



Bacterial Diversity and Nitrogen Utilization Strategies in the Upper Layer of the Northwestern Pacific Ocean

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OPEN ACCESS

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Specialty section:
This article was submitted to
Aquatic Microbiology,
a section of the journal
Frontiers in Microbiology

Received: 23 November 2017

Accepted: 10 April 2018

Published: 25 April 2018

Citation:
Li Y-Y, Chen X-H, Xie Z-X, Li D-X,
Wu P-F, Kong L-F, Lin L, Kao S-J and
Wang D-Z (2018) Bacterial Diversity
and Nitrogen Utilization Strategies in
the Upper Layer of the Northwestern
Pacific Ocean. *Front. Microbiol.* 9:797.
doi: 10.3389/fmicb.2018.00797

Nitrogen (N) is a primary limiting nutrient for bacterial growth and productivity in the ocean. To better understand bacterial community and their N utilization strategy in different N regimes of the ocean, we examined bacterial diversity, diazotrophic diversity, and N utilization gene expressions in the northwestern Pacific Ocean (NWPO) using a combination of high-throughput sequencing and real-time qPCR methods. 521 and 204 different operational taxonomic units (OTUs) were identified in the 16s rRNA and nifH libraries from nine surface samples. Of the 16s rRNA gene OTUs, 11.9% were observed in all samples while 3.5 and 15.9% were detected only in N-sufficient and N-deficient samples. *Proteobacteria*, *Cyanobacteria* and *Bacteroidetes* dominated the bacterial community. *Prochlorococcus* and *Pseudoalteromonas* were the most abundant at the genus level in N-deficient regimes, while SAR86, *Synechococcus* and SAR92 were predominant in the Kuroshio-Oyashio confluence region. The distribution of the nifH gene presented great divergence among sampling stations: *Cyanobacterium_UCYN-A* dominated the N-deficient stations, while clusters related to the *Alpha*-, *Beta*-, and *Gamma-Proteobacteria* were abundant in other stations. Temperature was the main factor that determined bacterial community structure and diversity while concentration of NO_x-N was significantly correlated with structure and distribution of N₂-fixing microorganisms. Expression of the *ammonium transporter* was much higher than that of *urea transporter subunit A (urtA)* and *ferredoxin-nitrate reductase*, while *urtA* had an increased expression in N-deficient surface water. The predicted ammonium transporter and ammonium assimilation enzymes were most abundant in surface samples while urease and nitrogenase were more abundant in the N-deficient regions. These findings underscore the fact that marine bacteria have evolved diverse N utilization strategies to adapt to different N habitats, and that urea metabolism is of vital ecological importance in N-deficient regimes.

Keywords: Northwestern Pacific Ocean, bacterial diversity, nitrogen utilization genes, urea, cyanobacteria