhl counting chamber. The general procedure for phytoplankton enumeration followed the inverted microscope technique (Lund et al., 1958; Utermöhl, 1958). All phytoplankton genera were identified and counted using a Wild inverted microscope at 400×. Transects were counted until 100 algal units (cells, filaments, or colonies) of the most common taxa were recorded. However, at least two transects were counted for each sample. Measurements were recorded for the first 20 algal units for each taxon. For filamentous algal taxa, however, all filament lengths were measured and then summed and recorded as the total filament length for each taxon. All of the recorded data were entered into a spreadsheet program that calculated the density and biomass of each algal taxon, as well as the critical dimensions that were measured for each algal species or category, and the biomass for each taxon was calculated and appropriately summed for PPL and cyanobacterial biomass (Cyano). Additional details can be found in Kane (2004).

Nutrient loading determination

Water-year soluble reactive phosphorus (SRP) and nitrate (NO_3) loads were calculated for the Maumee and Sandusky rivers based on the National Center for Water Quality Research (NCWQR) tributary monitoring program (Richards et al., 2009). The NCWQR collects samples for sediment and nutrient analysis at U.S. Geological Survey gaging stations on the Maumee River at Waterville, OH and on the Sandusky River at Fremont, OH. Three samples per day are taken using refrigerated Isco autosamplers. During periods of high flow or high turbidity, all samples are analyzed; at other times only one sample per day is analyzed. Typically, this program provides 450 to 500 analyzed samples per year. Data can be accessed at http://www.heidelberg.edu/academiclife/distinctive/ncwqr/data.

The NCWQR's routine analytical schedule includes two forms of phosphorus, total phosphorus (TP) and dissolved reactive phosphorus (DRP, also known as SRP). TP is determined by digesting the sample including its particulate matter with a strong oxidizing agent (ammonium persulfate) in an acidic solution, filtering the resulting solution through a glass fiber filter, and analyzing the filtrate colorimetrically using the molybdate blue reaction. SRP is determined by filtering a sample through a 0.45 μm pore size filter and analyzing the filtrate by the same colorimetric procedure, but without digestion. SRP is mostly orthophosphate (PO_4^{---}) (except at very low P concentrations where SRP and orthophosphate can diverge, Tarapchak and Rubitschun, 1982). SRP is analyzed on a Bran + Luebbe TRAACS 800, using two working ranges: 0.01 to 0.1 mg L^{-1} and 0.1 to 0.5 mg L^{-1}. The concentration obtained from the lower working range is retained, unless it is off scale, in which case the concentration from the higher working range is used. Nitrogen forms routinely analyzed by NCWQR are nitrate, nitrite, ammonia, and total Kjeldahl nitrogen. Nitrate and nitrite are analyzed according to EPA method 300.1 using a Dionex ion chromatograph and a filtered sample; working ranges are 0 to 50 mg L^{-1} and 0 to 10 mg L^{-1} respectively. For all analyses, samples are diluted and reanalyzed if their concentrations are outside of the previously stated ranges.

Annual loads are calculated using a custom version of the Beale Ratio Estimator called Autobeale (Richards et al., 1996). For days on which sample concentrations are available, daily loads are calculated as the product of the daily mean discharge from USGS records and a flow weighted average concentration for that day. The year is divided into time strata, within which the daily loads are fairly consistent with each other. Within each stratum, an average daily load is computed from the days with samples; this load is adjusted by the ratio of the average discharge for all days in the stratum divided by the average

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