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Microbial metatranscriptomes from the thermally stratified Gulf of Aqaba/Eilat during summer

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ABSTRACT

The water column in the oligotrophic Gulf of Aqaba/Eilat experiences distinct seasonal cycles with the cooling air and water temperatures of late fall and winter destabilizing the thermocline and forming mixed layer depths reaching 300 to 700 m. As air temperatures warm thermal re-stratification results in a stable thermocline throughout the summer which physically separates a photic, nutrient-poor surface layer from an aphotic, nutrient-rich deep layer. Here we present the first metatranscriptome dataset, and its taxonomic assignments, sampled from three depths of the 700 m deep Station A in the Gulf of Aqaba during the summer stratification (surface – 10 m, deep chlorophyll maximum (DCM) – 85 m, deep aphotic zone — 500 m). Intensive transcriptional activity was attributed to *Prochlorococcus* - the most abundant photosynthetic organism in the RNA-seq dataset - both at the surface and at the DCM. In contrast, cDNA reads related to picoeukaryotic algae were detected almost exclusively at the DCM. The metatranscriptomes presented here provide a basis for examining the seasonal differences in microbial gene expression by comparison with the published metatranscriptomes sampled during the winter deep-mixing from the same station.

1. Introduction

The Gulf of Aqaba/Eilat (hereafter the Gulf) situated along the Syrian-African Rift Valley is a long (180 km), narrow (5–25 km), very deep basin (1800 m in its deepest point) connected to the Red Sea by the shallow straits of Tiran (242 m deep). This arid region is characterized by high temperatures, higher evaporation than precipitation rates, and low riverine runoff. These factors contribute to the high salinity (~40.3–40.9), and low availability of inorganic nutrients (Genin et al., 1995; Lazar et al., 2008; Monismith and Genin, 2004) observed in the Gulf. The Gulf's topography combined with its physical and chemical characteristics create an oligotrophic marine environment that resembles the open ocean despite its vicinity to the shore. During summer, thermal stratification occurs with surface water reaching 28 °C and relatively high temperatures (~21 °C) below the seasonal thermocline which can reach 200–250 m depth (Biton and Gildor, 2011; Paldor and Anati, 1979; Wolf-Vecht et al., 1992). Station A at the northern tip of the Gulf (29°28′N 34°55′E, bottom depth ~700 m) is monitored monthly within the framework of the Israeli National Monitoring Program for physical, chemical, and biological parameters (http://iui-eilat.ac.il/Research/NMPAbout.aspx). Seasonal changes in nutrient concentrations, chlorophyll distribution and population composition (based on flow cytometry) have been characterized (Foster et al., 2009; Kimor and Golandsky, 1977; Kimor and Golandsky-Baras, 1981; Lindell and Post, 1995; Post et al., 2011). Yet, little information exists on the environmental gene pool and microbial gene expression. We recently reported a metatranscriptome dataset from three different depths sampled from station A during deep winter-mixing (Pfreundt et al., 2014). These samples were analyzed further to compare different methods of library preparation (Hou et al., 2016) and depth dependent differences in gene expression for the deep-mixing period (Miller et al., *unpublished results*). A metatranscriptomic dataset taken at Station A in September 2010 focused on *Prochlorococcus* with a selective enrichment protocol for shorter and non-coding RNAs (Steglich et al., 2015). Here we report an additional metatranscriptome-dataset sampled from three depths (surface, deep chlorophyll maximum - DCM, aphotic zone) during the thermally-stratified summer. The availability of this dataset can help expand our understanding of seasonally and depth induced changes in gene expression of the microbial communities from the Gulf.

2. Data description

2.1. Site description and collection of samples

Sampling H)(H)(occurred on July 28th 2012 at 15:00 (UTC + 2:00), at station A (29°28′N 34°55′E, ~720 m bottom depth, Fig. 1a) at 10 m

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(surface), 85 m (DCM) and 500 m (aphotic) depths. Surface water temperatures of 28.6 °C declined with depth to reach 21 °C below the ~200 m thermocline (Fig. 1b). Photosynthetic active radiation (PAR) declined from 2812 μmol quanta m^{-2} s^{-1} at the sea surface to 1% and 0.01% at 30 m and 71.5 m, respectively, resulting in an absorption coefficient (Kd) of 0.052 m^{-1} (Fig. 1b). Nutrient-concentrations were the lowest at 10 m depth with measurements of 0.06 μmol L^{-1} NO_3 + NO_2 (hereafter dissolved inorganic nitrogen – DIN), 0.02 μmol L^{-1} PO_4, and 0.81 μmol L^{-1} $Si(OH)_4$. Nutrient concentrations increased with depth. The nitrocline was observed between 160 and 300 m, with DIN concentrations of 0.63 and 4.2 μmol L^{-1} respectively. DIN concentrations remained ~4.2 μmol L^{-1} at 500 m and declined slightly to 3.9 μmol L^{-1} above the sediment (720 m) (Fig. 1c). PO_4 and $Si(OH)_4$ concentrations were 0.22 and 2.29 μmol L^{-1}, respectively, at 500 m depth and 0.21 μmol L^{-1} (PO_4) and 2.34 μmol L^{-1} ($Si(OH)_4$) above the sediment (Fig. 1c). Chl *a* concentrations ranged between 0.07 μg Chl *a* L^{-1} in the deep, aphotic layer to 0.17 μg Chl *a* L^{-1} at approximately 80 m, with a prominent DCM observed between 70 and 90 m (Fig. 1b). The DCM was further characterized by maximal picophytoplankton cells and biomass measured at 85 m. (Fig. S1, 1d). The carbon-based biomass of *Synechococcus* (calculated from flow cytometry measurements according to Campbell (2001)) was the highest of the three assessed phytoplankton fractions and varied between 0.3 ng C L^{-1} at 720 m and 2456 ng C L^{-1} at the DCM (85 m) (Fig. 1d). *Prochlorococcus* biomass varied between 0.8 and 1515 ng C L^{-1} at 720 m and the DCM, respectively. Picoeukaryotic algae biomass ranged between non-detectable levels at 500 and 720 m to 1150 ng C L^{-1} at the DCM (Fig. 1d). To extract environmental RNA, 10 L of sea water were collected from 10, 85, and 500 m depths using Niskin bottles and immediately filtered in the shade through a 20 μm mesh onto polyethersulfone filters (PALL Supor, 47 mm diameter, 0.45 μm pore size). Filtration time did not exceed 15 min to reduce filtration induced gene expression. Filters were

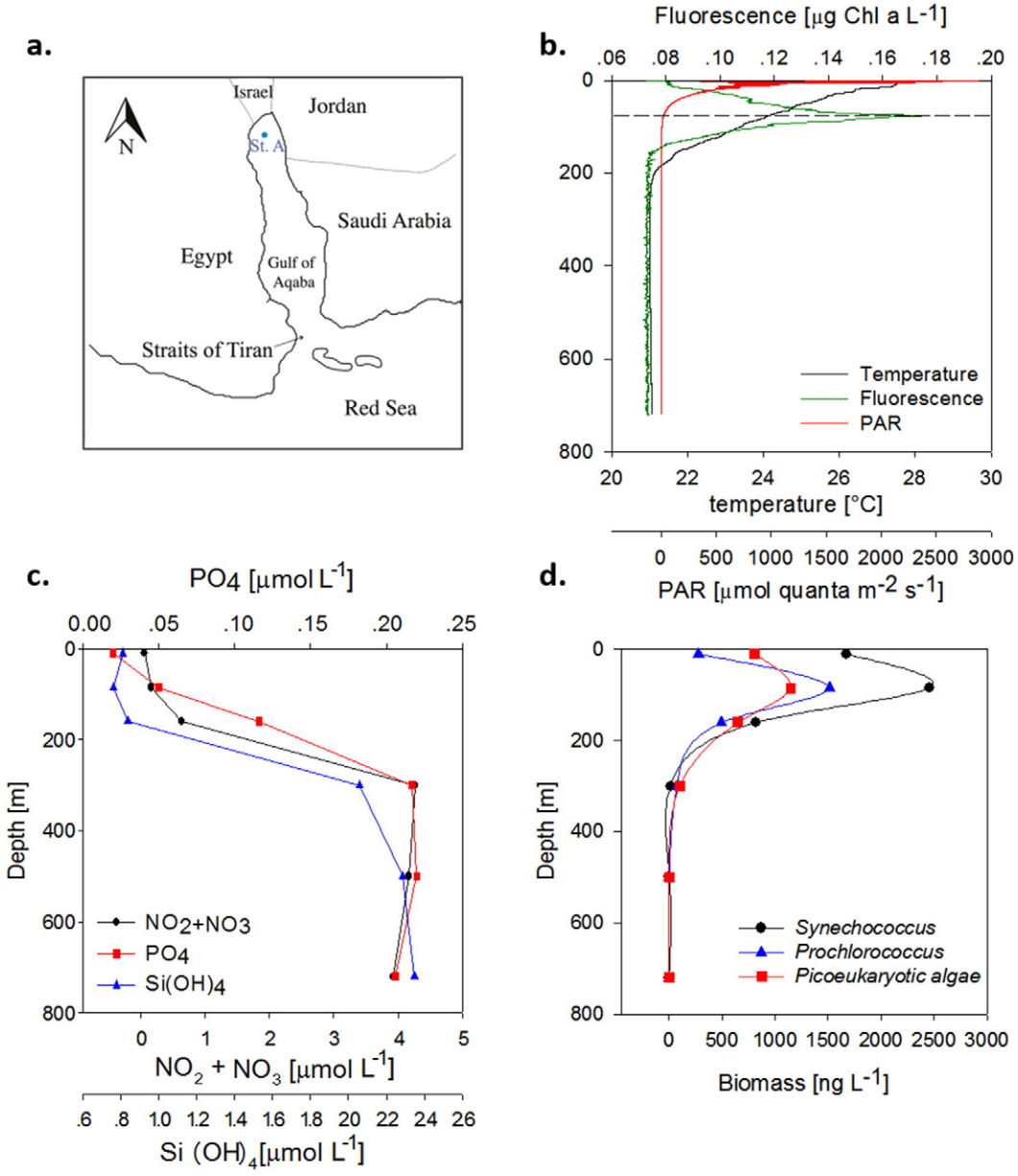

Fig. 1. Sampling site and water column characteristics. (a) Location of Station A in the Gulf of Aqaba. (b) Changes in temperature (black), photosynthetically active radiation (PAR) (red) and Chlorophyll *a* fluorescence (green) along the water column on 28/07/2012 at station A with 700 m maximal water depth. (c) Distribution of macronutrients along the water column (NO_3 + NO_2 in black, PO_4 in red, and $Si(OH)_4$ in blue). (d) Picophytoplankton carbon biomass calculated from cell counts (see Fig. S1 for a plot of cell counts). The deep chlorophyll maximum (DCM) at ~85 m is marked with a dashed line in b and d.