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Resilience of estuarine phytoplankton and their temporal variability along salinity gradients during drought and hypersalinity

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ABSTRACT

In South African estuaries, there is no knowledge on the resilience and variability in phytoplankton communities under conditions of hypersalinity, extended droughts and reverse salinity gradients. Phytoplankton composition, abundance and biomass vary with changes in environmental variables and taxa richness declines specifically under hypersaline conditions. This research thus investigated the phytoplankton community composition, its resilience and variability under highly variable and extreme environmental conditions in an estuarine lake system (Lake St. Lucia, South Africa) over one year. The lake system was characterised by a reverse salinity gradient with hypersalinity furthest from the estuarine inlet during the study period. During this study, 78 taxa were recorded: 56 diatoms, eight green algae, one cryptophyte, seven cyanobacteria and six dinoflagellates. Taxon variability and resilience depended on their ability to tolerate high salinities. Consequently, the phytoplankton communities as well as total abundance and biomass differed along the salinity gradient and over time with salinity as the main determinant. Cyanobacteria were dominant in hypersaline conditions, dinoflagellates in marine-brackish salinities, green algae and cryptophytes in lower salinities (brackish) and diatoms were abundant in marine-brackish salinities but survived in hypersaline conditions. Total abundance and biomass ranged from 3.66×10^3 to 1.11×10^9 Cells/L and 1.21×10^6 to 1.46×10^{10} pgC/L respectively, with the highest values observed under hypersaline conditions. Therefore, even under highly variable, extreme environmental conditions and hypersalinity the phytoplankton community as a whole was resilient enough to maintain a relatively high biomass throughout the study period. The resilience of few dominant taxa, such as *Cyanothece*, *Spirulina*, *Protoperidinium* and *Nitzschia* and the dominance of other common genera such as *Chlamydomonas*, *Chroomonas*, *Navicula*, *Gyrosigma*, *Oxyrrhis*, and *Prorocentrum*, provided the carbon at the base of the food web in the system and showed that even during the extended period of drought, a foundation for productivity can be provided for once conditions improve.

1. Introduction

Phytoplankton undergo continual changes in their community composition and structure in aquatic systems with varying environmental conditions (Reynolds, 2006). Factors affecting the biological variables (composition, abundance, biovolume and biomass) of phytoplankton in estuaries include nutrients, light, turbidity, temperature, salinity (Haris, 1986; Reynolds, 2006; O'Boyle and Silke, 2010) and grazing (Alpine and Cloern, 1992; Mortazavi et al., 2000; Froneman, 2001). Estuarine systems with relatively stable environmental variables are characterised by very little variation in biological variables, while systems with highly varying to extreme physico-chemical variables are characterised by high variability in biomass (Naselli-Flores et al., 2003).

Two of the main environmental variables influencing estuarine phytoplankton communities are salinity and nutrients which relate to freshwater inflow into estuaries (Lancelot and Muylaert, 2011). Estuarine phytoplankton abundance and biomass correlates with salinity and succession is mostly characterised by diatoms dominating during periods of high nutrient concentrations and dinoflagellates during lower nutrient concentrations (Gallegos, 1992; Chan et al., 2002; Reynolds, 2006). In estuaries with ordinary salinity gradients, higher species richness towards the fresh water region and lower richness in the estuarine mouth (marine) is observed with few species occurring along the entire estuarine gradient (Lancelot and Muylaert, 2011). Hypersalinity, further

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reduces species richness (Williams, 1998; Pedrós-Alió et al., 2000). As salinity changes, phytoplankton composition changes and is dominated by species able to resist such salinities (Hammer, 1986). Estuaries and lakes under extreme saline to hypersaline (>50) conditions have previously been characterised by halotolerant taxa such as the chlorophyte *Dunaliella* and the ciliate *Fabrea* (Por, 1980) while systems with relatively lower salinities (<20) have been dominated by taxa such as the chlorophyte *Chlamydomonas* (Tomas, 1997; Bazin et al., 2014; Jendyk et al., 2014).

Changes in phytoplankton species composition strongly influence the biomass and community structure of higher trophic levels as well as various ecosystem processes (Duffy and Stachowicz, 2006). However, little is known about the phytoplankton community structure, dynamics and resilience in South African estuarine systems, especially during extended drought periods such as that experienced recently in the St. Lucia estuarine lake system of KwaZulu-Natal, South Africa (Taylor, 2013). The St. Lucia estuarine lake system was separated from its main source of freshwater, the Mfolozi River and had, since 2002, a prolonged closure of the estuarine mouth from the sea. Evaporation and limited fresh water inflow led to an extended drought period (2002–2012) characterised by hypersaline conditions and reversed salinity gradients during periods of low rainfall (Lawrie and Stretch, 2011). Interestingly, the few studies that investigated chl *a* concentrations during this period reported significantly different chl *a* concentrations between the lake compartments and overall high chl *a* concentrations (0.5–132 mg chl *a* m^{-3}) (Perissinotto et al., 2010; Tirok and Scharler, 2013), implying some phytoplankton species adapted and were resilient even to such extreme conditions. The overall importance of estuaries in their protection and hosting of juvenile marine fish, post-larva prawns and other planktonic organisms have been noted previously (e.g. Whitfield, 1988; Sheaves et al., 2014). The importance of estuaries in general as high productivity regions, the results from previous studies on Lake St. Lucia and the importance of phytoplankton as one of the main providers of energy at the base of the food web (Fielding et al., 1991; Ramdani et al., 2009) prompted this study. The objectives of this study were to 1) investigate the temporal variability of the nano- and microphytoplankton community at three sites of the lake along a reverse salinity gradient, 2) investigate the relationship between the nano- and microplankton community structure (composition, abundance, biovolume and biomass) and physico-chemical variables, and 3) to determine the taxa resilient enough to dominate during conditions of hypersalinity thereby providing the energy at the base of the food web under such extreme conditions.

2. Materials and methods

2.1. Study site

The St. Lucia estuarine lake system (between 27° 52′S, 28° 24′S and 32° 21′E, 32° 34′E), situated in the northern parts of the KwaZulu-Natal province of South Africa, is the largest estuarine system in southern Africa and one of the largest estuarine lake systems in Africa (Day, 1981). The estuarine system is part of the iSimangaliso Wetland Park which gained World Heritage Site status in 1999 (Taylor, 2006) after being declared a RAMSAR site in 1991 (Taylor, 1991). For the purposes of this study, the system was divided into three compartments: the northern embayments (which are comprised of False Bay and North Lake), the South Lake, and the channel (Fig. 1). Depending on water levels, the surface area of the entire lake varies from 300 to 360 km^2 (Begg, 1978). Its three interconnected shallow lakes (False Bay, North Lake and South Lake) have a maximum depth of 2 m and an average depth of 0.9 m (Fielding et al., 1991). The lakes discharge into a 21 km long channel which connects to the Indian Ocean (Orme, 1973). Sampling was conducted monthly from October 2010–September 2011, with one station in each of the compartments, namely Listers Point (LP), Charters Creek (CC) and Mouth (MT) (Fig. 1) as representatives of the system following previous studies (e.g Perissinotto et al., 2013; Tirok and Scharler, 2013) and available data on the system. However, given the large size of the system these three sites cannot comprehensively cover the spatial dynamics of the entire system, we here however focus on the temporal dynamics at the three sites.

2.2. Physico-chemical measurements

Sampling was conducted monthly at the three sites. Salinity, temperature (°C) and turbidity (NTU) were measured at each site using a YSI 6920 Multiprobe system. Depth (m) of LP and CC were measured using a ruler and average depth of MT was estimated at 2 m (Tirok and Scharler, 2013). Photosynthetic available radiation (PAR) (μmol photons m^{-2} s^{-1}) was measured at the surface and bottom of all sites using an LI-COR light meter, fitted either with LI-189 or LI-193SA quantum sensor. The light attenuation coefficient (Kd) was calculated using the following formula: $Kd = -Ln(Iz_2/Iz_1)/(z_2 - z_1)$ where Iz_2 is the irradiance (μmol photons m^{-2} s^{-1}) at depth z_2 (m, surface) and Iz_1 is the irradiance at depth z_1 (m, bottom).

Duplicate subsurface water samples were analysed for dissolved inorganic nitrogen (DIN: nitrate, nitrite and ammonia) and dissolved inorganic phosphorus (DIP: orthophosphate). The samples were collected in 100 ml polyethylene bottles, filtered through a Whatman GF/F glass-fiber filter and stored at <−20 °C until analysis.

2.3. Abundance, biovolume and biomass

During the monthly sampling, duplicate subsurface water samples for phytoplankton composition, abundance, biovolume and biomass were collected in 250 ml acid washed iodine proof polyethylene bottles and fixed with acid Lugol's solution. The Utermöhl (1958) method was used to settle cells for microscopy. Depending on the abundance of cells and amount of detritus in the sample, 2–100 ml was settled and viewed under a Nikon *ECLIPSE Ti Series* inverted microscope fitted with a DS-Fi1c camera and a Differential Interference Contrast (DIC) attachment powered by the NIS-Elements BR software at magnifications of 100× to 400×. Cells were identified to the lowest taxonomic level possible with the aid of taxonomic guides which included Round et al. (1990), Rippka et al. (1979) and Tomas (1997). At least 50 cells per taxa and a sum of at least 500 cells were counted per sample following Hillebrand et al. (1999). Abundance was calculated using the equation: Abundance (Cells/L) = $[A(mm^2)*1000/(a(mm^2)*V(ml))]*n$, where n was the number of cells counted, A was the area of the whole chamber, a was the area counted, and V was the volume settled. Where a taxon was abundant in some samples and beyond detection in others, a zero replacement value was used since it could not be assumed that the taxon was truly absent in the system. The zero replacement value was set to half the detection limit, i.e. zero replacement value (Cells/L) = $0.5*(1/V)*1000$, where V was the volume (ml) of sample settled which differed for different samples.

In order to calculate the cell volume, linear dimensions (length, width, height) of taxa were measured using the NIS-Elements BR software and fitted into geometric models according to Lecce-Monteroni (2007), Sun (2003) and Hillebrand et al. (1999). Total biovolume per taxa (μm^3/L) was calculated by multiplying the mean cell volume for each taxon by the abundance of that taxon (Felip and Catalan, 2000). Similarly, zero replacement values for biovolume were calculated by multiplying the abundance zero