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Chasing after Non-cyanobacterial Nitrogen Fixation in Marine Pelagic Environments

Pia H. Moisander 1*, Mar Benavides 2, Sophie Bonnet 3, Iilana Berman-Frank 4, Angelique E. White 5 and Lasse Riemann 2

1 Department of Biology, University of Massachusetts Dartmouth, North Dartmouth, MA, United States, 2 Marine Biology Section, Department of Biology, University of Copenhagen, Helsingør, Denmark, 3 Centre National de la Recherche Scientifique, IFREMER, Brest, France, 4 Mina and Everard Goodman Faculty of Life Sciences, Bar-Ilan University, Ramat Gan, Israel, 5 College of Earth, Ocean, and Atmospheric Sciences, Oregon State University, Corvallis, OR, United States

Traditionally, cyanobacterial activity in oceanic photic layers was considered responsible for the marine pelagic dinitrogen (N2) fixation. Other potentially N2-fixing bacteria and archaea have also been detected in the pelagic water column, however, the activity and importance of these non-cyanobacterial diazotrophs (NCDs) remain poorly constrained. In this perspective we summarize the N2 fixation rates from recently published studies on photic and aphotic layers that have been attributed to NCD activity via parallel molecular measurements, and discuss the status, challenges, and data gaps in estimating non-cyanobacterial N2 fixation (NCNF) in the ocean. Rates attributed to NCNF have generally been near the detection limit thus far (< 1 nmol N L−1 d−1). Yet, if considering the large volume of the dark ocean, even low rates of NCNF could make a significant contribution to the new nitrogen input to the ocean. The synthesis here shows that nifH transcription data for NCDs have been reported in only a few studies where N2 fixation rates were detected in the absence of diazotrophic cyanobacteria. In addition, high apparent diversity and regional variability in the NCDs complicate investigations of these communities. Future studies should focus on further investigating impacts of environmental drivers including oxygen, dissolved organic matter, and dissolved inorganic nitrogen on NCNF. Describing the ecology of NCDs and accurately measuring NCNF rates, are critical for a future evaluation of the contribution of NCNF to the marine nitrogen budget.

Keywords: bacteria, diazotroph, DOM, mesopelagic, nifH, nitrogenase, oxygen minimum zone

INTRODUCTION

Biological dinitrogen (N2) fixation produces biologically available nitrogen (N) through reduction of atmospheric N2 to ammonium (NH4+) (Postgate, 1998). In oligotrophic marine environments, N2 fixation can provide ~50% of the “new” N (Karl et al., 2002; Capone et al., 2005; Berthelot et al., 2017), and probably contributes more in hot spots such as the Western Tropical South Pacific (Bonnet et al., 2017). N2 fixation (diazotrophy) is catalyzed by the enzyme nitrogenase (Mortenson and Thorneley, 1979; Postgate, 1998). The nifH gene that encodes the dinitrogenase reductase is distributed in many phylogenetic groups of bacteria and archaea (Chien and Zinder, 1996), and used to assess the diversity and expression of the enzyme in marine diazotrophs (Zehr et al., 2003).
Cyanobacteria have traditionally been considered the most important diazotrophs in the ocean. The predominantly described taxa include the filamentous, bloom-forming *Trichodesmium*, heterocystous, symbiotic groups (e.g., diatom-diazotroph associations), and the unicellular cyanobacteria UCYN-A (*Candidatus Atelocyanobacterium thalassa*), UCYN-B (*Crocosphaera watsonii*), and UCYN-C (Zehr, 2011). Early molecular studies also reported the presence of non-cyanobacterial diazotrophs (NCDs) (Kirshtein et al., 1991; Zehr et al., 1995, 1998). These findings stimulated recent research on diversity, composition, and ecology of marine NCDs (Bombar et al., 2016), leading to a currently perceived emergence of a new paradigm: non-cyanobacterial N$_2$ fixation (NCNF). Extensive research on free-living and symbiotic NCDs in soils has provided evidence of the activity, regulation, and the significance of these processes in terrestrial ecosystems (Postgate, 1998; Herridge et al., 2008; Hayat et al., 2010). While the diversity and abundance of marine NCDs indicate that NCNF could potentially have a large impact on the marine N budget, at present, the activity and contribution of marine NCNF to total N$_2$ fixation remain poorly constrained.

In many oceanic waters, NCD sequences dominate the *nifH* gene pool (Riemann et al., 2010; Farnelid et al., 2011), and detection of transcripts of some of the NCD *nifH* genes suggests that at least some of the NCDs fix N$_2$ in the oceanic water column and sediments (Bird et al., 2005; Church et al., 2005b; Halm et al., 2012; Brown and Jenkins, 2014; Moisander et al., 2014; Bentzon-Tilia et al., 2015b). However, gene expression cannot be equated with active N$_2$ fixation rates without evidence of cell-specific activity. Current broadly available methods cannot discern the relative contribution of cyanobacteria and NCDs to measured N$_2$ fixation rates. The contribution of NCNF could be studied by parallel rate measurements and molecular detection in areas where cyanobacterial diazotrophs are typically not present (such as the ocean water column below the euphotic layer, i.e., aphotic waters). Here we summarize data from studies where N$_2$ fixation rates were reported in parallel to molecular characterization of NCDs when cyanobacterial diazotrophs were not detected (presence and/or expression of the *nifH* gene; Table 1). Presumed NCNF rates ranged from undetectable to 8 and 0.89 nmol N L$^{-1}$ d$^{-1}$ in photic and aphotic studies, respectively (Table 1). The goal of this perspective is to synthesize emerging trends and data gaps from these studies and highlight future research directions.

### NCNF IN PHOTIC WATERS

Most early studies of oceanic N$_2$ fixation (Montoya et al., 1996; Karl et al., 2002; Hood et al., 2004; Mahaffey et al., 2005; Mulholland et al., 2006) and diazotroph diversity and activity (Zehr, 2011) focused on photic waters and cyanobacterial diazotrophs. Traditionally, the photic layer has been considered an optimal environment for cyanobacterial N$_2$ fixation, as abundant light energy (harnessed via photosynthesis) supplies the high energetic demands of the N$_2$ fixation process, while dissolved inorganic nitrogen (DIN) limits non-diazotrophic autotrophs. Yet, since the first molecular studies (Zehr et al., 1998), *nifH* sequence libraries have revealed diverse NCD phytophylotypes from surface waters of various oceans and estuaries (Falcon et al., 2004; Church et al., 2005a; Langlois et al., 2005; Hewson et al., 2007; Moisander et al., 2008; Foster et al., 2009; Farnelid et al., 2011; Halm et al., 2012; Bentzon-Tilia et al., 2015b; Messer et al., 2016). Transcripts from a range of NCD groups have been recovered in surface layers (Man-Aharonovich et al., 2007; Halm et al., 2012; Loescher et al., 2014). One of the few consistent NCDs in photic layers is a gamma-proteobacterial cluster of sequences (termed γ-24774A11, Gamma A, or UMB; representatives of the same phylotype). Gamma A shows a wide distribution and expression of the *nifH* gene (Bird et al., 2005; Church et al., 2005b; Moisander et al., 2014; Langlois et al., 2015). This group appears to be broadly distributed across tropical and subtropical surface waters compared with cyanobacterial diazotrophs (Moisander et al., 2014; Bonnet et al., 2015; Langlois et al., 2015). Its presence exclusively in surface layers suggests either reliance on a photosynthetic machinery, rhodopsin, or photosynthesis products from other organisms. Once cultivated or its genome assembled, we can learn more about its autecology. A few other studies have detected N$_2$ fixation from photic layers in the reported absence of cyanobacterial sequences (Yogev et al., 2011; Blais et al., 2012). However, due to the difficulty of demonstrating the absence of cyanobacterial diazotrophs, it has generally been difficult to prove that NCNF is active in photic layers.

The nitrogenase enzyme may be downregulated or inactivated by NH$_4^+$ (Zehr et al., 1997). As typically assumed for cyanobacterial diazotrophs (Zehr, 2011), DIN could negatively impact NCDs directly (physiological inhibition) or indirectly (NCDs outcompeted by faster growing non-diazotrophs). However, DIN availability may not always have immediate negative effects on NCDs. For example, Gamma A transcripts and Cluster III diazotrophs (Chien and Zinder, 1996) were found in the presence of micromolar concentrations of DIN in the upper layers of the Arabian Sea (Bird and Wyman, 2013). N$_2$ fixation rates were also detected in the Benguela Upwelling System in the presence of micromolar nitrate and in the absence of cyanobacterial diazotrophs (Sohm et al., 2011). In other surface waters (Eastern Tropical South Pacific; ETSP), N$_2$ fixation rates were similarly reported in the absence of cyanobacterial diazotrophs and presence of high DIN (Fernandez et al., 2011; Dekaezemacker et al., 2013; Gradoville et al., 2017). In Indian Ocean surface waters with a shallow nitracline, N$_2$ fixation rates were reported in parallel with up to 10$^4$ *nifH* gene copies L$^{-1}$ of Gamma A, while cyanobacterial groups were undetectable (Shiozaki et al., 2014). Collectively these field studies suggest that NCDs may have a low sensitivity to DIN (Knapp, 2012), but recent work with cultivated NCDs suggest that responses to DIN may be strain specific (Bentzon-Tilia et al., 2015a).

PCR amplification biases likely influence our current data and conclusions of studies on NCDs. A recent study using metagenomic data from the TARA Oceans survey reports
TABLE 1 | Compilation of photic and aphotic N\textsubscript{2} fixation rates published with molecular data and associated with non-cyanobacterial diazotrophs in waters reportedly devoid of cyanobacterial diazotrophs.

<table>
<thead>
<tr>
<th>References</th>
<th>Location</th>
<th>Latitude</th>
<th>Longitude</th>
<th>Average rate or range of rates (nmol N L\textsuperscript{-1} d\textsuperscript{-1})</th>
<th>Depth (m)</th>
<th>Sequencing: Associated non-cyanobacterial phylotype genes and transcripts</th>
<th>qPCR: non-cyanobacterial diazotroph gene and transcript abundance (nifH copies L\textsuperscript{-1})</th>
</tr>
</thead>
<tbody>
<tr>
<td>SOUTH AND NORTH PACIFIC OCEAN</td>
<td></td>
<td></td>
<td></td>
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<td></td>
<td></td>
</tr>
<tr>
<td>Benavides et al., 2015</td>
<td>Western South Pacific</td>
<td>3–9°S</td>
<td>146–153°E</td>
<td>0.08–0.89</td>
<td>200–1000</td>
<td>Cluster I, III, IV, and Trichodesmium</td>
<td>0–900</td>
</tr>
<tr>
<td>Hall et al., 2012</td>
<td>South Pacific Gyre</td>
<td>20–50°S</td>
<td>180°E– 120°W</td>
<td>0.41.5</td>
<td>0–200</td>
<td>Cluster I, III, IV, and Trichodesmium</td>
<td>0–7*10\textsuperscript{6}</td>
</tr>
<tr>
<td>Fernandez et al., 2011</td>
<td>Eastern Tropical South Pacific</td>
<td>1.5°N–17.8°S</td>
<td>86.9–70.8°W</td>
<td>0.01–3.5</td>
<td>70–400\textsuperscript{a}</td>
<td>Cluster I, II, III, and Trichodesmium</td>
<td>0–8*10\textsuperscript{6}</td>
</tr>
<tr>
<td>Dekaezemacker et al., 2013</td>
<td>Eastern Tropical South Pacific</td>
<td>10–20°S</td>
<td>100–80°W</td>
<td>0–0.88</td>
<td>15–150</td>
<td>Cluster I</td>
<td>nd</td>
</tr>
<tr>
<td>Turk-Kubo et al., 2014</td>
<td>Eastern Tropical South Pacific</td>
<td>10–20°S</td>
<td>100–80°W</td>
<td>b</td>
<td>10–200</td>
<td>Cluster I, III, IV, and Trichodesmium</td>
<td>0.40</td>
</tr>
<tr>
<td>Loecher et al., 2014</td>
<td>Eastern Tropical South Pacific</td>
<td>2°N–16°S</td>
<td>85–74°W</td>
<td>0.4</td>
<td>0–350</td>
<td>Cluster I, III, IV, and Trichodesmium</td>
<td>0–10\textsuperscript{6}</td>
</tr>
<tr>
<td>Bonnet et al., 2013</td>
<td>Eastern Tropical South Pacific</td>
<td>10–20°S</td>
<td>100–80°W</td>
<td>0–0.8</td>
<td>200–2,000</td>
<td>Cluster I, III, IV, and Trichodesmium</td>
<td>1.5 x 10\textsuperscript{2} – 1.4 x 10\textsuperscript{4}</td>
</tr>
<tr>
<td>Gradoville et al., 2017</td>
<td>Eastern Tropical South Pacific</td>
<td>20.1–26.3°S</td>
<td>104–77°W</td>
<td>0.5–5.1</td>
<td>5 m for N\textsubscript{2} fix, 5–420 m for nifH</td>
<td>Cluster I, III, IV, and Trichodesmium</td>
<td>1.5 x 10\textsuperscript{2} – 1.4 x 10\textsuperscript{4}</td>
</tr>
<tr>
<td>Hamersley et al., 2011</td>
<td>Southern California Bight</td>
<td>33.55°N</td>
<td>118.4°W</td>
<td>0.07</td>
<td>500–885</td>
<td>Cluster I, III, IV, and Trichodesmium</td>
<td>nd</td>
</tr>
<tr>
<td>ATLANTIC OCEAN, ARCTIC OCEAN</td>
<td></td>
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<td></td>
</tr>
<tr>
<td>Sohm et al., 2011</td>
<td>South Atlantic Gyre and Benguela upwelling system</td>
<td>11–25°S</td>
<td>29°W–15°E</td>
<td>0.06–8</td>
<td>8 m for N\textsubscript{2} fix, 8–110 m for nifH</td>
<td>nd</td>
<td>nd</td>
</tr>
<tr>
<td>Blais et al., 2012</td>
<td>Arctic Ocean coastal</td>
<td>69.3–75°N</td>
<td>69–134°W</td>
<td>0.02–4.45</td>
<td>5 m, DCM (30–57)</td>
<td>Cluster I, III, IV, and Trichodesmium</td>
<td>nd</td>
</tr>
<tr>
<td>INDIAN OCEAN</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Shiozaki et al., 2014</td>
<td>Indian Ocean</td>
<td>4°N–20°S</td>
<td>65–70°E</td>
<td>0.18–0.23</td>
<td>0–90</td>
<td>Cluster I</td>
<td>10\textsuperscript{3}</td>
</tr>
</tbody>
</table>

(Continued)
Several studies have recently reported N\textsubscript{2} fixation rates in the aphotic ocean where active autotrophic cyanobacterial diazotrophy is not expected. Early evidence for aphotic N\textsubscript{2} fixation showed proteobacterial and archaeal diazotrophy in hydrothermal vent fluids (Millero et al., 2006), and deep-sea sediment microbial communities (Diles et al., 2009; 2014). Proteobacterial \textit{nifH} sequences were reported from mesopelagic waters down to 2,000 m (Forning et al., 2011; Loescher et al., 2014). However, mesopelagic waters down to 400 and 800 m, and abyssopelagic waters remain poorly known.

In recent work, hydrogenases (i.e., \textit{nifH}2 fixation and denitrification has been proposed. Collectively, these studies suggest that NCNF is occurring in aphotic waters and may correlate with oxygen availability (Gardner et al., 2014). However, mesopelagic waters down to 2,000 m (Forning et al., 2011; Loescher et al., 2014). Nevertheless, mesopelagic waters down to 400 and 800 m, and abyssopelagic waters remain poorly known.

## Table 1: Association of NCNF in Aphotic Waters and Oxygen Deficient Zones

<table>
<thead>
<tr>
<th>References</th>
<th>Location</th>
<th>Latitude</th>
<th>Longitude</th>
<th>Average rate or range of rates (nmol N L\textsuperscript{-1} d\textsuperscript{-1})</th>
<th>Depth (m)</th>
<th>Sequencing: Associated non-cyanobacterial phylotype genes and transcripts</th>
<th>qPCR: non-cyanobacterial diazotroph gene and transcript abundance (\textit{nifH} copies L\textsuperscript{-1})</th>
</tr>
</thead>
<tbody>
<tr>
<td>Jayakumar et al., 2012</td>
<td>Indian Ocean</td>
<td>13–19°N</td>
<td>64°–66°E</td>
<td>nd</td>
<td>110–175 (OMZ)</td>
<td>Cluster I, III, IV</td>
<td>nd</td>
</tr>
<tr>
<td>Rahav et al., 2013a</td>
<td>Mediterranean Sea, Red Sea, and Baltic Sea</td>
<td>29°–59°N</td>
<td>34°–29°E</td>
<td>0.01–0.38</td>
<td>150–720</td>
<td>Pseudomonas stutzeri-related</td>
<td>nd</td>
</tr>
<tr>
<td>Rahav et al., 2016</td>
<td>Eastern Mediterranean Sea</td>
<td>32°N</td>
<td>34°E</td>
<td>0.1–0.15</td>
<td>5</td>
<td>nd</td>
<td>Cluster I (\textit{Alpha}–), and “other”</td>
</tr>
<tr>
<td>Yogev et al., 2011</td>
<td>Eastern Mediterranean Sea</td>
<td>33.14°–34.00°N</td>
<td>25°–33°E</td>
<td>0–0.3</td>
<td>0–160 m</td>
<td>Cluster I, II</td>
<td>Cluster I, II</td>
</tr>
<tr>
<td>Farnelid et al., 2013</td>
<td>Baltic Sea</td>
<td>57.20°N</td>
<td>20.03°E</td>
<td>0.44</td>
<td>200</td>
<td>Cluster I, II, III</td>
<td>0–2*10\textsuperscript{7}</td>
</tr>
<tr>
<td>Delmont et al., 2017</td>
<td>MEDITERRANEAN SEA, RED SEA, AND BALTIC SEA</td>
<td></td>
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<td></td>
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</tbody>
</table>

All rates are based on the \textsuperscript{15}N\textsubscript{2} method and no conversions were made to originally reported values. The station location and depth information is specific for locations where non-cyanobacterial diazotrophs were detected (unless otherwise indicated). Red letters indicate transcripts. Clusters I, II, III, and IV follow Chien and Zinder (1996).

* Depths range from photic to aphotic.

* Delaere (2013) reported rates and Turk-Kubo et al. (2014) reported corresponding molecular data.

* nd, data not available/not done.

* Nodularia transcripts were detected at abundances below the level of quantification via RT-qPCR and its transcripts were not detected by sequencing.

### Notes

- Several studies have recently reported N\textsubscript{2} fixation rates in the aphotic ocean where active autotrophic cyanobacterial diazotrophy is not expected. Early evidence for aphotic N\textsubscript{2} fixation showed proteobacterial and archaeal diazotrophy in hydrothermal vent fluids (Millero et al., 2006), and deep-sea sediment microbial communities (Diles et al., 2009; 2014). Proteobacterial \textit{nifH} sequences were reported from mesopelagic waters down to 2,000 m (Forning et al., 2011; Loescher et al., 2014). However, mesopelagic waters down to 400 and 800 m, and abyssopelagic waters remain poorly known.

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THE POTENTIAL ROLE OF DISSOLVED ORGANIC MATTER (DOM) IN SUPPORTING NCNF

Organic particles may provide a site of low oxygen and a source of DOM that both can benefit specific bacterial attachment (Thiele et al., 2015; Dang and Lovell, 2016). If NCDs are heterotrophic (Riemann et al., 2010), overall DOM availability should play a role in controlling their growth and activity (Kirchman, 1990). Genomic and physiological analyses have confirmed that gamma- and alphaproteobacterial diazotrophs isolated from the Baltic Sea are heterotrophic and contain genes responsible for DOM metabolism (Bentzon-Tilia et al., 2015a). Evidence for DOM influence on NCDs was reported from the South Pacific Gyre (SPG) photic layers (Halm et al., 2012) and in the Mediterranean Sea (Rahav et al., 2016), where DOM originating from primary production was suggested to impact N2 fixation. Most of the SPG sequences were gammaproteobacterial, but represented different groups from those found in the ETSP (Fernandez et al., 2011; Turk-Kubo et al., 2014). Mesopelagic N2 fixation rates had a positive correlation with relatively labile DOM (Benavides et al., 2015), and were enhanced upon the addition of sugars, amino acids, or transparent exopolymeric particles (Bonnet et al., 2013; Rahav et al., 2013a; Loescher et al., 2014; Benavides et al., 2015).

In the eastern Mediterranean Sea, N2 fixation in the photic zone was uncoupled from primary production and correlated significantly and positively with bacterial production (Rahav et al., 2013b). However, even in coastal waters with high dissolved inorganic nutrient loads, organic carbon stimulated light and dark N2 fixation in a community containing cyanobacterial and NCD nifH phylotypes (Rahav et al., 2016). Saharan dust addition (serving potentially as a source of trace elements, nutrients, and/or DOM) enhanced N2 fixation and both NCD (Gamma A) and cyanobacterial diazotroph abundances in the North Atlantic (Langlois et al., 2012). Gamma A abundances were also enhanced by addition of sugars in the South Pacific (Moisander et al., 2012). Many cyanobacteria, including diazotrophs, take up organic forms of carbon (Hietanen et al., 2002; Church et al., 2004; Moisander et al., 2012; Benavides et al., 2017) thus rates of N2 fixation in mixed communities, measured after DOM amendments, may reflect responses of both cyanobacterial and NCDs. Whether some marine NCDs also use light as an energy source remains to be demonstrated (Bombar et al., 2016).

CURRENT AND FUTURE CHALLENGES

The data synthesis here shows that while N2 fixation rates have been reported by several studies in waters dominated by NCD nifH sequences (Table 1), most studies of NCDs did not measure transcription. The nifH DNA sequences often do not appear as transcripams in the same samples, suggesting that some of the organisms are not active (Moisander et al., 2006; Short and Zehr, 2007; Yoge et al., 2011; Halm et al., 2012; Severin et al., 2015), thus it would be misleading to use nifH gene (DNA) data as proof for NCNF. Despite the common detection of cyanobacterial and NCD nifH in DNA sequence libraries and, at times, in transcripts, only a few studies from surface layers reported the absence of cyanobacterial diazotrophs when N2 fixation rates were detected (Table 1). Due to various methodological constraints, proving the absence of low numbers of cyanobacterial cells in a sample is difficult, if not impossible, yet such low abundance may be sufficient to result in detectable N2 fixation rates. Aphotic waters may be considered a good case study for NCNF, as photoautotrophic N2 fixation in these waters is conceivably absent. However, the common detection of diazotrophic cyanobacteria in aphotic layers (Hamersley et al., 2011; Farnelid et al., 2013; Benavides et al., 2015), possibly due to either settling material that could be viable upon experimental incubations (Agusti et al., 2015), or caused by contamination during sampling, complicate attributing measured aphotic N2 fixation rates to NCDs alone. Overall, the measured rates of in situ aphotic N2 fixation are higher than the parallel abundance and transcript numbers of NCDs would potentially support. Moreover, the reported cell-specific rates of NCDs are under debate (Turk-Kubo et al., 2014; Benavides et al., 2015; Bentzon-Tilia et al., 2015a; Gradoville et al., 2017).

Various factors of the 15N-N2 method, such as uncertainties in the 15N-labeling step, influence N2 fixation rate determination (Mohr et al., 2010; Grosskopf et al., 2012; Wilson et al., 2012). In addition, commercially available 15N2 gases are at times contaminated with substrates other than N2 (Dabundo et al., 2014), which could lead to false positive NCNF rates. An additional source of uncertainty that must be considered when assessing minimum quantifiable N2 fixation rates is the concentration and isotopic composition of particulate organic N (PON), which at typical concentrations requires large volumes in incubations (usually >4 L) to constrain rates in deep waters. While N2 fixation rates per volume are most informative for budgetary calculations, rates normalized to PON concentration would provide an additional measure for comparing rates across studies. Further, variability of the natural 815N background of PON, changes in the 815N of PON that may occur over the incubation period or due to substrate additions, and 815N of the N2 pool, should be considered (Montoya et al., 1996; Gradoville et al., 2017). These sources of uncertainty are not routinely reported and detection limits are infrequently calculated. Taking into account these sources of error, Gradoville et al. (2017) estimated the minimum quantifiable N2 fixation rate in their study at ~0.4 nmol L−1 d−1 which is higher than many reported rates of NCNF (Table 1).

To our knowledge, direct field measurements of N2 fixation per cell are currently lacking for marine NCDs; such measurements would be important in assessing their contribution to N2 fixation rates, along with other efforts to separate signals of NCNF and cyanobacterial N2 fixation (see also Bombar et al., 2016). High NCD nifH diversity renders identification and quantification of biogeochemically significant individual groups challenging. The combination of in situ hybridization approaches using halogenated probes together with single-cell mass spectrometry (nanoscale secondary ion mass spectrometry; nanoSIMS) has recently advanced quantification of single-cell N2 fixation rates in UCYN-A.
(Thompson et al., 2012; Krupke et al., 2013). Similar approaches could provide insights into the NCNF in marine environments. Stable isotope probing and isotope microarrays could lead to valuable future insights (Seyler et al., 2014; Arandia-Gorostidi et al., 2017).

In describing the communities, sequencing depth and primer specificity influence what portion of the NCD community is detected. In addition, the detection limit for diazotroph transcripts or genes and the detection limit for N₂ fixation are not necessarily equal. The quantification limit of quantitative PCR is often on the order of 10² nifH gene copies L⁻¹ (and often unreported), which could potentially result in false negatives for cyanobacterial diazotrophs, and subsequently, lead to false positive NCNF rates. Using small water volumes when abundance of cyanobacterial diazotrophs is low would increase the chances of reporting false negatives for these organisms. On the other hand, metabolic rate measurements of microbial samples brought to the surface from aphotic depths may be underestimated (Tamburini et al., 2013), making both rate and transcription analyses of deep communities challenging.

CONCLUSIONS

Our compiled analysis of data illustrates that low N₂ fixation rates were reported from marine environments where NCD abundance was high and cyanobacterial diazotrophs were low or undetected. NCD nifH sequences show a wider geographical and depth distribution in pelagic environments overall than their cyanobacterial counterparts. The emerging data suggest that the NCD communities are diverse but only a few groups have been identified that appear in several studies (Farnelid et al., 2011; Turk-Kubo et al., 2014). Studies on NCD nifH transcripts in aphotic layers are scarce or missing for many areas of the oceans. We currently lack a fundamental understanding of the key players and environmental regulation of NCNF in the ocean. Ecophysiological data of the organisms contributing to these rates are still preliminary and incomplete. Moreover, the measured rates in most environments are generally “snapshots” determined during a cruise/sampling foray and have not been examined over seasonal and annual cycles. In addition, several methodological concerns complicate interpretation of N₂ fixation rate data. Modeling the significance of NCNF in marine N₂ fixation remains a challenge due to these various constraints. If these rates are confirmed, however, NCNF could contribute significantly to new N inputs to the ocean. How factors such as temperature, DIN, oxygen, trace elements, and hydrostatic pressure drive the metabolic capacities and adaptations of NCNF are currently only partially revealed. The actual activities and taxon specific roles of marine NCDs remain enigmatic at present, as do their contributions to regional and global N₂ fixation.

AUTHOR CONTRIBUTIONS

PM and LR designed the study, wrote the initial drafts, and compiled the majority of Table 1. All authors wrote sections of the manuscript and contributed to Table 1.

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