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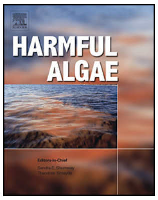

Cyanobacteria and cyanotoxins at the river-estuarine transition

Paul A. Bukaveckas[a,*], Rima Franklin[a], Spencer Tassone[a], Brendan Trache[a], Todd Egerton[b]

[a] *Virginia Commonwealth University, Department of Biology and Center for Environmental Studies, United States*
[b] *Virginia Department of Health, United States*

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ABSTRACT

We examined seasonal and longitudinal patterns in the occurrence of toxic cyanobacteria in the James River Estuary (Virginia). Highest chlorophyll and cyanobacteria levels were observed in the tidal freshwater segment, particularly during dry summers when freshwater replacement time was long. Cyanobacteria accounted for a small proportion of phytoplankton biomass (7–15%), and *Microcystis* comprised a small proportion of the cyanobacteria (<1%). Despite this, measureable levels of microcystin were commonly observed in water (>85% of samples in July, August and September), fish tissues (87% of planktivorous fishes) and shellfish (83% of individuals). Generic indicators of algal blooms (chlorophyll and algal biomass) had limited utility for predicting microcystin concentrations. However, chlorophyll was found to be a useful predictor for the probability of exceeding specific toxin thresholds. Tissue microcystin concentrations were highest in fish and shellfish collected from the tidal fresh segment, but were detectable in biota collected from the oligohaline at distances 50 km seaward.

1. Introduction

There is widespread concern regarding the presence of algal toxins in surface waters and their potential effects on human and aquatic health (Ibelings and Chorus, 2007; Zanchett and Oliveira-Filho, 2013; Boopathi and Ki, 2014; Rastogi et al., 2014; Schmidt et al., 2014). In eutrophic freshwaters, cyanobacteria often dominate the phytoplankton community, and include many toxin-producing forms (Smith, 2003; O'Neil et al., 2012; Paerl and Otten, 2013). Studies of harmful cyanobacteria have largely focused on lentic (lake) environments where phytoplankton blooms often form conspicuous surface scums that raise public concern and response from monitoring and regulatory agencies. Harmful algal blooms in flowing waters (rivers, river impoundments) have received less attention, perhaps in part because phytoplankton blooms are less apparent in well-mixed waters (i.e., in the absence of surface scums), and because blooms may be masked by the presence of non-algal suspended matter. Rivers are considered less susceptible to eutrophication because short water residence and low water clarity constrain phytoplankton responses to nutrient enrichment (Soballe and Kimmel, 1987; Smith, 2003; Sellers and Bukaveckas, 2003; Koch et al., 2004; Lucas et al., 2009). Despite these constraints, phytoplankton blooms are common in rivers (Basu and Pick, 1996; Reynolds and Descy, 1996; Kennedy and Whalen, 2008; Bukaveckas et al., 2011a) and merit consideration of risks posed by the occurrence of harmful algae. A better understanding of the factors regulating harmful algal blooms in rivers may also provide insights regarding environmental conditions favoring their occurrence over the continuum of water residence conditions among waterbodies.

Factors contributing to harmful algal blooms include the quantity and forms of nutrients delivered from the watershed, and changes in food webs that affect grazing rates on various forms of algae (Davis et al., 2010; Goleski et al., 2010; Heisler et al., 2011). In addition to these general factors acting across lentic and lotic systems, there are system-specific attributes that influence the abundance of harmful algae. In lakes and coastal lagoons, cyanobacteria typically dominate the phytoplankton community in summer (Johnk et al., 2008; O'Neil et al., 2012). Several factors may contribute to their dominance including their ability to sustain high growth rates at warmer temperature, their capacity to regulate buoyancy to obtain favorable (near-surface) light conditions, and their potential to resist or avoid grazing by consumers (Huisman et al., 2004; Paerl and Otten, 2013). A key difference between lentic and lotic systems is that greater mixing in lotic systems, due to fluvial, and in some cases, tidal forces, negates the buoyancy advantage of cyanobacteria. Diatoms are typically the dominant phytoplankton in flowing waters because turbulent mixing maintains these heavier (silica-based) cells in suspension (Admiraal et al., 1990; Garnier et al., 1995). Despite accounting for a small proportion of algal biomass, the presence of

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[*] Corresponding author.
E-mail address: pabukaveckas@vcu.edu (P.A. Bukaveckas).

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toxic cyanobacteria in rivers may have important implications for human and aquatic health. Our prior work in the James River has shown that cyanotoxins are consistently present in fish and shellfish, as well as terrestrial consumers that feed on emergent insects (Wood et al., 2014; Moy et al., 2016; Bukaveckas et al., 2017).

An appreciation of hydrologic processes in river networks is relevant to understanding bloom initiation and development in lotic environments. River networks integrate flow, often over large geographic areas that differ in their physical-chemical conditions. Blooms that initiate in one segment of the network may be transported, and subsequently propagate in areas distant from their source. For example, Morse et al. (2011) reported that the Lafayette and Elizabeth Rivers acted as initiation grounds for outbreaks of the toxic dinoflagellate *Cochlodinium polykrikoides*, which subsequently formed blooms in the lower portion of the James River. Spatial displacements between bloom initiation and development pose a challenge when attempting to link factors promoting bloom occurrence with local environmental conditions. In addition to transporting algae, rivers transport products of algal biosynthesis, including toxins. Preece et al. (2017) recently reviewed studies of cyanotoxin transport in rivers to coastal waters, including a case where mortality of sea otters was attributed to microcystin from inland freshwaters (Miller et al., 2010). Thus, in contrast to lakes, where blooms arise in situ in response to local conditions, riverine blooms, and their toxic by-products, may originate from distant sources and propagate throughout the drainage network. Therefore impacts to designated uses (e.g., drinking water, recreational contact, aquatic life) may extend beyond the location where blooms originate.

Here, we present the results of an 8-year study focusing on harmful cyanobacteria in the James River of Virginia. The data are used to address the following questions: What are the effects of salinity, temperature, and water residence time on total phytoplankton biomass, the abundance of cyanobacteria, and microcystin concentrations? Second, what are the best indicators for elevated cyanotoxin concentrations? We examine relationships among chlorophyll-*a* (CHL*a*), microcystin (MC), algal counts and genetic markers to assess their utility for monitoring and for enhancing our understanding of algal bloom dynamics. In addition, we present results from longitudinal studies characterizing transport of harmful algae and their toxins to the saline portions of the James Estuary. Lastly, we compare cyanotoxin concentrations in tissues of fish and shellfish from the tidal fresh and oligohaline segments of the estuary.

2. Materials and methods

2.1. Study area

Prior work has characterized the occurrence of cyanotoxins in tributaries of Chesapeake Bay (Tango and Butler, 2008). Our focus here is on the James River, the southernmost and third largest tributary of Chesapeake Bay (Fig. 1). The James receives nutrients from a large contributing area that includes much of Virginia, as well as local point sources associated with major metropolitan areas in Richmond and Hampton Roads (Bukaveckas and Isenberg, 2013; Bukaveckas et al., 2018). The tidal portion of the James has high levels of algal production, and is considered impaired on the basis of exceeding site-specific chlorophyll standards. Harmful algal blooms include periodic outbreaks of dinoflagellates in the lower, saline portions of the James, and toxic cyanobacteria in the upper, tidal freshwater segment (Marshall et al., 2009; Mulholland et al., 2009). We previously documented the occurrence of a longitudinal CHL*a* maximum in the tidal fresh segment, which

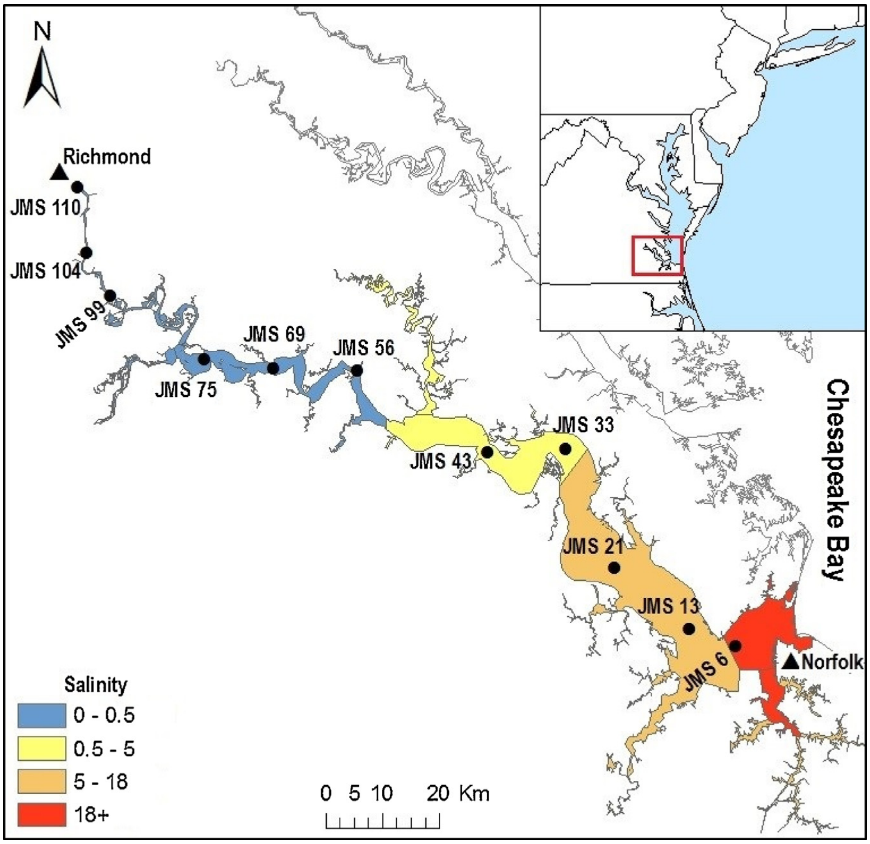

Fig. 1. Map of the tidal James River showing sampling locations in the tidal fresh (0–0.5), oligohaline (0.5–5), mesohaline (5–18) and polyhaline (>18) segments.