



Phytoplankton, bacterioplankton and virioplankton structure and function across the southern Great Barrier Reef shelf



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ABSTRACT

Bacterioplankton and phytoplankton dynamics, pelagic respiration, virioplankton abundance, and the diversity of pelagic diazotrophs and other bacteria were examined in relation to water-column nutrients and vertical mixing across the southern Great Barrier Reef (GBR) shelf where sharp inshore to offshore gradients in water chemistry and hydrology prevail. A principal component analysis (PCA) revealed station groups clustered geographically, suggesting across-shelf differences in plankton function and structure driven by changes in mixing intensity, sediment resuspension, and the relative contributions of terrestrial, reef and oceanic nutrients. At most stations and sampling periods, microbial abundance and activities peaked both inshore and at channels between outer shelf reefs of the Pompey Reef complex. PCA also revealed that virioplankton numbers and biomass correlated with bacterioplankton numbers and production, and that bacterial growth and respiration correlated with net primary production, suggesting close virus–bacteria–phytoplankton interactions; all plankton groups correlated with particulate C, N, and P. Strong vertical mixing facilitates tight coupling of pelagic and benthic shelf processes as, on average, 37% and 56% of N and P demands of phytoplankton are derived from benthic nutrient regeneration and resuspension. These across-shelf planktonic trends mirror those of the benthic microbial community.

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1. Introduction

Microbes are the key players in processing carbon through food webs, recycling most organic matter in the sea. Organic matter and energy is funneled through highly diverse, actively growing, assemblages of Archaea, bacteria, ciliates, nano- and dinoflagellates, and amoebae – many of mixed trophic states sometimes mediated by viral lysis – and subsequently transferred to higher consumers via a chain of small grazers (Legendre and Rivkin, 2008; Strom, 2008). Production and consumption within microbial food webs are largely passed to higher consumers via multiple trophic transfers or lost via remineralization within the euphotic zone.

The functional role of heterotrophic marine bacterioplankton is fairly well understood (Ducklow, 2000). Factors regulating bacterial growth rates and productivity have been identified for temperate bays and estuaries, and for the open sea (Ogbebo and Ochs, 2008), as well as for tropical convergence zones and gyres (Morán et al., 2004; Riemann et al., 2011). However, in tropical shelf waters, the drivers of

phytoplankton and bacterioplankton growth and productivity have rarely been investigated (Alongi and McKinnon, 2005). Most studies available have focused on estuarine and inshore waters of South and Southeast Asia (Bhaskar and Bhosle, 2008; Bong and Lee, 2011; Lee and Bong, 2008; Lee et al., 2009; Ram et al., 2003) where rates of phytoplankton and bacterial growth and production are rapid due to organic pollution.

Bacterioplankton are critical to energy flow and biogeochemical processes in the water column, with their role in coral reef and reef-associated waters exacerbated by the availability of substrates such as mucus and other organics produced by corals and their symbionts (Patten et al., 2008; Sorokin and Sorokin, 2009). However, the role of bacterioplankton in GBR shelf waters has been inferred more often from carbon and nutrient budgets than from empirical measurements (Alongi and McKinnon, 2005; Furnas et al., 1995). It is not known if the same or a different set of drivers control bacterioplankton dynamics in coral reef versus non-coral reef waters.

The plankton communities of the GBR shelf are dominated by rapidly dividing cells in the nano- and pico-plankton size classes (Crosbie and Furnas, 2001; Furnas et al., 2011). The sparse data for GBR bacterioplankton indicate production rates on the order of 20–455 mg C m⁻² d⁻¹ (Alongi and McKinnon, 2005) with the ratio of bacterial to phytoplankton production ranging from 12–161%.

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Factors that drive the functional relationships between phytoplankton and bacteria and further, the roles that viruses play in GBR microbial structure and function are unclear. In other marine systems, including coral reef and reef-associated waters, viruses can play major roles in microbial mortality (Patten et al., 2008; Payet et al., 2014; Seymour et al., 2005). Further, specific functional groups, especially the diazotrophic bacteria and Archaea, can be influenced strongly by benthic–pelagic coupling as they fix nitrogen at rates exceeded only by some cyanobacteria (Bourne and Webster, 2013).

The southern section of the GBR shelf, like the rest of the shelf, is characterized by an across-shelf gradient of sedimentary facies and habitats, yet has several unique characteristics, such as (1) the largest number of coral reefs, and the largest individual reefs, on the entire GBR shelf; (2) relatively high dissolved and particulate nutrient concentrations, partly owing to the fact that most terrestrial materials enter the southern GBR; (3) strong turbulent mixing driven by a large tidal prism (Wolanski, 1994); and (4) the Pompey Reef complex, composed of a large number of individual reefs (many between 50 km² and 100 km² in area) extending over a distance of 140 km. In narrow channels through the Pompey Reef complex (Hopley, 2006), tidal currents of up to 4 m s⁻¹ scour the bottom and sustain gardens of numerous and highly diverse, suspension-feeding benthic communities that thrive on the hard-bottom carbonate platforms at both ends of each channel (Pitcher et al., 2009). These invertebrate gardens benefit from high loads of suspended food particles stimulated by strong tidal currents and sustained periods of turbulent mixing (Alongi et al., 2011).

In this paper, we describe measurements taken at 14 stations across the southern GBR shelf to test the hypothesis that the phytoplankton, virioplankton and bacterioplankton communities will exhibit two peaks in abundance and activity – one inshore peak where high concentrations of terrestrially-derived nutrients and turbulent mixing

foster rapid growth via resuspension, and a second offshore peak within channels of the Pompey Reef Complex, where strong vertical mixing and resuspension of benthic material prevails. We thus hypothesize that the pattern of plankton activity across the shelf mirrors the across-shelf pattern of benthic microbial activity (Alongi et al., 2011).

2. Methods

2.1. Study site description

Inshore stations IS9 (20°57.1'S, 149°04.8'E, 5 m) and IS10 (21°29.7'S, 149°26.6'E, 5 m) were located north of Shoal Point in Sand Bay and near Cape Palmerston in Ince Bay, respectively. Stas. MS7 (20°37.5'S, 149°43.3'E, 49 m) and MS8 (21°19.1'S, 150°18.2'S, 55 m) were located mid-shelf, south of Parker Reef, and southwest of Pompey Reef, respectively. Stas. BR1 (20°29.4'S, 150°04.5'E, 44 m), GR1 (20°45.9'S, 150°22.4'E, 42 m), and PR1 (21°01.9'S, 150°24.8'E, 37 m) were located within mid-shelf reef lagoons (Fig. 1). Sta. BR1 was located within the lagoon formed by Box, Stevens, Credlin, Cannan, and Nixon Reefs; Sta. GR1 was located with the lagoon enclosed by Chavel, Goble, Cole, Briggs, and McIntyre Reefs. Sta. PR1 was situated on the northern leeward side of Pompey Reef. Stations PRC4 (20°26.1'S, 150°31.6'E, 65 m), PRC5 (20°37.4'S, 150°40.2'E, 56 m), and PRC6 (20°44.4'S, 150°48.1'E, 57 m) were established within the outer lagoon of the greater Pompey Reef complex, in close proximity to channels formed between the outer shelf reefs. This complex parallels the shelf edge and is 10–15 km wide. The entire reef tract is not on the shelf edge, which lies another 20 km seaward.

The outer shelf margin is dominated by a series of fault-controlled steps where sediments scoured from the Pompey Reef complex have accumulated (Hopley et al., 2007). Stas. OS1 (20°12.2'S, 150°34.3'E, 60 m)

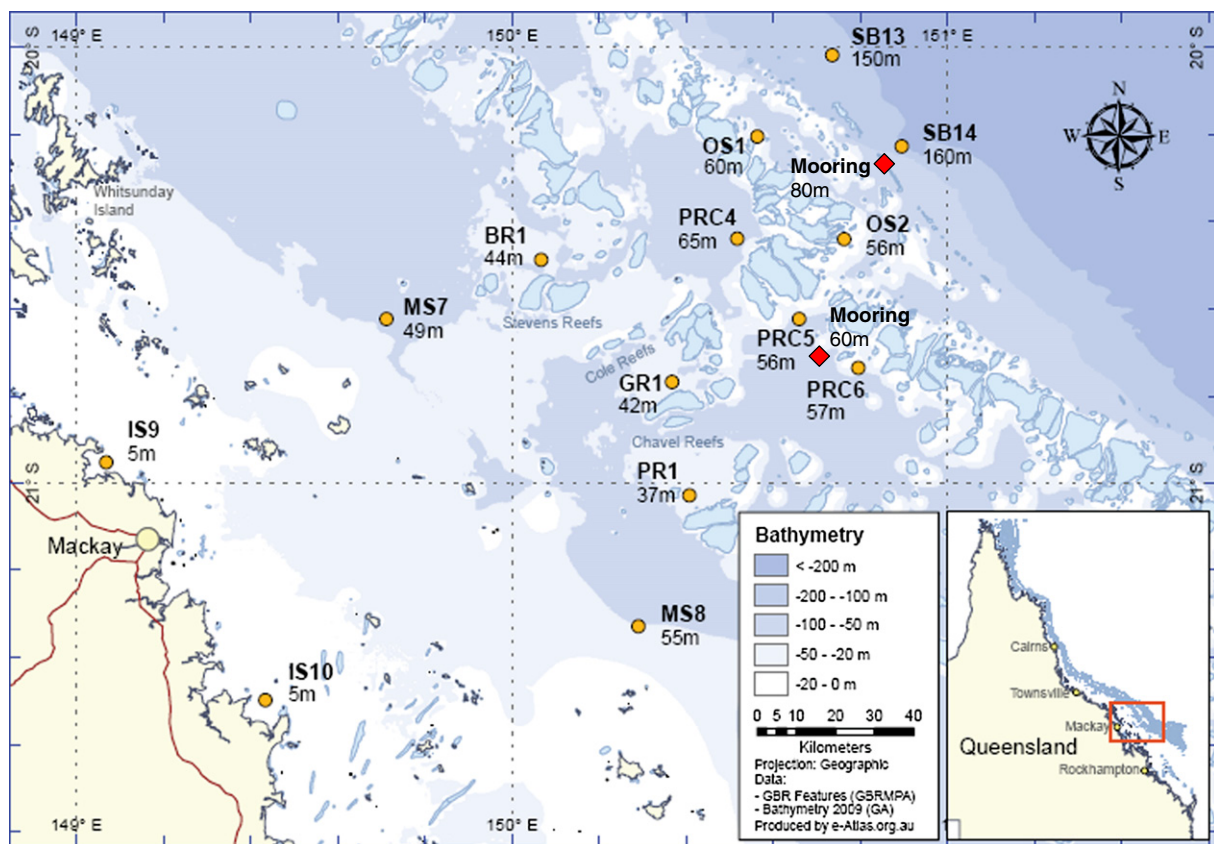


Fig. 1. Map of the pelagic stations sampled across the southern Great Barrier Reef shelf. Two oceanographic mooring sites are designated as sites 'POMP60m' and 'POMP80m'. The third mooring is south of this immediate area (see location in Section 2.1).

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