

# Diversity of coastal phytoplankton assemblages – Cross ecosystem comparison



Kalle Olli <sup>a,\*</sup>, Hans W. Paerl <sup>b</sup>, Riina Klais <sup>a</sup>

<sup>a</sup> Institute of Ecology and Earth Sciences, University of Tartu, Lai 40, 51005, Tartu, Estonia

<sup>b</sup> Institute of Marine Sciences, University of North Carolina at Chapel Hill, 3431 Arendell Street, Morehead City, NC 28557, USA

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## ABSTRACT

Phytoplankton plays a massively important role in the oceanic carbon cycling and biogeochemistry. Despite its far-reaching importance, regional cross-ecosystem comparisons remain incomplete because the data sets are often scattered and fragmented. Here we compiled and harmonized decadal scale phytoplankton monitoring data sets from seven geographic regions of the world ocean, covering ca 45 thousand quantitative samples from European, North- and South American coastal waters. Nonmetric multidimensional scaling revealed clear regional clustering of sampling locations, both when using compositional relatedness or phylogenetic turnover of communities. Compositional and phylogenetic relatedness of phytoplankton communities had a strong correlation with salinity and temperature gradients ( $R^2 = 0.6–0.8$ ). The regional taxon richness ( $S$ ) varied by almost an order of magnitude, and scaled with the ecosystem size ( $A$ ) according to a power law:  $S = 62 \times A^{0.35}$ . The compositional turnover of species (beta-diversity) was also positively related to ecosystem size, but also to mean regional salinity.

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## 1. Introduction

The oceans provide approximately half of the planetary carbon fixation and oxygen production (Field et al., 1998). Marine coastal zones are among the most productive ecosystems of the planet, accounting for at least 15% of oceanic primary production, 80% of organic matter burial, and at least 40% of the value of the world's ecosystem services (Gattuso et al., 2011). Like other earth systems, oceans are undergoing change — warming and coastal eutrophication are impacting community structure and ecosystem function.

Unlike plant-dominated terrestrial environments, marine photosynthesis is dominated by single-celled microbes — phytoplankton. The demographic traits and high turnover of phytoplankton are reflected in immediate community response to external pressures, like climate change or the input of nutrients to coastal ecosystems. Phytoplankton community itself strongly influences climate processes and global biogeochemical cycles, and sets the upper limit to ocean productivity and fishery yields (Chassot et al., 2010).

Recent modeling advances have revealed that physically mediated dispersal and variability of the environment are the most important ecological controls on global marine phytoplankton gradients (Barton et al., 2010). Further, phytoplankton diversity patterns determine important ecosystem functions, like primary production in the global ocean (Prowse et al., 2014), as well as response to predicted climate change (Dutkiewicz et al., 2013). However, field data remain indispensable to provide a test of the hypothesized patterns and mechanisms that emerge from modeling studies.

Phytoplankton can be quantified by relatively simple and intercomparable sampling methods (Lund et al., 1958; Utermöhl, 1958). Many data sets are available now and have been presented in conferences and research papers (Mallin et al., 1991; Wasmund and Uhlig, 2003; Cloern and Dufford, 2005; Olli et al., 2013). However, regional cross-ecosystem comparisons remain hampered, because the data sets are to a large extent scattered and fragmented. In a recent paper we shared our experience in procedures of combining and harmonizing heterogeneous phytoplankton data sets from several countries and institutions around the Baltic Sea (Olli et al., 2013). Here we extend our scope to coastal ecosystems in different continents and oceans, and provide a cross ecosystem comparison by using compositional and phylogenetic information on coastal phytoplankton assemblages.

\* Corresponding author.

E-mail address: [kalle.oli@ut.ee](mailto:kalle.oli@ut.ee) (K. Olli).

The ecological interactions and ecosystem functions within communities are predicted by community composition and the functional traits of the constituent species. Functional traits, which are more directly linked to ecosystem functioning, are not readily available for a wide variety of phytoplankton species, and/or can't be easily measured. Phylogenies reflect the integrated functional differences among taxa, and may be a more encapsulating measure than singular, discretely measured traits (Vane-Wright et al., 1991). Ecosystem functions may differ depending on whether abundances are phylogenetically clustered, so that one or a few clades dominate, or are evenly dispersed across the phylogenetic tree connecting the species. Conditions favoring high abundance within a particular species, could also favor higher abundance among its close relatives (Cadotte et al., 2010).

The aim of this study was a comparative analysis of phytoplankton data sets from seven geographic regions of the world coastal ocean, incorporating over 40 thousand quantitative samples, two thousand taxa and 1.2 million records. After careful taxonomic harmonization we analyzed if the regional taxon richness, compositional and phylogenetic turnover of communities reveals any large-scale geographic pattern. Resource competition of phytoplankton may lead to chaotic fluctuations in species abundances, allowing stochastic coexistence of many species (Huisman and Weissing, 1999). We thus expected high compositional and phylogenetic diversity within each coastal region, and asked if this within region variation is equal or comparable to the overall variation of coastal phytoplankton communities. Alternatively, the geographic regions could show idiosyncratic phylogenetic and community composition patterns, which could be driven by differences in environmental conditions (environmental filtering), or dispersal limitation due to large distances.

## 2. Material and methods

### 2.1. Data compilation and taxonomic harmonization

We used microscopy derived species-specific quantitative phytoplankton data from seven coastal regions of the world ocean (Fig. 1, Table 1). All the regions are coastal or estuarine habitats strongly influenced by river inflows, with time-varying mixtures of seawater and freshwater, exchanges across the sediment–water interface, steep spatial salinity gradients, and some with pronounced seasonality (Table 1).

Phytoplankton were sampled from surface layer and aliquots preserved in acid Lugol's solution or formalin. Cell enumeration was done from plankton settling chambers using inverted microscopes (Utermöhl, 1958) by counting random grid fields, strips or whole chamber bottom, at magnifications ranging from 125 $\times$  to 1250 $\times$  (for method details see Cloern and Dufford, 2005; Hall et al., 2008; Olli et al., 2013). The number of cells counted is rarely presented on a per record basis in routine phytoplankton monitoring data sets. The counting effort varied between institutions, but in general was better than 100 cells of the most numerous taxon. Species-specific cell volumes were estimated from cell size and respective geometric formulas (Edler, 1979; Hillebrand et al., 1999), and were converted to wet weight biomass by assuming a density of 1.

Phytoplankton samples were always taken from fixed statutory monitoring stations, except for the Baltic Sea, which was a combination of fixed, and spatially scattered coastal samples (Olli et al., 2013). Sampling frequency varied between the time series from monthly (Patos Lagoon Estuary) to weekly or biweekly in intensively sampled stations (e.g. in Chesapeake Bay). In regions with strong seasonality sampling frequency was lower during winter months.

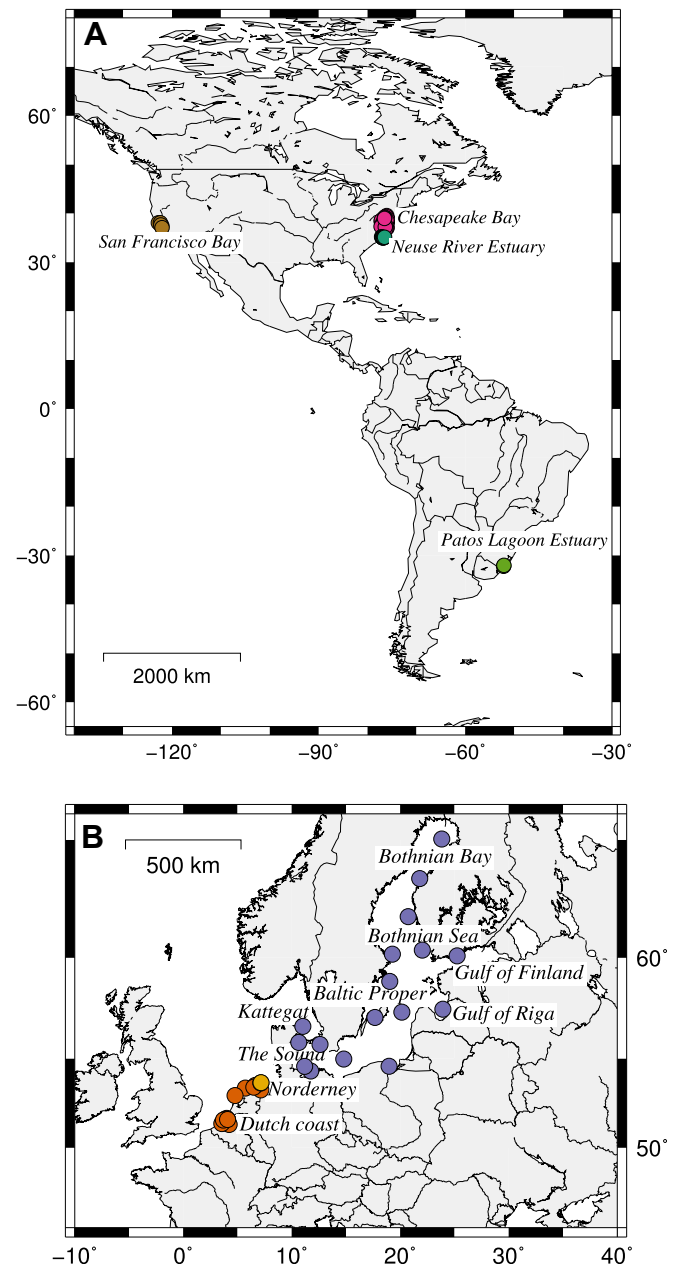


Fig. 1. Spatial distribution of phytoplankton sampling locations in the joint data set.

The mean and range of regional salinities and temperatures, as the main determinants of environmental heterogeneity, are given in Table 1. Another potential predictor of heterogeneity and diversity, the regional ecosystem surface area, is hard to define due to lack of clear borders, except for landlocked embayment. Therefore for consistency of cross-regional comparison we used the length of the minimum spanning tree (MST) connecting the sampling stations. MST (km) is a combination of vertices connecting all the sampling stations in the geographic space, constrained to have the shortest total length.

Harmonization of taxonomic naming conventions preceded data analysis. Firstly, a unique list of original taxon names was compiled, and corrected for typing errors. Information about the presence or absence of flagella, photo- or heterotrophy, and presence or absence of theca in dinoflagellates was retained to narrow down the distinctiveness of unidentified or partly identified taxa.

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