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Authors

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Nitrogen fixation in sediments along a depth transect through the Peruvian oxygen minimum zone

Jessica Gier^{[1](#page-1-0)}, Stefan Sommer¹, Carolin R. Löscher^{[1,a](#page-1-0)}, Andrew W. Dale¹, Ruth A. Schmitz^{[2](#page-1-0)}, and Tina Treude^{[1,b](#page-1-0)}

¹GEOMAR Helmholtz Centre for Ocean Research Kiel, Germany

²Institute for Microbiology, Christian-Albrechts-University Kiel, Germany

^apresent address: Nordic Center for Earth Evolution, University of Southern Denmark, 5230 Odense M, Denmark

^bpresent address: University of California, Los Angeles, Department of Earth, Planetary & Space Sciences and Department of Atmospheric & Oceanic Sciences, CA, USA

Correspondence to: Jessica Gier (jgier@geomar.de) and Tina Treude (ttreude@g.ucla.edu)

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Abstract. The potential coupling of nitrogen (N_2) fixation and sulfate reduction (SR) was explored in sediments of the Peruvian oxygen minimum zone (OMZ). Sediment samples were retrieved by a multiple corer at six stations along a depth transect (70–1025 m water depth) at 12◦ S, covering anoxic and hypoxic bottom water conditions. Benthic N_2 fixation, determined by the acetylene reduction assay, was detected at all sites, with highest rates between 70 and 253 m and lower rates at greater depth. SR rates decreased with increasing water depth. N_2 fixation and SR overlapped in sediments, suggesting a potential coupling of both processes. However, a weak positive correlation of their activity distribution was detected by principle component analysis. A potential link between N_2 fixation and sulfate-reducing bacteria was indicated by the molecular analysis of *nifH* genes. Detected *nifH* sequences clustered with the sulfate-reducing bacteria *Desulfonema limicola* at the 253 m station. However, *nifH* sequences of other stations clustered with uncultured organisms, Gammaproteobacteria, and Firmicutes (Clostridia) rather than with known sulfate reducers. The principle component analysis revealed that benthic N_2 fixation in the Peruvian OMZ is controlled by organic matter (positive) and free sulfide (negative). No correlation was found between N² fixation and ammonium concentrations (even at levels $> 2022 \mu M$). N₂ fixation rates in the Peruvian OMZ sediments were in the same range as those measured in other organic-rich sediments.

1 Introduction

Only 6 % of nitrogen (N) in seawater is bioavailable (Gruber, 2008). This bioavailable N is mainly present in the form of nitrate $(NO₃⁻)$, whereas the large pool of atmospheric dinitrogen gas (N_2) is only available for N_2 fixing microorganisms (diazotrophs). N often limits marine productivity (Ward and Bronk, 2001; Gruber, 2008) and the largest source of bioavailable N (i.e., ammonium; $NH₄⁺$) in the marine environment is N₂ fixation (Falkowski et al., 1998; Strous et al., 1999; Brandes and Devol, 2002).

To date, the quantitative contribution of diazotrophs in the marine N cycle remains unclear and numerous estimates of global sources and sinks of global N have led to an unbalanced budget with deficits of around 200 Tg N yr−¹ (Codispoti, 2007). This suggests that either previous N_2 fixation rate determinations have been underestimated (Großkopf et al., 2012) or that N loss processes are overestimated (Codispoti, 2007). However, also balanced budgets such as \sim 265 Tg N yr⁻¹ for N sources and \sim 275 Tg N yr⁻¹ for N sinks exist (Gruber, 2004). These budget discrepancies illustrate that the current knowledge on diazotrophy and the marine N cycle is still limited.

Recent investigations argue that N_2 fixation in the water column cannot be totally attributed to phototrophic cyanobacteria, but that also heterotrophic prokaryotes contribute substantially (Riemann et al., 2010; Farnelid et al., 2011; Dekaezemacker et al., 2013; Löscher et al., 2014; Fernandez et al., 2015). This was shown for the Peruvian oxygen minimum zone (OMZ), where proteobacterial clades dominated with heterotrophic diazotrophs, indicating that cyanobacterial diazotrophs are of minor importance in this area (Löscher et al., 2014).

Pelagic N_2 fixation has been studied mostly in the oligotrophic surface oceans, but it was not until the past decade that benthic habitats began to receive more attention (Fulweiler et al., 2007; Bertics et al., 2010, 2013). Most studies on benthic N_2 fixation focused on coastal environments (Capone et al., 2008 and references therein). For example, subtidal sediments in Narragansett Bay (Rhode Island) were found to switch from being a net sink in the form of denitrification to being a net source of bioavailable N by N_2 fixation, caused by a decrease of organic matter deposition to the sediments (Fulweiler et al., 2007). Shallow brackish-water sediments off the Swedish coast revealed benthic N_2 fixation along with a diverse diazotrophic community (Andersson et al., 2014). N₂ fixation was positively influenced by a variety of environmental factors, such as salinity and dissolved inorganic Nitrogen, while wave exposure had a negative influence. Recent work revealed that benthic N_2 fixation is often linked to sulfate-reducing bacteria. For instance, bioturbated coastal sediments showed enhanced N_2 fixation activity mediated by sulfate-reducing bacteria, adding new dissolved inorganic N to the system (Bertics et al., 2010; Bertics and Ziebis, 2010). Further coupling of N_2 fixation to SR was observed in organic-rich sediments of the seasonal hypoxic Eckernförde Bay (Baltic Sea, Bertics et al., 2013), as well as in the sub-tidal, heterotrophic sediments of Narragansett Bay (Rhode Island, USA; Fulweiler et al., 2013). Several sulfate-reducing bacteria carry the functional gene marker for N² fixation, the *nifH* gene (Sisler and Zo-Bell, 1951; Riederer-Henderson and Wilson, 1970; Zehr and Turner, 2001) and were shown to actively fix N_2 in culture experiments (Riederer-Henderson and Wilson, 1970). However, information on sulfate-reducing bacteria and their contribution to N_2 fixation in the environment is still sparse and restricted to a small selection of environments.

So far, the distribution of benthic N_2 fixation and its relevance for N cycling in the Peruvian oxygen minimum zone (OMZ), defined by dissolved oxygen < 20μ mol kg⁻¹ (Fuenzalida et al., 2009), are unknown. The shelf and the upper slope in the Peruvian OMZ represent recycling sites of dissolved inorganic N with dissimilatory NO_3^- reduction to NH_4^+ being the dominant process (~ 15 mmol N m⁻² d⁻¹) in the benthic N cycle (Dale et al., 2016). This process is mediated by the filamentous sulfide-oxidizing *Thioploca* bacteria (Schulz, 1999; Schulz and Jørgensen, 2001). Benthic denitrification, which is mediated by foraminifera at water depth between 80 and 250 m of the Peruvian OMZ, represent a sink for bioavailable N in sediments, accounting for a potential NO₃ flux, i.e., N loss, of 0.01 to 1.5 mmol N m⁻² d⁻¹ (Glock et al., 2013; Dale et al., 2016).

The high input of labile organic carbon to Peruvian OMZ sediments (Dale et al., 2015) and subsequent SR should favor benthic N_2 fixation. Sulfate-reducing bacteria could considerably contribute to N_2 fixation in these organic-rich OMZ sediments, given that several sulfate-reducing bacteria (e.g., *Desulfovibrio* spp.; Riederer-Henderson and Wilson, 1970; Muyzer and Stams, 2008) carry the genetic ability to fix N2, and provide an important bioavailable N source for nondiazotrophic organisms (Bertics et al., 2010; Sohm et al., 2011; Fulweiler et al., 2013). We therefore hypothesize a possible coupling of N_2 fixation and SR in sediments off Peru. The aim of the present study was to identify and quantify benthic N_2 fixation along a depth transect through the Peruvian OMZ, together with SR, and compare its distribution with environmental factors, such as organic matter, to study its control mechanisms. The identification of bacteria carrying the genetic ability to perform N_2 fixation should further deliver information about benthic diazotrophic community structures at the different stations. The overall knowledge gained is needed to better constrain benthic N cycling in OMZs and to improve our knowledge on sources and sinks of fixed N.

2 Materials and methods

2.1 Study area

The most extensive OMZ worldwide is found in the eastern tropical south Pacific Ocean at the central Peruvian coast (Kamykowski and Zentara, 1990). The Peruvian OMZ ranges between 50 and 700 m water depth with oxygen (O_2) concentrations below the detection limit in the mid-waters (Stramma et al., 2008). The mean water depth of the upper OMZ boundary deepens during intense El Niño Southern Oscillation years and can reach a depth of 200 m (Levin et al., 2002) with oxygenation episodes reaching concentrations of up to 100 μM O₂ (Gutiérrez et al., 2008). O₂ concentrations (Fig. 1, Table 1) off Peru are modulated by coastal trapped waves (Gutiérrez et al., 2008), trade winds (Deutsch et al., 2014) and subtropical–tropical cells (Duteil et al., 2014), and can vary on monthly to interannual timescales (Gutiérrez et al., 2008).

At 12◦ S, the OMZ extends from water depths between 50 and 550 m (Dale et al., 2015; Fig. 1). During our field work, bottom water O_2 concentrations varied greatly with water depth and were below the detection limit $(5 \mu M)$ at stations from 70 to 407 m water depth. Bottom water O_2 increased to 19 µM at 770 m water depth and 53 µM at 1025 m water depth, indicating the increase of dissolved O_2 below the lower boundary of the OMZ (Dale et al., 2015). Between 70 and 300 m water depth, the sediment surface was colonized by dense filamentous mats of sulfur-oxidizing bacteria, presumably of the genera *Marithioploca* spp. These bacteria are able to glide up to 1 cm h^{-1} through the sediment in

Figure 1. Cross-section of dissolved O₂ concentrations (μ M) along the continental margin of the Peruvian OMZ at 12[°] S. The vertical lines represent CTD cast for O2 measurement during the cruise M92. Stations 1 to 10 for multicorer (MUC) sampling are indicated by station numbers according to Dale et al. (2015).

Table 1. Sampling deployments, including station number according to Dale et al. (2015), core ID, sampling date and coordinates. Water depth (m) recorded by the ship's winch and bottom water temperature ($°C$) and bottom water O₂ concentration ($µM$; bdl = below detection limit: 5 µM) measured on the CTD.

Station	Core ID	Date (2013)	Latitude (S)	Longitude (W)	Depth (m)	Temp. $(^{\circ}C)$	$O2$ (µM)
	MUC 13	January 11	$12^{\circ}13.492'$	$77^{\circ}10.511'$	70	14	bdl
4	MUC 11	January 9	$12^{\circ}18.704'$	$77^{\circ}17.790'$	144	13.4	bdl
6	MUC 6	January 7	$12^{\circ}23.322'$	$77^{\circ}24.181'$	253	12	bdl
8	MUC ₂₃	January 15	12°27.198'	77°29.497'	407	10.6	bdl
9	MUC ₁₇	January 13	$12^{\circ}31.374'$	$77^{\circ}35.183'$	770	5.5	19
10	MUC ₂₈	January 19	$12^{\circ}35.377'$	$77^{\circ}40.975'$	1025	4.4	53

order to access hydrogen sulfide (Fossing et al., 1995; Jørgensen and Gallardo, 1999; Schulz, 1999). Sediments at the lower boundary (770 and 1025 m) of the OMZ host a variety of macrofaunal organisms, e.g., ophiuroids, gastropods, and crustaceans (Mosch et al., 2012).

The 12◦ S region is in the center of an extensive upwelling zone and features high primary productivity (Pennington et al., 2006). Sediments at 12◦ S have higher rates of particulate organic carbon accumulation (2–5 times) compared to other continental margins and a high carbon burial efficiency, indicating preferential preservation of organic matter in the Peruvian OMZ (Dale et al., 2015). The shelf (74 m) of the Peruvian OMZ is characterized by high sedimentation rates of 0.45 cm yr−¹ , while mid-waters and below the OMZ show rates between 0.07 and 0.011 cm yr^{-1} .

2.2 Sampling

Sediment samples were taken in January 2013 at six stations (70, 144, 253, 407, 770, and 1025 m) along a depth transect at 12◦ S in the OMZ off Peru (Fig. 1) during an expedition on RV *Meteor* (M92). January represents austral summer, i.e., the low upwelling, high productivity season in this area (Kessler, 2006). Samples were retrieved using a TV-guided multiple corer (MUC) equipped with seven core liners. The core liners had a length of 60 cm and an inner diameter of 10 cm. Location, water depth, temperature, and O_2 concentration (from Dale et al., 2015) at the six sampling stations are listed in Table 1. Retrieved cores for microbial rate measurements were immediately transferred to cold rooms (4– 9 °C) for further processing.

2.3 Geochemical analyses

Porewater analysis and the determination of sediment properties and geochemical data have been previously described in detail by Dale et al. (2015). In short, the first core was subsampled under anoxic conditions using an argonfilled glove bag, to preserve redox sensitive constituents. $NH₄⁺$ and sulfide concentrations were analyzed on a Hitachi U2800 UV/VIS spectrophotometer using standard photometric procedures (Grasshoff et al., 1999), while sulfate $(SO₄²)$ concentrations were determined by ion chromatography (Methrom 761).

The second replicate core was sampled to determine porosity by the weight difference of the fresh sediment sub-

Figure 2. Biogeochemical porewater profiles in MUC cores from sampling stations along the 12° S depth transect. Graphs show NH⁺ (μ M), SO₄⁻ (mM), sulfide (µM), organic carbon content (C_{org}, wt%) and the C / N ratio (molar). Water depths and bottom water O₂ concentrations (BW O_2 , μ M) are detailed on the right.

samples before and after freeze-drying. Particulate organic carbon and particulate organic nitrogen contents were analyzed using a Carlo-Erba element analyzer (NA 1500).

2.4 Benthic nitrogen fixation

At each of the six stations, one MUC core was sliced in a refrigerated container (9 \degree C) in 1 cm intervals from 0 to 6 cm, in 2 cm intervals from 6 to 10 cm, and in 5 cm intervals from 10 to 20 cm. The acetylene reduction assay (Capone, 1993; Bertics et al., 2013) was applied to quantify nitrogenase activity. This application is based on the reduction of acetylene (C_2H_2) to ethylene (C_2H_4) by the nitrogenase enzyme (Dilworth, 1966; Stewart et al., 1967; Capone, 1993). To convert from nitrogenase activity to N_2 fixation, a conversion factor of 3 C_2H_4 : 1 N_2 was applied (Patriquin and Knowles, 1972; Donohue et al., 1991; Orcutt et al., 2001; Capone et al., 2005), which was previously used to measure N_2 fixation in sediments (Welsh et al., 1996; Bertics et al., 2013).

Serum vials (60 mL) were flushed with N_2 and filled with 10 cm³ sediment from each sampling depth (triplicates). The samples were flushed again with N_2 , crimp sealed with butyl stoppers and injected with $5 \text{ mL of } C_2H_2$ to saturate the nitrogenase enzyme. Serum vials were stored in the dark at 9 ◦C, which reflected the average in situ temperature along the transect (compare with Table 1). Two sets of triplicate controls (10 cm^3) were processed for every station. Sediment was collected from each core liner from 0 to 5, 5 to 10, and from 10 to 20 cm and placed in 60 mL serum vials. One set of controls was used to identify natural C_2H_4 production without the injection of acetylene, and the second control set was fixed with 1 mL 37.5 % formaldehyde solution.

The increase of C_2H_4 in each sediment slice was measured onboard over 1 week (in total five time points, including time zero) using gas chromatography (Hewlett Packard 6890 Series II). From each serum vial, a 100 µL headspace sample was injected into the gas chromatograph and the results were analyzed with the HP ChemStation gas chromatograph software. The gas chromatograph was equipped with a packed column (Haye SepT, 6 ft, 3.1 mm ID, Resteck) and a flame ionization detector. The carrier gas was helium and the combustion gases were synthetic air $(20\% \text{ O}_2 \text{ in } \text{N}_2)$ and hydrogen. The column had a temperature of 75 ◦C and the detector temperature was 160 ◦C.

Standard deviation of individual N_2 fixation rates was calculated from three replicates determined per sediment depth in one multicorer. Standard deviation of depth-integrated N_2 fixation was calculated from the three replicate integrated rates.

It should be mentioned that the incubation with C_2H_2 can potentially lead to a lack of fixed N caused by the saturation of the nitrogenase enzyme, which leads to a reduction of cell viability and consequently N_2 fixation (Seitzinger and Garber, 1987). These effects are expected to cause an underestimation of N_2 fixation rates. However, the acetylene reducabove the natural δ^{15} N abundance of sediments.

2.5 Sulfate reduction rates

One MUC core per station was used for determination of SR activity (same MUC cast as for N_2 fixation, but different core). First, two replicate push cores (length 30 cm, inner diameter 2.6 cm) were subsampled from one MUC core. The actual push core length varied from 21 to 25 cm total length. Then, 6 µL of the carrier-free ${}^{35}SO_4^{2-}$ radio tracer (dissolved in water, 150 kBq, specific activity 37 TBq mmol−¹) was injected into the replicate push cores in 1 cm depth intervals according to the whole-core injection method (Jørgensen, 1978). The push cores were incubated for \sim 12 h at 9 °C. After incubation, bacterial activity was stopped by slicing the push core into 1 cm intervals and transferring each sediment layer into 50 mL plastic centrifuge tubes filled with 20 mL zinc acetate $(20\% \t w/w)$. Controls were done in triplicates from different depths and first fixed with zinc acetate before adding the tracer. Rates for SR were determined using the cold chromium distillation procedure according to Kallmeyer et al. (2004).

tion method is to the best of our knowledge still the standard method for the determination of benthic N_2 fixation (Bertics et al., 2013). The δ^{15} N rate determinations are not feasible in sediments, as they would require incubation times of several weeks to months to achieve signals that are statistically

It should be mentioned that the yielded SR rates have to be treated with caution due to long (up to 3 half-life times of ³⁵S) and unfrozen storage. Storage of SR samples without freezing has recently been shown to result in the re-oxidation of ³⁵S-sulfides (Røy et al., 2014). In this reaction, FeS is converted to ZnS. The released Fe^{2+} reacts with O_2 and forms reactive Fe(III). The Fe(III) oxidizes ZnS and FeS, which are the major components of the total reduced inorganic sulfur species, resulting in the generation of SO_4^{2-} and hence an underestimation of SR rates. However, because all SR samples in the present study were treated the same way, we trust the relative distribution of activity along sediment depth profiles and recognize potential underestimation of absolute rates.

2.6 *nifH* gene analysis

Core samples for DNA analysis were retrieved from the six stations and were sliced in the same sampling scheme as described for benthic N_2 fixation. Approximately 5 mL sediment from each depth horizon was transferred to plastic whirl-paks® (Nasco, Fort Atkinson, USA), frozen at −20 ◦C and transported back to the home laboratory. To

check for the presence of the *nifH* gene, DNA was extracted using the FastDNA® SPIN Kit for Soil (MP Biomedicals, CA, USA) following the manufacturer's instructions with a small modification. Sample homogenization was done in a Mini-Beadbeater™ (Biospec Products, Bartlesville, USA) for 15 s. PCR amplification, including primers and PCR conditions, was done as described by Zehr et al. (1998), using the GoTaq kit (Promega, Fitchburg, USA) and additionally 1 µL bovine serum albumin (20 mg mL⁻¹; Fermentas). The TopoTA Cloning® Kit (Invitrogen, Carlsbad, USA) was used for cloning of PCR amplicons, according to the manufacturer's protocol. Sanger sequencing (122 *nifH* sequences) was performed by the Institute of Clinical Molecular Biology, Kiel, Germany. For the sampling sites 70, 144, 253, 407, 770, and 1025 m water depth the number of obtained sequences was 22, 24, 24, 13, 18, and 21, respectively. Negative controls were performed using the PCR mixture as described without template DNA; no amplification was detected. Sequences were ClustalW aligned in MEGA 6.0 (Tamura et al., 2007), and a maximum likelihood tree was constructed on a 321 base pair fragment and visualized in iTOL (Letunic and Bork, 2007, 2011). Reference sequences were obtained using BlastX on the NCBI database. Sequences were submitted to Genbank (Accession numbers: KU302519 – KU302594).

2.7 Statistical analysis

A principle component analysis (PCA) was applied to microbial rates and environmental parameters to determine most likely explanatory variables for active N_2 fixation at the sampling St. 1 to 9. The deepest St. 10 was excluded from the analysis because at this site SR rates were below the detection limit and the PCA only allows complete datasets, which otherwise would have resulted in the exclusion of all SR rates. Prior to PCA, the dataset was Hellinger transformed in order to make it compatible with PCA. The PCA was performed in R v3.0.2 by using the R package "Vegan" (Oksanen et al., 2013) according to the approach described in Löscher et al. (2014).

For the depth profiles of N₂ fixation rates (mmol m⁻² d⁻¹) the variables water depth (m), sediment depth (cm), sulfate reduction (mmol m⁻² d⁻¹), organic carbon content (wt%), C/N ratio (molar), ammonium (μ M), and sulfide (μ M) were tested. A PCA of integrated $(0-20 \text{ cm})$ N₂ fixation rates (mmol $m^{-2} d^{-1}$) and environmental parameters could not be done due to the lack of sufficient data points.

Finally, two biplots for the depth profiles were produced, which allowed having two different views from two different angles, i.e., one biplot for principle component 1 and 2, and one biplot for principle component 2 and 3. These biplots graphically reveal a potential negative, positive or zero correlation between N_2 fixation and the tested variables.

3 Results

3.1 Sediment properties

Although sediments were sampled down to the bottom of the core, the focus here is on the 0–20 cm depth interval where benthic N_2 fixation was investigated.

Sediments at the shelf station (St.) $1(70 \text{ m})$ were black between 0 and 1 cm and then olive green until 20 cm. Only a few metazoans (polychaetes) were observed in the surface sediment. The sediment surface was colonized by dense filamentous mats of sulfur-oxidizing *Marithioploca* spp. These bacteria extended down to a sediment depth of 36 cm. The sediment on the outer shelf St. 4 (144 m) was dark olive green from 0 to 13 cm and dark grey until 20 cm. At St. 6 (253 m), which was located within the core of the OMZ, the sediment appeared dark olive green between 0 and 17 cm and olive green with white patches between 17 and 20 cm. At this station, *Marithioploca* spp. was abundant. Uniquely, surface sediments $(0-3 \text{ cm})$ at St. 8 (407 m), consisted of a fluffy, dark olive-green layer mixed with white foraminiferal ooze. This layer also contained centimeter-sized phosphorite nodules with several perforations (ca. 1–3 mm in diameter). Below 2 cm, the sediment consisted of a dark olive green, sticky clay layer. No *Marithioploca* mats were found here. St. 9 (770 m) was below the OMZ, and sediments were brown to dark olive green with white particles between 0 and 12 cm, and brown to olive green without white particles below this depth. Organisms such as anemones, copepods, shrimps and various mussels were visible with the TV-guided MUC and in the sediment cores. The deepest St. (10; 1025 m) had dark olive green sediment from 0 to 20 cm and black patches from 17 to 20 cm. The sediment was slightly sandy and was colonized with polychaete tubes at the surface and organisms that were also present at St. 9. For further sediment core descriptions see also Dale et al. (2015).

Geochemical porewater profiles of NH⁺₄, SO²⁻₁, sulfide, organic carbon content, and organic C/N ratio between 0 and 20 cm at the six stations are shown in Fig. 2. In all cores, NH₄⁺ concentrations increased with sediment depth. The highest NH_4^+ concentration was reached at St. 1 (70 m), increasing from $316 \mu M$ in the upper cm to $2022 \mu M$ at 20 cm. St. 4 and 6 showed intermediate $NH₄⁺$ concentrations between 300 and 800 μ M at 20 cm, respectively. At St. 8 (407 m) the NH₄⁺ concentration increased from 0.7 μ M at the surface to 107 μ M at 20 cm. The two deep stations (St. 9 and 10) had the lowest NH⁺ concentrations with 33 and 22 μ M at 20 m sediment depth, respectively.

The SO_4^{2-} concentrations remained relatively constant in the surface sediments along the transect. A decrease was only observed at St. 1; from 28.7 µM in the surface layer to 19.4 μM at 20 cm. In parallel with the decrease in SO_4^{2-} , only St. 1 revealed considerable porewater sulfide accumulation, whereby sulfide increased from 280 μ M at the surface sediment to 1229 µM at 20 cm.

Figure 3. Sediment profiles of N₂ fixation (nmol N₂ cm⁻³ d⁻¹, average of three replicates) and sulfate reduction rates (SR, nmol SO₄⁻ cm⁻³ d⁻¹, two replicates; R1 and R2) from 0 to 20 cm at the six stations. The upper x axis represents the N₂ fixation, while the lower x axis represents the SR. Error bars indicate standard deviation of N_2 fixation.

Organic carbon content decreased with increasing sediment depth at St. 1 (70 m), 9 (770 m), and 10 (1025 m). The highest surface organic carbon content (∼ 15 wt %) was found at St. 6, whereas the lowest (\sim 2.6 wt%) was detected at the deep St. 10. The average (0–20 cm) organic carbon content (Fig. 5) increased from St. 1 to St. 6 (15 \pm 1.7 wt %) and decreased from St. 6 to the lowest value at St. 10 $(2.4 \pm 0.4 \text{ wt\%})$.

 C/N ratios, as a proxy for the freshness of the organic matter, increased with increasing sediment depth (Fig. 5). The lowest surface C / N ratio (6.2) was measured at the shallow St. 1, while the highest surface C / N ratio (11) was found at St. 10.

3.2 Benthic nitrogen fixation and sulfate reduction

For a straightforward comparison of SR rates with benthic N_2 fixation only the sediment depths between 0 and 20 cm are considered. Sediment depth profiles are expressed as N_2 fixation, that is, with the conversion factor of $3 C_2H_4$: $1 N_2$.

Highest N_2 fixation and SR rates were detected in the surface sediments (0–5 cm) and both rates tended to decrease with increasing sediment depth (Fig. 3). N_2 fixation and SR rates were high at St. 1, 4, and 6 (70, 144, 253 m) and lowest at the deeper St. 8–10 (407, 770, 1025m).

At St. 1, N_2 fixation and SR rates showed different trends in the top layer of the cores, but depth profiles were more aligned below. Although St. 1 had the highest SR rates of all

Figure 4. Integrated nitrogen fixation (mmol N_2 m⁻² d⁻¹, grey bars, average of three replicates) and integrated sulfate reduction (mmol SO_4^{2-} m⁻² d⁻¹, green bars, two replicates) from 0 to 20 cm, including dissolved inorganic carbon flux (DIC, mmol m⁻² d⁻¹, red curve from Dale et al., 2015) and bottom water O₂ (µM, blue curve) along the depth transect (m). Error bars indicate standard deviation of N₂ fixation.

Figure 5. Integrated nitrogen fixation (mmol N_2 m⁻² d⁻¹, grey bars, average of three replicates), average organic carbon content (C_{org} , wt%, orange curve) and the average C / N molar ratio (yellow curve) from 0 to 20 cm along the depth transect (m). Error bars indicate standard deviation.

sites, reaching 248 nmol SO_4^{2-} cm⁻³ d⁻¹ at 0-1 cm, N₂ fixation was not highest at this station. At St. 4 (144 m), both N_2 fixation and SR revealed peaks close to the surface. N_2 fixation decreased between 0 and 8 cm and increased below 8 cm. This increase was not observed in SR rates, which were highest at the surface $(181 \text{ nmol } SO_4^{2-} \text{ cm}^{-3} \text{ d}^{-1})$ and decreased towards the bottom of the core. St. 6 (253 m) had the highest N_2 fixation of all stations, with rates of 4.0 ± 0.5 nmol N₂ cm⁻³ d⁻¹ in the surface centimeter. Yet, although N_2 fixation and SR had overlapping activity profiles, the highest SR rate of all stations was not detected at St. 6. Very low N_2 fixation rates were measured at St. 8 (407 m; 0.5 ± 0.25 nmol N₂ cm⁻³ d⁻¹ in the surface), as well as very low SR rates $(0-4.3 \text{ nmol SO}_4^{2-} \text{ cm}^{-3} \text{ d}^{-1})$. As mentioned, this station was unique due to the presence of foraminiferal ooze, phosphorite nodules and a sticky clay layer below 2 cm. N² fixation and SR rates showed a peak at 5 and at 7 cm, re-

spectively. At St. 9 (770 m) N_2 fixation was low in the surface and at 20 cm sediment depth, with a peak in activity at 4–5 cm (0.8 ± 0.08 nmol N₂ cm⁻³ d⁻¹). At St. 10 (1025 m), N² fixation rates were low throughout the sediment core, not exceeding 0.16 ± 0.02 nmol N₂ cm⁻³ d⁻¹. This site had the lowest organic carbon content throughout the core (between 2.6 wt % at the surface and 1.9 wt % at 20 cm), as well as low NH⁺ concentrations. At St. 9 (below 9 cm depth) and St. 10 (entire core) SR rates were below detection, which could point either to the absence of SR or to the complete loss of total reduced inorganic sulfur due to the long, unfrozen storage (see methods).

Integrated N_2 fixation (0–20 cm) increased from St. 1 to St. 6, with the highest rate $(0.4 \pm 0.06 \text{ N}_2 \text{ m}^{-2} \text{ d}^{-1})$ at St. 6 (253 m), and decreased from St. 6 (407 m) to St. 10 (1025 m; Fig. 4). Integrated SR rates (0 to 20 cm) ranged from \sim 4.6 mmol SO₄⁻ m⁻² d⁻¹ at St. 1 to below detection at St. 9 (Fig. 4). Overall, integrated SR rates decreased with increasing water depth. Integrated N_2 fixation rates and SR were in general inversely correlated between St. 1 and St. 6, and followed the organic carbon content from St. 1 to St. 6 (70–253 m; Fig. 5). Both parameters had the highest value at St. 6. This pattern did not hold for the relatively low integrated SR rate at St. 6. The C / N ratio, averaged over 20 cm, increased with increasing water depth (Fig. 5). Regarding the three deep stations, the lowest integrated N₂ fixation rate $(0.008 \pm 0.002 \text{ N}_2 \text{ m}^{-2} \text{ d}^{-1})$ was detected at St. 8 (407 m). Also the integrated SR rate was low at this site (\sim 0.46 mmol SO₄² m⁻² d⁻¹). At St. 9 and 10 (770 and 1025 m), integrated N₂ fixation was low at 0.05 ± 0.005 and 0.01 ± 0.001 N₂ m⁻² d⁻¹, respectively, and integrated SR rates were also lowest at St. 9 (770 m). From St. 8 to 10 a decrease of integrated N_2 fixation and SR together with the average organic carbon content was detected.

J. Gier et al.: Nitrogen fixation in sediment 4073

No activity was detected in controls for N_2 fixation and SR.

3.3 Statistical analysis

The PCA of N_2 fixation depth profiles (Fig. 6a and b) showed a weak positive correlation with sulfate reduction rates (Fig. 6a) and a strong positive correlation between N_2 fixation and the organic matter content in sediments (Fig. 6b). A negative correlation between N_2 fixation and sediment depth (Fig. 6a), as well as between N_2 fixation and sulfide concentration for St. 1 (Fig. 6b) was found. Furthermore, a weak negative correlation was detected between N_2 fixation and the C/N ratio (Fig. 6a). No correlation was found between N_2 fixation and ammonium concentration and water depth (Fig. 6a and b).

3.4 Molecular analysis of the *nifH* gene

Sequences for the *nifH* gene analysis were pooled for each of the six stations, making about 20 sequences per sample and 120 in total. *NifH* gene sequences were detected at all six sampling sites and clustered with Cluster I proteobacterial sequences and Cluster III sequences as defined by Zehr and Turner (2001) (Fig. 7). In Cluster I and Cluster III, three and seven novel clades were detected, respectively. In general, most of the previously unidentified clades belonged to uncultured bacteria. One distinct novel clade was found for St. 1–6. No Cluster I cyanobacterial *nifH* sequences were detected and no potential PCR contaminants were present (Turk et al., 2011). Sequences clustered with only one identified sulfate-reducing bacterium, *Desulfonema limicola* (Fukui et al., 1999, OMZ 253). Other sequences from several stations (OMZ 70, 144, 253, 770) were distantly related to *Desulfovibrio vulgaris* (Riederer-Henderson and Wilson, 1970; Muyzer and Stams, 2008). One cluster (OMZ 144 m) was closely related to the anaerobic marine bacterium *Vibrio diazotrophicus* (Guerinot et al., 1982). Other organisms with which OMZ sequences clustered belonged to the genera of fermenting bacteria, namely *Clostridium beijerincki* (Chen, 2005), and to the genera of iron-reducing bacteria, namely *Geobacter bemidjiensis* (Nevin et al., 2005). In addition, several sequences were phylogenetically related to a gamma proteobacterium (Zehr and Turner, 2001) from the Pacific Ocean.

4 Discussion

4.1 Coupling of benthic nitrogen fixation and sulfate reduction

Based on the high organic matter input to Peruvian sediments underneath the OMZ we hypothesized a presence of N_2 fixation and its coupling to sulfate reduction (SR). We confirmed the presence of N_2 fixation in sediments at all sampled sta-

Figure 6. Principle component analysis (PCA) from two different angles of Hellinger transformed data of N_2 fixation and environmental parameters along vertical profiles. Correlation biplots (a) of principle components 1 and 2 and of (b) principle components 2 and 3 in a multidimensional space are shown. Samples are displayed as dots while variables are displayed as lines. Parameters pointing into the same direction are positively related; parameters pointing in the opposite direction are negatively related.

tions along the depth transect. N_2 fixation activity was often enhanced where SR peaked and sometimes both activity depth profiles revealed similar trends. However, while peaks in SR were very pronounced, maximum N_2 fixation showed a much broader distribution over depth. These findings are in line with the PCA of depth profiles, which revealed a weak positive correlation between activities of N_2 fixation and sulfate reduction. But it should be kept in mind that the N_2 fixation and SR were determined in replicate MUC cores, which were taken up to 50 cm apart, depending on where the core liners were situated in the multicorer. Nonetheless, it appears that the observed N_2 fixation is not exclusively fueled by SR activity.

The coupling between N_2 fixation and SR has been previously suggested for coastal sediments off California, where N_2 fixation significantly decreased when SR was inhibited (Bertics and Ziebis, 2010). Different studies confirmed that sulfate-reducing bacteria, such as *Desulfovibrio vulgaris* can supply organic-rich marine sediments with bioavailable N through N² fixation (Welsh et al., 1996; Nielsen et al., 2001;

Figure 7. Phylogenetic tree of *nifH* genes based on the analysis of 122 sequences (∼ 20 sequences per sample) from the six sampling stations between 70 and 1025 m water depth. Novel detected clusters consisting of several sequences from the same sampling depth are indicated by grey triangles. Reference sequences consist of the alternative nitrogenase $an f D$, $an f G$, $an f K$. Cluster III sequences as defined by Zehr and Turner (2001) are highlighted in blue; Cluster I cyanobacterial sequences are highlighted in green and Cluster I proteobacterial sequences are highlighted in orange. The scale bar indicates the 10 % sequences divergence. Sequences marked with an asterisk represent potential PCR contaminated products, with novel clusters distant from those clusters. Sequences determined in this study are termed OMZ plus the corresponding water depth.

J. Gier et al.: Nitrogen fixation in sediment 4075

Steppe and Paerl, 2002; Fulweiler et al., 2007; Bertics et al., 2013; Fulweiler et al., 2013). Fulweiler et al. (2013) conducted a study in sediments of the Narrangaset Bay and found several *nifH* genes related to sulfate-reducing bacteria, such as *Desulfovibrio* spp., *Desulfobacter* spp. and *Desulfonema* spp., suggesting that sulfate-reducing bacteria were the dominant diazotrophs.

The more surprising finding in this study is that integrated rates of N_2 fixation and SR showed opposite trends at the three shallowest stations, pointing to potential environmental control mechanisms (see Sect. 5.2). Overall, these findings indicate that N_2 fixation might be partly coupled to processes other than SR or that the two processes are controlled by different parameters. The *nifH* gene sequence analyses indicated only a weak potential of sulfate reducers to conduct N_2 fixation in the Peruvian sediments. Sequences clustered only with the sulfate-reducing bacteria *Desulfonema limicola* (Fukui et al., 1999) exclusively at the 253 m Station. *D. limicola* is known from other benthic environments through *nifH* gene analyses (Mussmann et al., 2005; Bertics et al., 2010, 2013). A distant relation to the confirmed diazotrophic sulfate reducer *Desulfovibrio vulgaris* (Sisler and ZoBell, 1951; Riederer-Henderson and Wilson, 1970) was detected at several stations. *D. limicola* and *D. vulgaris* clustered with sequences taken from the seasonally hypoxic Eckernförde Bay in the Baltic Sea (Bertics et al., 2013), suggesting a major involvement of these sulfate-reducing bacteria in N_2 fixation in organic-rich sediments. Further, sequences related to *Vibrio* diazotrophicus were detected, which has the unique ability for a known *Vibrio* species to perform N² fixation and which was found previously in the water column of the OMZ off Peru (Fernandez et al., 2011; Löscher et al., 2014). Interestingly, we detected several new *nifH* gene clusters in the Peruvian OMZ that have not been identified yet and which have, consequently, yet unknown metabolic processes (Fig. 7). Thus, a coupling of N_2 fixation to processes other than SR is also possible, which might also explain some of the discrepancies between N_2 fixation and SR activity (see above). However, the coupling to heterotrophic metabolic processes such as denitrification or methanogenesis was not supported by our molecular data.

4.2 Environmental factors controlling benthic N_2 fixation

The observed differences between integrated N_2 fixation and SR along the depth transect indicate potential environmental factors that control the extent of benthic N_2 fixation, which will be discussed in the following section.

4.2.1 Organic matter

A major driver for microbial processes such as SR and N² fixation by potentially heterotrophic organisms is the availability of the organic material (Jørgensen, 1983; Howarth et al., 1988; Fulweiler et al., 2007). Integrated N_2 fixation and average organic carbon content showed similar trends along the Peruvian OMZ depth transect (Fig. 5), and a strong positive correlation was detected by PCA in the sediment depth profiles (Fig. 6). Thus, organic matter availability appears to be a major factor controlling N_2 fixation at this study site. Low organic matter content was previously shown to result in low N₂ fixation rates in slope sediments in the Atlantic Ocean (Hartwig and Stanley, 1978). Correlation to organic matter was further confirmed by the study of Bertics et al. (2010), which showed that burrow systems of the bioturbating ghost shrimp *Neotrypaea californiensis* can lead to enhanced organic matter availability in deeper sediment layers, resulting in high rates of N_2 fixation. However, high organic matter availability does not always result in enhanced N_2 fixation rates. Subtidal sediments in the Narragansett Bay were found to switch from being a net sink via denitrification to being a net source of bioavailable N via N_2 fixation (Fulweiler et al., 2007). This switch was caused by a decrease of organic matter deposition to the sediments, which was in turn triggered by low primary productivity in the surface waters.

Besides quantity also the quality of organic matter in sediments is a major factor influencing microbial degradation processes (Westrich and Berner, 1984). In the Peruvian OMZ sediments, the average C/N ratio increased with water depth indicating that the shallow stations received a higher input of fresh, labile organic material compared to the deeper stations. Similar trends were reported for a different depth transect off Peru (Levin et al., 2002). The C/ N ratios did not follow the pattern of integrated N_2 fixation (Fig. 5), which is in line with the PCA of depth profiles, which showed a weak negative correlation between N_2 fixation and the C / N ratio. These results indicate that the C/N ratio is not a major factor controlling N_2 fixation in Peruvian OMZ sediments.

DIC fluxes, which were determined in benthic chamber lander incubations at the same stations and during the same expedition as our study (Dale et al., 2015), can be used as an indicator for organic matter degradation rates, e.g., by SR. The DIC flux did not follow the pattern of the integrated N_2 fixation rates (Fig. 4) and thus does not indicate that N_2 fixation and SR are coupled. Instead, the benthic DIC flux roughly followed the pattern of SR rates along the depth transect. The highest integrated SR rate and DIC flux were found at St. 1 (70 m), whereas the lowest occurred at St. 10 (1025 m). Assuming that SR is largely responsible for organic matter remineralization in the sediments below the OMZ (Bohlen et al., 2011; Dale et al., 2015), the difference between integrated SR and DIC flux is expected to be mainly caused by the loss of $35S$ -sulfides during the long duration of unfrozen storage of the SR samples (see methods).

4.2.2 Ammonium

Interestingly, the highest N_2 fixation was measured in sediments colonized by the sulfur-oxidizing and nitratereducing filamentous bacteria *Marithioploca* spp. (Schulz, 1999; Schulz and Jørgensen, 2001; Gutiérrez et al., 2008; Salman et al., 2011; Mosch et al., 2012). *Marithioploca* facilitates dissimilatory NO_3^- reduction to NH_4^+ , which preserves fixed N in the form of $NH₄⁺$ in the environment (Kartal et al., 2007). OMZ sediments off Peru are generally rich in $NH₄⁺$ (Bohlen et al., 2011; Dale et al., 2016). This cooccurrence of *Marithioploca* and N₂ fixation was puzzling since high concentrations of $NH₄⁺$ were expected to inhibit N² fixation (Postgate, 1982; Capone, 1988; Knapp, 2012). It remains questionable why microorganisms should fix N_2 in marine sediments, when reduced N species are abundant. Some doubt remains as to the critical $NH₄⁺$ concentration that inhibits N_2 fixation and whether the inhibitory effect is the same for all environments (Knapp, 2012). For example, NH_4^+ concentrations up to 1000 μ M did not fully suppress benthic N_2 fixation in a hypoxic basin in the Baltic Sea (Bertics et al., 2013), indicating that additional environmental factors must control the distribution and performance of benthic diazotrophs (Knapp, 2012). We observed high porewater NH⁺₄ concentrations at the shallow St. 1 with 316 μ M at the sediment surface $(0-1 \text{ cm})$ increasing to $2022 \mu M$ at 20 cm (Fig. 2), while no inhibition of N_2 fixation was found. This observation is verified by the PCA, which showed no correlation with ammonium for the N_2 fixation depth profiles. Hence, ammonium did not seem to have a significant influence on benthic N_2 fixation rates in the Peruvian OMZ.

One debated explanation for why diazotrophs still fix N under high NH_4^+ concentrations is that bacteria fix N₂ to remove excess electrons and to preserve their intracellular redox state, particularly with a deficient Calvin–Benson– Bassham pathway, as shown for photoheterotrophic nonsulfur purple bacteria (Tichi and Tabita, 2000). Another explanation could be that microniches, depleted in NH_4^+ , exist between sediment grains, which we were unable to track with the applied porewater extraction techniques (Bertics et al., 2013).

4.2.3 Sulfide

Sulfide is a known inhibitor for many biological processes (Reis, et al., 1992; Joye and Hollibaugh, 1995) and could potentially affect N_2 fixation (Tam et al., 1982). The shallow St. 1 was the only station with sulfide in the porewater, reaching 280μ M in surface sediments and 1229μ M in 20 cm (Fig. 2). The presence of relatively high concentrations of sulfide at St. 1 might explain why N_2 fixation was lower at this site when compared to St. 6, which had the highest N_2 fixation rates. Statistically, depth profiles of N_2 fixation and sulfide showed a negative correlation (Fig. 6b). Generally, interactions of sulfide with benthic N_2 fixation have so far not been investigated, and the PCA did not provide a complete pattern, as sulfide was not widespread in the sediments along the transect and thus does not allow robust interpretation.

4.2.4 Oxygen

Dissolved O_2 can have a considerable influence on N_2 fixation due to the O_2 sensitivity of the key enzyme nitrogenase (Postgate, 1998; Dixon and Kahn, 2004). Bioturbating and bioirrigating organisms can transport O_2 much deeper into sediments than molecular diffusion (Orsi et al., 1996; Dale et al., 2011). In coastal waters, the bioturbation and bioirrigation activity of ghost shrimps was found to reduce N_2 fixation when sediments were highly colonized by these animals (Bertics et al., 2010). While bottom water O_2 concentrations in the Peruvian OMZ were below the detection limit at St. 1 to 8 (70 to 407 m), thereby mainly excluding benthic macrofauna, O_2 concentrations increased to above $40 \mu M$ at St. 10 (1025 m) where a diverse bioturbating and bioirrigating benthic macrofauna community was observed (Mosch et al., 2012). Accordingly, St. 10 revealed some of the lowest N_2 fixation activity. We speculate that the low organic matter content at this St. was mainly responsible for the low N_2 fixation rates and not the high bottom water O_2 concentrations, as the statistics showed a positive correlation between integrated N_2 fixation and organic carbon content.

4.3 Comparison of benthic N_2 fixation in different environments

We compiled a list of N_2 fixation rates from different marine sedimentary environments to gain an overview of the magnitude of N_2 fixation rates measured in the Peruvian OMZ sediments (Table 2). We found that N_2 fixation rates from the Peruvian sediments exceed those reported for open ocean sediments (2800 m; Howarth et al., 1988), bioturbated coastal lagoon sediment (Bertics et al., 2010) and sediments > 200 m water depth from various sites worldwide (Capone, 1988). The highest integrated N_2 fixation rate determined in our study (0.4 mmol N_2 m⁻² d⁻¹, St. 6) closely resembles highest rates found in salt marshes (0.38 mmol N_2 m⁻² d⁻¹) and Zostera estuarine sediments $(0.39 \text{ mmol N}_2 \text{ m}^{-2} \text{ d}^{-1})$ (Capone, 1988). Further, our rates were characterized by a similar range of N_2 fixation rates that were previously measured in an organic-rich hypoxic basin in the Baltic Sea (0.08–0.22 mmol N₂ m⁻² d⁻¹, Bertics et al., 2013). In contrast to the above examples, our N_2 fixation rates were 8.5 times lower compared to shallow $(< 1 \,\mathrm{m})$ soft-bottom sediment off the Swedish coast (Andersson et al., 2014) and 17 times lower than coral reef sediments (Capone, 1988). However, in these environments, phototrophic cyanobacterial mats contributed to benthic N_2 fixation. Given the dark incubation, N_2 fixation of the present study seems to be attributed to heterotrophic diazotrophs, which is additionally confirmed by the *nifH* gene analysis, where none of the sequences clustered with cyanobacteria (Fig. 7).

Table 2. Integrated rates of benthic N₂ fixation (mmol N₂ m⁻² d¹) in the Peruvian OMZ sediments from this study compared to other marine benthic environments. Only the highest and lowest integrated rates are shown, as well as the integrated sediment depth (cm) and the method used $(ARA = acetylene reduction assay, MIMS = membrane inlet mass spectrometry).$

Benthic environment	$N2$ fixation (mmol N_2 m ⁻² d ⁻¹)	Depth of integration (cm)	Method	Reference
Peru OMZ	$0.01 - 0.4$	$0 - 20$	ARA	This study
Coastal region				
Baltic Sea, hypoxic basin	$0.08 - 0.22$	$0 - 18$	ARA	Bertics et al. (2013)
Bioturbated coastal lagoon	$0.8 - 8.5$	$0 - 10$	ARA	Bertics et al. (2010)
Brackish-water	$0.03 - 3.4$	$0 - 1$	ARA	Andersson et al. (2014)
Coral reef	$6.09 \ (\pm 5.62)$			Capone (1983)
Eelgrass meadow	$0.15 - 0.39$	$0 - 5$	ARA	Cole and McGlathery (2012)
Eutrophic estuary	$0 - 18$	$0 - 20$	MIMS	Rao and Charette (2012)
Mangrove	$0 - 1.21$	$0 - 1$	ARA	Lee and Joye (2006)
Salt marsh	$0.38 \ (\pm 0.41)$			Capone (1983)
Subtidal	$0.6 - 15.6$	$0 - 30$	MIMS	Fulweiler et al. (2007)
Zostera estuary	0.39			Capone (1983)
Open ocean				
Atlantic Ocean (2800 m)	0.00008		ARA	Howarth et al. (1988)
$<$ 200 m, various sites	$0.02 \ (\pm 0.01)$			Capone (1983)
Mauritania OMZ	$0.05 - 0.24$	$0 - 20$	ARA	Bertics and Treude, unpubl.

5 Summary

To the best of our knowledge, this is the first study combining N² fixation and SR rate measurements together with molecular analysis in OMZ sediments. We have shown that N_2 fixation occurred throughout the sediment and that activity often overlapped with SR. The PCA showed a weak positive correlation between activity depth profiles of N_2 fixation and SR. The molecular analysis of the *nifH* gene confirmed the presence of heterotrophic diazotrophs at all sampling sites, but only a few of the sequences were related to known sulfate reducers. Instead, many sequences clustered with uncultured organisms. In combination, our results indicate that N_2 fixation and SR were coupled to some extent, but additional coupling to other metabolic pathways is very likely. The major environmental factor controlling benthic diazotrophs in the OMZ appears to be the organic matter content. Sulfide was identified as a potential inhibitor for N_2 fixation. We further found no inhibition of N₂ fixation by high NH₄⁺ concentration, highlighting gaps in our understanding of the relationship between NH_4^+ availability and the stimulation of N₂ fixation. N_2 fixation rates determined in the Peruvian OMZ sediments were in the same range of other organic-rich benthic environments, underlining the relation between organic matter, heterotrophic activity, and N_2 fixation.

Author contributions. Jessica Gier and Tina Treude collected samples and designed experiments. Jessica Gier performed nitrogen fixation experiments and Tina Treude conducted sulfate reduction experiments. Stefan Sommer and Andrew W. Dale measured porosity, DIC, organic carbon content and C / N. Jessica Gier, Tina Treude, Carolin R. Löscher and Stefan Sommer analyzed the data. Jessica Gier and Carolin R. Löscher performed molecular analysis and statistical analysis. Jessica Gier prepared the manuscript with contributions from all co-authors and Tina Treude supervised the work.

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J. Gier et al.: Nitrogen fixation in sediment 4079

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