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Seasonal variability of picoplankton in the Northern South China Sea at the SEATS station

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Abstract

Flow cytometric analysis of picoplankton from the Southeast Asia Time-series Station (SEATS) in the South China Sea was performed for samples collected every 1–4 months during October 2001 to September 2002 (six cruises) and between November 2004 and December 2005 (four cruises). *Prochlorococcus* was the most abundant autotrophic picoplankton with the maximum abundance occurring in summer. *Synechococcus* and picoeukaryotes were 1 or 2 orders of magnitude less abundant during most of the year, but showed a much larger seasonal variation, with maximum abundance occurring in winter to early spring. The winter peak of *Synechococcus* and picoeukaryotes coincided with the deepening of the mixed-layer depth caused by surface cooling and the strong NE monsoon winds. Maximum bacterial biomass was observed in spring, and generally followed the winter peak of *Synechococcus* and picoeukaryotes with a time lag. *Prochlorococcus* contributed up to 80% of the total autotrophic biomass during summer, but *Synechococcus* and picoeukaryotes accounted for 60–80% of the total autotrophic biomass in winter. Bacterial biomass was less than the autotrophic biomass and the two were only weakly correlated. The interannual variability in the structure and composition of the picoplankton community may be related to the El Niño-Southern Oscillation (ENSO) cycle. During an El Niño year (2001–2002), with higher sea-surface temperature, chlorophyll *a* was lower and *Prochlorococcus* and bacterial biomass were higher. In contrast, the higher picoeukaryote biomass during winter was probably responsible for the higher chlorophyll *a* during the La Niña year of 2004–2005.

Keywords: Picoplankton; Community structure; Seasonal variation; South China Sea; Flow cytometry

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1. Introduction

The picophytoplankton (<2 μm), including the cyanobacteria *Prochlorococcus* and *Synechococcus* and the small eukaryotic algae, contribute substantially to both phytoplankton biomass and production in marine ecosystems (Li et al., 1983; Campbell

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et al., 1994; Liu et al., 2004). Because their rapid growth rates are closely matched by mortality losses due to grazing by microzooplankton, they play an important role in nutrient regeneration and cycling in the ocean. Because of its indisputable importance in marine primary production and biogeochemical cycling of carbon and nutrients, the dynamics of picoplankton, and its control mechanisms have been widely studied in various types of aquatic ecosystems in the last two decades. However, there is no report on the seasonal and interannual variation of picoplankton community structure in the South China Sea (SCS), the world's second largest marginal sea.

The SCS is a semi-enclosed basin with extensive continental shelves on the west and south sides and a deep basin over 3000 m deep. Several large rivers, including the Mekong River and the Pearl River, discharge to it. Climatic variations in the atmosphere and in the upper ocean of the SCS are primarily controlled by the East Asian monsoon, which follows closely the climatic variations in the equatorial central Pacific (Shaw and Chao, 1994). In addition, SCS is also subject to frequent passage of typhoons, and strong internal waves (Liu A.K. et al., 1998). All of these physical disturbances could influence water-column stability and the magnitude of vertical mixing in different time and spatial scales. This would in turn affect the upward flux of inorganic nutrients from deep water to the surface, and sequential biological processes in the upper water column. Therefore, SCS is a very good site to monitor the response of the oceanic ecosystem to climate change during various time scales, from episodic events to seasonal, interannual, and decadal. Based on the above consensus, scientists in Taiwan (Republic of China) established the Southeast Asia Time-series Station (SEATS) in the SCS in 1999. The primary station is located at 18 °N, 116 °E, about 700 km southwest of Taiwan (see map in Wong et al., 2007a). In this paper, we report flow cytometric analysis of picoplankton from the SEATS site and the elucidation of the seasonal and interannual variability in the structure and composition of the picoplankton community.

2. Materials and methods

Samples were collected at the SEATS station (18 °N, 116 °E) in the SCS on six cruises between October 2001 and September 2002, and again on four cruises between November 2004 and July 2005. Seawater was collected from eight depths within the upper 150 m of the water column using Go-Flo or Niskin bottles attached to a CTD rosette system; sub-samples (2 ml) were preserved with paraformaldehyde (0.2% final concentration), quick frozen, and stored in liquid nitrogen until analysis.

An LSR flow cytometer (Becton Dickinson) equipped with a 488-nm laser was used to enumerate the picoplankton. Forward and side light scatters (FSC and SSC) and green (515–545 nm), orange (564–606 nm), and red (>650 nm) fluorescence were collected, saved, and analyzed with CYTOWIN software (Vaulot, 1989). All signals were normalized to that of the 1-μm Fluoresbrite YG beads (Polysciences, Warrington, PA) that were added to each sample. Three major groups of picophytoplankton, *Prochlocococcus*, *Synechococcus* and picoeukaryotes, were distinguished based on their autofluorescence properties. Heterotrophic bacteria were enumerated in a separate sub-sample stained with the nucleic acid stain SYBR Green I (Molecular Probes) (Marie et al., 1997).

Sizes of each picoplankton category were estimated by counting cell numbers that pass through 0.4, 0.6, 0.8, 1.0, 2.0, and 3.0-μm polycarbonate membrane filters (Zubkov et al., 1998). These measurements were deployed only during July and September 2002 cruises and the resulting size estimates were applied to all cruises. For bacteria, *Prochlorococcus* and *Synechococcus* cell volumes were converted to carbon using a conversion factor of 280 fg C μm^{-3} (Heldal et al., 2003). Because the size fractionation method we employed in this study is not suitable for picoeukaryotes due to the breaking of delicate cells during the filtration, we used a carbon content of 1500 fg C $cell^{-1}$ determined by Zubkov et al. (1998).

Hydrographic, nutrients and chlorophyll *a* (chl *a*) data were provided by the SEATS core program (see Tseng et al., 2005). The mixed-layer depth (MLD) during each cruise was estimated as the depth above which the density gradient was 0.1 unit m^{-1}. Chl *a* was measured by the fluorometric method (Strickland and Parsons, 1984) using GF/F filters.

3. Results

3.1. SST, MLD and chlorophyll a concentrations

Details of physical and chemical characteristics at the SEATS site are reported elsewhere (Tseng et al.,