



# Time series models of decadal trends in the harmful algal species *Karlodinium veneficum* in Chesapeake Bay



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## ABSTRACT

The harmful dinoflagellate, *Karlodinium veneficum*, has been implicated in fish-kill and other toxic, harmful algal bloom (HAB) events in waters worldwide. Blooms of *K. veneficum* are known to be related to coastal nutrient enrichment but the relationship is complex because this HAB taxon relies not only on dissolved nutrients but also particulate prey, both of which have also changed over time. Here, applying cross-correlations of climate-related physical factors, nutrients and prey, with abundance of *K. veneficum* over a 10-year (2002–2011) period, a synthesis of the interactive effects of multiple factors on this species was developed for Chesapeake Bay, where blooms of the HAB have been increasing. Significant upward trends in the time series of *K. veneficum* were observed in the mesohaline stations of the Bay, but not in oligohaline tributary stations. For the mesohaline regions, riverine sources of nutrients with seasonal lags, together with particulate prey with zero lag, explained 15%–46% of the variation in the *K. veneficum* time series. For the oligohaline regions, nutrients and particulate prey generally showed significant decreasing trends with time, likely a reflection of nutrient reduction efforts. A conceptual model of mid-Bay blooms is presented, in which *K. veneficum*, derived from the oceanic end member of the Bay, may experience enhanced growth if it encounters prey originating from the tributaries with different patterns of nutrient loading and which are enriched in nitrogen. For all correlation models developed herein, prey abundance was a primary factor in predicting *K. veneficum* abundance.

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## 1. Introduction

Harmful algal blooms (HABs) are escalating worldwide, recognized to be significantly associated with human-induced nutrient pollution as well as global climate change (Anderson et al., 2002; Glibert et al., 2005; Heisler et al., 2008; Hallegraeff, 2010; Wells et al., 2015; Glibert and Burford, 2017). There is a need to quantify these relationships but there is inherent inconsistency and variability in and/or between time-series data of algal taxa and of the associated environmental factors (Cloern and Jassby, 2010). New quantitative tools that can integrate multifactorial data are needed to unambiguously parameterize HAB species responses to dynamic environmental conditions, while accounting for natural variability and confounding factors.

Of the many HAB taxa, the toxic dinoflagellate *Karlodinium veneficum* is of particular concern worldwide due to its

ichthyotoxic properties (Deeds et al., 2002, 2006; Place et al., 2012). Blooms of *K. veneficum* (formerly *Gyrodinium galatheanum*, *Gymnodinium galatheanum* and *K. micrum*) have been reported in a wide range of estuarine systems, including the South African, Europe, Western Australia and the eastern United States seaboard (Adolf et al., 2009; Place et al., 2012, and reference therein). In Chesapeake Bay, toxicity of *K. veneficum* has been implicated in fish kills (Deeds et al., 2002, 2006) and in the failure of oyster spawning and in the growth of early life stages of oysters (Glibert et al., 2007; Stoecker et al., 2008). The Chesapeake Bay has been negatively impacted by anthropogenic nutrient enrichment over the past several decades, as evidenced by recurrent low dissolved oxygen (DO) conditions, losses of submersed aquatic vegetation (SAV; Cooper and Brush, 1991; Boynton et al., 1995; Hagy et al., 2004; Kemp et al., 2005; Gurbisz and Kemp, 2014) and increasing observations of *K. veneficum* as well as other HAB taxa are a manifestation of these nutrient effects (HABs; e.g. Glibert et al., 2001; Marshall et al., 2005; Li et al., 2015). As a well-monitored estuary, Chesapeake Bay provides an excellent model system with which to explore how dynamic environmental conditions affect this HAB species.

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A number of previous studies have examined the factors that can influence *K. veneficum* occurrence, but these have yet to be collectively quantified in such a way as to allow predictive power for this dinoflagellate in an estuarine system such as Chesapeake Bay. The abundance of *K. veneficum* is positively associated with temperature, and negatively with depth and salinity, based on field observations (Li et al., 2000a); it commonly occurs over a broad salinity range (7–17) in the mid and upper Bay regions during late summer when temperatures are high (Li et al., 2000a, 2015). High ambient dissolved inorganic phosphate (DIP), and resultant low N:P ratios in summer, also show some correspondence with bloom occurrence (Li et al., 2000a, 2015). These trends are supported by laboratory studies showing a high P demand by these cells (Nielsen, 1996; Li et al., 2000b). It has also been noted that *K. veneficum* blooms are favored when there is a predominance of  $\text{NH}_4^+$  or other reduced forms of nitrogen (N, e.g., urea, dissolved organic N) over  $\text{NO}_3^-$  and  $\text{NO}_2^-$  concentrations (Glibert and Terlizzi, 1999; Kempton et al., 2002). Furthermore, because *K. veneficum* is a mixotroph (Li et al., 2000b; Place et al., 2012), prey availability and prey quality also affect its abundance and its rate of growth (Adolf et al., 2008). Moreover, recent laboratory experiments have shown that the physiological or nutritional conditions of both predator and prey affect the feeding behavior and growth rate of *K. veneficum* (Lin et al., 2017).

Adding further complexity, it is conceivable that HABs such as *K. veneficum* may have increased in frequency in Chesapeake Bay due to climate-induced changes in hydrology and nutrient loading. Future climate scenarios project increases in spring river flows to Chesapeake Bay, a trajectory that may undermine efforts for eutrophication recovery and that may strengthen nonlinear interactions among biogeochemical processes (Najjar et al., 2010). Such changes may alter competitive outcomes that are favorable for initiation and development of HAB species (Wells et al., 2015).

Here, using the extensive time series data from Chesapeake Bay, this study extends the previously documented trends in *K. veneficum* and quantifies the relationships between abundance of this HAB taxon in time and space in relation to physical factors, nutrient concentrations, forms and ratios, as well as prey availability. Advanced time-series models with multiplicative and lagged terms were used to address the hypothesis that a combination of increasing N, altered nutrient ratios, and concentrations and nutritional quality of prey have contributed significantly to increased *K. veneficum* abundance in mid-Chesapeake Bay. These quantitative tools may help to guide managers in predicting how these blooms may change as they can be applied in future scenarios of climate change and nutrient management actions.

## 2. Material and methods

### 2.1. Overview of datasets and study stations

Data from 2002 to 2011 on phytoplankton abundance and water quality were acquired from the Chesapeake Bay Program (link: <http://www.chesapeakebay.net>) and flow data were acquired from USGS (<http://md.water.usgs.gov>). Phytoplankton and water quality data acquisition was restricted to near-surface samples at seven stations in mid-Chesapeake Bay and tributaries that were selected because they experienced a reoccurrence of *K. veneficum* for more than five years and thus represent the broad spatial distribution of this species in the estuary (Fig. 1). The oligohaline and mesohaline salinity zone was defined based on Harding and Perry (1997). The stations analyzed included the main-channel stations of CB3.3C, CB4.3C and CB5.2 and the tributary stations of the Patapsco River (WT5.1), Choptank River (ET 5.2), Patuxent River (LE1.1) and Potomac River (LE2.2).

Routine sampling by the Chesapeake Bay Program was conducted on a biweekly to monthly basis. Phytoplankton abundance in the Chesapeake Bay Program is enumerated with conventional light microscopy. Phytoplankton data were mainly available from biweekly sampling in April, May, July and August, and monthly sampling in March, June, September, October, and December for each station, each year. The data analyzed here encompassed only the period from 2002 to 2011 because prior to 2002 the presence of *K. veneficum* was variably reported with different names, including *Gyrodinium estuarali*, *Gymnodinium galatheanum* or *Gymnodinium veneficum* and thus its presence, while documented, is difficult to unravel with certainty in the database. Since 2002, this species was reported as *Karlodinium micrum*, or more recently as *K. veneficum* (Bergholtz et al., 2006). Frequency of sampling and enumeration has declined since 2011, thus making the window from 2002 to 2011 the most complete data set. Data on the common prey for *K. veneficum*, *Cryptomonas* spp. and unidentified microphytoflagellates ( $<10\ \mu\text{m}$ ), were also retrieved from the database. Nutrient data in the Chesapeake Bay Program database were available from biweekly sampling in April, May, July and August, and monthly sampling for the other months. Variables included dissolved inorganic nitrogen (DIN: sum of  $\text{NO}_3^-$ ,  $\text{NO}_2^-$  and  $\text{NH}_4^+$ ), DIP, total N, total P, dissolved organic N and P (DON, DOP). Physical and climate-related variables included temperature, salinity and flow (the sum of measures for Susquehanna and Potomac River).

### 2.2. Statistical analyses

Several approaches were taken for data analysis, and all data processing was conducted using the R language (R Core Team, 2016). Where data availability was more frequent than monthly, averages were calculated so that all datasets and variables from different sources were comparable for any month during the 10-year studying period.

First, in order to determine the relationship between river flow and nutrient concentrations, linear correlations between flow and nutrient variables were calculated and significance was estimated using Pearson's product moment coefficients. Second, the non-parametric seasonal Mann-Kendall (SMK) test was applied to detect monotonic trends in time series of *K. veneficum* and other variables. This test, somewhat analogous to regression analysis, is better suited for water-quality data sets with irregular sampling intervals, non-normality and missing data and it is less affected by extreme values because it is based on sign differences, not actual values.

Next, Fourier sine and cosine series were used to remove the seasonal components from the time series data. Then, the Wang-Akritas-Van Keilegom (WAVK) test was further applied to assess potentially non-monotonic parametric trends in weakly stationary time-series (Lyubchich et al., 2013). Thus, the time series were detrended, deseasonalized and statistically tested to obtain stationary residuals. After such decomposition, autocorrelation and partial autocorrelation functions were used to examine the temporal persistence of all variables at each station.

The detrended time series of *K. veneficum* were then modeled using transfer functions to relate the change in abundance with the other detrended, environmental, nutrient and biological variables. Relationships were compared contemporaneously and with time lags. To explore both non-lagged and lagged relations between variables, cross-correlation functions (CCF) were applied to the stationarized time-series of the abundance of *K. veneficum* and 1) nutrient concentrations, including DIP, different N forms (e.g.  $\text{NO}_3^-$ ,  $\text{NH}_4^+$  and DON) and nutrient ratios (DIN:DIP, DON:DOP, and TN:TP) and 2) the abundance of prey, the cryptophyte *Cryptomonas* spp. and unidentified microphytoflagellates. Overall,

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