

NH₂OH Disproportionation Mediated by Anaerobic Ammonium-oxidizing (Anammox) Bacteria

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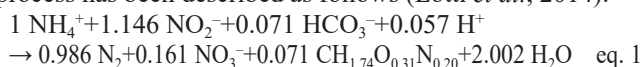
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Anammox bacteria produce N₂ gas by oxidizing NH₄⁺ with NO₂⁻, and hydroxylamine (NH₂OH) is a potential intermediate of the anammox process. N₂ gas production occurs when anammox bacteria are incubated with NH₂OH only, indicating their capacity for NH₂OH disproportionation with NH₂OH serving as both the electron donor and acceptor. Limited information is currently available on NH₂OH disproportionation by anammox bacteria; therefore, the stoichiometry of anammox bacterial NH₂OH disproportionation was examined in the present study using ¹⁵N-tracing techniques. The anammox bacteria, *Brocadia sinica*, *Jettenia caeni*, and *Scalindua* sp. were incubated with the addition of ¹⁵NH₂OH, and the production of ¹⁵N-labeled nitrogenous compounds was assessed. The anammox bacteria tested performed NH₂OH disproportionation and produced ¹⁵-¹⁵N₂ gas and NH₄⁺ as reaction products. The addition of acetylene, an inhibitor of the anammox process, reduced the activity of NH₂OH disproportionation, but not completely. The growth of *B. sinica* by NH₂OH disproportionation (-240.3 kJ mol NH₂OH⁻¹ under standard conditions) was also tested in 3 up-flow column anammox reactors fed with 1) 0.7 mM NH₂OH only, 2) 0.7 mM NH₂OH and 0.5 mM NH₄⁺, and 3) 0.7 mM NH₂OH and 0.5 mM NO₂⁻. NH₂OH consumption activities were markedly reduced after 7 d of operation, indicating that *B. sinica* was unable to maintain its activity or biomass by NH₂OH disproportionation.

Key words: anammox bacteria, hydroxylamine (NH₂OH), NH₂OH disproportionation, ¹⁵N-tracing technique, up-flow column reactor

Anaerobic ammonium-oxidizing (anammox) bacteria were initially discovered in a denitrifying bioreactor in 1995 (Mulder *et al.*, 1995), and are now recognized as the main players in the global nitrogen cycle (Kuypers *et al.*, 2003; 2005; Amano *et al.*, 2007; Yoshinaga *et al.*, 2011). In the anammox process, NH₄⁺ is oxidized to N₂ gas using NO₂⁻ as an electron acceptor, and the stoichiometry of the anammox process has been described as follows (Lotti *et al.*, 2014):



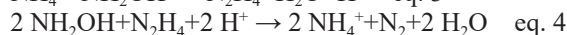
As an intermediate, hydrazine (N₂H₄) is synthesized from NH₄⁺ and NO or NH₂OH by hydrazine synthase, and its biosynthesis appears to be unique to metabolism by anammox bacteria (Strous *et al.*, 2006; Kartal *et al.*, 2011; Oshiki *et al.*, 2016a). Anammox bacteria are monophyletically affiliated into the bacterial order *Brocadiales* in the phylum *Planctomycetota* (Strous *et al.*, 1999), and five candidate genera have been proposed: *Candidatus Brocadia*, *Kuenenia*, *Jettenia*, *Anammoxoglobus*, and *Scalindua* (Egli *et al.*, 2003; Kuypers *et al.*, 2003; Quan *et al.*, 2008). These anammox bacteria have been detected in various natural and man-made ecosystems and are significantly involved in

nitrogen loss (Oshiki *et al.*, 2016b).

Hydroxylamine (NH₂OH), a well-known intermediate of the aerobic NH₃ oxidation reaction (Madigan *et al.*, 2019), is also a potential intermediate of the anammox process (van de Graaf *et al.*, 1997). The anammox bacterium, *Brocadia sinica* reduced NO₂⁻ to NH₂OH (Oshiki *et al.*, 2016a) potentially by using reductive hydroxylamine dehydrogenase (rHao) (Ferousi *et al.*, 2021), and synthesized N₂H₄ from the NH₂OH and NH₄⁺ using hydrazine synthase (Oshiki *et al.*, 2016a). *Kuenenia stuttgartiensis* reduced NO₂⁻ to NO (Kartal *et al.*, 2011), and NO was further reduced to NH₂OH by hydrazine synthase to synthesize N₂H₄ (Dietl *et al.*, 2015). Apart from the anammox process, the nitrogen transformation reaction, NH₂OH disproportionation, has been reported in anammox bacteria (van der Star *et al.*, 2008). A disproportionation reaction is a reaction in which a chemical compound serves as both an electron donor and acceptor, and the disproportionation reaction of inorganic sulfur (Finster, 2008) is an example of a microbial disproportionation reaction. In NH₂OH disproportionation, NH₂OH is converted to N₂ gas and NH₄⁺ using the following stoichiometry (Pacheco *et al.*, 2011):



NH₂OH disproportionation involves the following 2 reactions, N₂H₄ production and consumption (Soler-Jofra *et al.*, 2020):



Although NH₂OH disproportionation by *K. stuttgartiensis* (van der Star *et al.*, 2008; Soler-Jofra *et al.*, 2020) and *B. sinica* (Oshiki *et al.*, 2016a) has been described, further studies are required to obtain a more detailed understanding of anammox bacterial NH₂OH disproportionation for the

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following reasons. Although the kinetics of NH_2OH disproportionation have been investigated using *K. stuttgartiensis* (van der Star *et al.*, 2008; Soler-Jofra *et al.*, 2020), the amounts of N_2 gas produced in NH_2OH disproportionation (see eq. 2) were not measured in previous studies and the stoichiometry of NH_2OH disproportionation was not established. Furthermore, we previously examined NH_2OH disproportionation by *B. sinica*; however, we only reported the occurrence of NH_2OH disproportionation (Oshiki *et al.*, 2016a) and did not investigate the effects of NH_2OH concentrations on NH_2OH disproportionation by repeating batch incubations. In addition, although eq. 2 yields $-240.3 \text{ kJ mol NH}_2\text{OH}^{-1}$ of free energy under standard conditions (Soler-Jofra *et al.*, 2020), the growth of anammox bacteria with NH_2OH disproportionation has not yet been examined.

Therefore, the present study investigated anammox bacterial NH_2OH disproportionation. The phylogenetically different anammox bacteria, *B. sinica*, *Jettenia caeni*, and *Scalindua* sp. were incubated with ^{15}N -labeled NH_2OH , and the stoichiometry of NH_2OH disproportionation was carefully assessed based on measurements of $^{15-15}\text{N}_2$ and NH_4^+ concentrations. NH_2OH disproportionation was also analyzed under acetylene inhibition conditions. Acetylene is a strong inhibitor of aerobic NH_3 oxidation, N_2O reduction to N_2 (*i.e.*, denitrification), and the anammox process (Jensen *et al.*, 2007); however, its effects on NH_2OH disproportionation currently remain unknown. *B. sinica* was cultured in up-flow column reactors with the addition of NH_2OH to establish whether it grows on NH_2OH , and the activity of NH_2OH consumption and the abundance of the anammox bacterial 16S rRNA gene were evaluated.

Materials and Methods

Anammox bacterial cultures

Planktonic cells of *B. sinica*, *J. caeni*, and *Scalindua* sp. were cultivated in membrane bioreactors (MBRs) equipped with a hollow fiber membrane module (pore size of $0.1 \mu\text{m}$, polyethylene) as previously described (Oshiki *et al.*, 2013; Zhang and Okabe, 2020). Culture media fed into MBRs contained KH_2PO_4 (24.4 mg L^{-1}), $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$ (60 mg L^{-1}), CaCl_2 (51 mg L^{-1}), yeast extract (Becton, Dickinson and Company) (1.0 mg L^{-1}), and 0.5 mL of trace element solutions I and II (van de Graaf *et al.*, 1996). The artificial sea salt SEALIFE (Marine Tech) (Kindaichi *et al.*, 2011) was supplemented into media for “*Ca. Scalindua* sp.” at a final concentration of 28 g L^{-1} . Equimolar amounts of $\text{NH}_4(\text{SO}_4)_2$ and NaNO_2 were supplemented into media at 10 mM for *B. sinica* and *Scalindua* sp. and 5 mM for *J. caeni*, and the nitrogen loading rates of the MBRs for *B. sinica*, *J. caeni*, and *Scalindua* sp. were set at 0.55 , 0.18 , and $0.45 \text{ kg N m}^{-3} \text{ d}^{-1}$, respectively. MBRs were operated at 37°C for *B. sinica* and at 25°C for *J. caeni* and *Scalindua* sp. pH was not controlled in MBRs, but was in the range of pH 7.6 – 8.0 . Anammox bacterial cells accounted for more than 90% of the total biomass in MBRs as measured by a fluorescence *in situ* hybridization (FISH) analysis using the oligonucleotide probes AMX820 (Schmid *et al.*, 2001) and EUBmix composed of equimolar EUB338, EUB338II, and EUB338III (Daims *et al.*, 1999). Anammox bacterial species were routinely checked based on the partial anammox bacterial 16S rRNA gene sequence using Sanger sequencing (Oshiki *et al.*, 2011).

Batch incubations of anammox bacteria

Standard anaerobic techniques were employed in an anaerobic chamber (Coy Laboratories Products) in which the concentration of oxygen was maintained at $<1 \text{ ppm}$. Culture media and stock solutions were prepared by purging N_2 gas for $>30 \text{ min}$, and then repeatedly vacuuming and purging He gas. The ^{15}N enrichment of $^{15}\text{NH}_2\text{OH} \cdot \text{HCl}$ (Cambridge Isotope Laboratories) was $>98\%$.

Anammox bacterial cells collected from MBRs were centrifuged at $13,420 \times g$ at 20°C for 10 min , washed, and then resuspended in the above culture media without NH_4^+ and NO_2^- at concentrations of $0.5 \text{ mg protein mL}^{-1}$. Twenty-five milliliters of the cell suspension was dispensed into 70-mL serum glass vials (Nichiden-Rika glass), and the headspace was replaced with He gas ($>99.99995\%$) after sealing with butyl rubber stoppers and aluminium caps. Vials were incubated after the addition of $^{15}\text{NH}_2\text{OH}$ (final concentration of 1.0 to 10 mM) and acetylene ($30 \mu\text{M}$) (Jensen *et al.*, 2007) in the dark at 37°C for *B. sinica* and at 25°C for *J. caeni* and *Scalindua* sp.. Liquid samples were collected using a 1-mL plastic disposable syringe, immediately filtered using a $0.2\text{-}\mu\text{m}$ cellulose acetate filter, and subjected to measurements of NH_4^+ , NO_2^- , NO_3^- , and NH_2OH concentrations. Gas samples were collected using a gas-tight glass syringe and immediately injected into a gas chromatograph to assess $^{14-15}\text{N}_2$ and $^{15-15}\text{N}_2$ concentrations.

Up-flow column reactors fed with NH_2OH

Three 255-mL up-flow column reactors were operated at 37°C in the dark with the continuous feeding of the above culture media containing 1) $0.7 \text{ mM } ^{14}\text{NH}_2\text{OH}$, 2) $0.7 \text{ mM } ^{14}\text{NH}_2\text{OH}$ and $0.5 \text{ mM } ^{14}\text{NH}_4^+$, or 3) $0.7 \text{ mM } ^{14}\text{NH}_2\text{OH}$ and $0.5 \text{ mM } ^{14}\text{NO}_2^-$. *B. sinica* cells immobilized on polyvinyl alcohol (PVA)-sodium alginate (SA) (6 and 2% [w/v], respectively) beads were inoculated into the column reactors at a packing ratio of 50% (v/v). The gel immobilization of *B. sinica* cells in PVA-SA gel beads was performed as previously described (Ali *et al.*, 2015). Briefly, the planktonic cells of *B. sinica* collected from the above MBR were resuspended in culture media, and mixed with an equal volume of PVA-alginate (FUJIFILM Wako) solution (12 and 4% [w/v], respectively). The gel solution was dropped using a disposable 50-mL plastic syringe (Terumo) into a 4% (w/v) CaCl_2 solution to form gel beads (diameter of *ca.* 2 mm). After an overnight incubation at 20°C , gel beads were washed with fresh inorganic medium. The gel beads obtained were inoculated into the up-flow column reactors.

Chemical analysis

NH_4^+ , NO_2^- , and NO_3^- concentrations were measured using the ion chromatograph IC-2010 equipped with the TSKgel SuperIC-Anion HS or TSKgel SuperIC-Cation HS column (Tosoh). NH_2OH concentrations were measured colorimetrically (Frear and Burrell, 1955). Briefly, liquid samples were mixed with 0.48% (w/v) trichloroacetic acid, 0.2% (w/v) 8-hydroxyquinoline, and 0.2 M Na_2CO_3 , heated at 100°C for 1 min , and absorbance was then measured at a wavelength of 705 nm using the spectrophotometer V-630bio (Jasco). N_2H_4 concentrations were measured colorimetrically using *p*-dimethyl-aminobenzaldehyde (Watt and Chrisp, 1952). Briefly, liquid samples were mixed with 0.12 M *p*-dimethyl-aminobenzaldehyde, and absorbance was measured at a wavelength of 460 nm .

$^{14-15}\text{N}_2$ and $^{15-15}\text{N}_2$ concentrations were measured by gas chromatography mass spectrometry (GC/MS) (Isobe *et al.*, 2011a; 2011b). Fifty microliters of the headspace gas was collected using a $100\text{-}\mu\text{L}$ gas-tight glass syringe and immediately injected into the gas chromatograph GCMS-QP 2010 SE (Shimadzu) equipped with a fused silica capillary column (Agilent Technologies). Peaks at $m/z=29$ and 30 corresponding to $^{14-15}\text{N}_2$ and $^{15-15}\text{N}_2$ were monitored, and concentrations were calculated using a standard curve prepared using $^{15-15}\text{N}_2$ gas (Cambridge Isotope Laboratories). The $^{14-15}\text{N}_2$ and $^{15-15}\text{N}_2$ concentrations of $^{15}\text{NH}_2\text{OH}$ were calculated by considering the ^{15}N enrichment of $^{15}\text{NH}_2\text{OH} \cdot \text{HCl}$ (^{15}N , 98%) and

the natural abundance of ¹⁴⁻¹⁵N₂ and ¹⁵⁻¹⁵N₂ in atmospheric N₂ gas contaminated at the injection of the gas sample.

qPCR assay

The copy numbers of the anammox bacterial 16S rRNA gene were measured using a qPCR assay. Genomic DNA was extracted from gel beads collected from the up-flow column reactors using the FastDNA SPIN kit (Qiagen) according to the instruction manual supplied by the manufacturer. The qPCR assay was conducted using the ABI7500 fast Real-Time PCR System (Thermo Fisher Scientific) and Premix Ex Taq (Probe qPCR) (TakaraBio) under previously described thermal conditions (Zhang and Okabe, 2017a). The oligonucleotide primers and TaqMan probe used for the PCR amplification of the *B. sinica* 16S rRNA gene were BRS95F, BRS170R, and BRS130P. Standard curves (10¹ to 10⁶ copies μL⁻¹) were prepared using a dilution series of plasmid DNAs containing a partial *B. sinica* 16S rRNA gene sequence.

Results

NH₂OH disproportionation by phylogenetically different anammox bacteria

Anammox bacterial cells of *B. sinica*, *J. caeni*, and *Scalindua* sp. were incubated with the addition of 1.0 to 2.5 mM ¹⁵NH₂OH. As shown in Fig. 1a, c, and e, ¹⁵NH₂OH consumption occurred in the culture concurrently with the production of ¹⁵⁻¹⁵N₂ gas and NH₄⁺. N₂H₄ was also produced and markedly increased when NH₂OH concentrations decreased below 0.1 mM (*i.e.*, a 60-min incubation for *B. sinica* and *Scalindua* sp. and a 120-min incubation for *J. caeni*). ¹⁴⁻¹⁵N₂, NO₂⁻, and NO₃⁻ were not detected during any incubations, and ¹⁵NH₂OH consumption was negligible in vials without anammox bacterial cells (*i.e.*, abiotic control incubation).

Batch incubations were repeated with the addition of 30 μM acetylene. Anammox bacterial cells consumed ¹⁵NH₂OH (Fig. 1b, d, and f), whereas consumption rates were >3-fold lower than those without acetylene. Although ¹⁵⁻¹⁵N₂ gas and NH₄⁺ were produced during the incubation, N₂H₄ was not produced in any anammox bacterial cultures.

The above batch incubation of *B. sinica* was repeated with an increase in the initial NH₂OH concentration (from 5 to 10 mM) with/without 30 μM acetylene. As shown in Fig. 2, ¹⁵NH₂OH consumption and the concomitant production of ¹⁵⁻¹⁵N₂ and NH₄⁺ occurred, similar to the batch incubation with the addition of 2.5 mM ¹⁵NH₂OH (*i.e.*, Fig. 1a and b). It is important to note that N₂H₄ production only occurred when NH₂OH concentrations decreased below 1.5 mM (Fig. 2a after 7.5 h of the incubation), and N₂H₄ production was not observed in Fig. 2c and e.

The stoichiometry and nitrogen mass balance of the above batch incubations are shown in Table 1. The theoretical values for Δ¹⁵⁻¹⁵N₂/Δ¹⁵NH₂OH and Δ¹⁵NH₄⁺/Δ¹⁵NH₂OH were 0.33 and 0.33, respectively when NH₂OH disproportionation occurred according to eq. 2. The values for Δ¹⁵⁻¹⁵N₂/Δ¹⁵NH₂OH and Δ¹⁵NH₄⁺/Δ¹⁵NH₂OH obtained from batch incubations with the addition of 2.5 or 5 mM ¹⁵NH₂OH were in the range of 0.19–0.45 and 0.17–0.36, respectively. These values were generally close to the theoretical values and those for Δ¹⁵NH₄⁺/Δ¹⁵NH₂OH in the *K. stuttgartiensis* culture (0.19–0.48), except for the following batch incu-

bations: *B. sinica* with 2.5 mM ¹⁵NH₂OH without acetylene (0.2 for Δ¹⁵NH₄⁺/Δ¹⁵NH₂OH), *B. sinica* with 5 mM ¹⁵NH₂OH with acetylene (0.19 for Δ¹⁵⁻¹⁵N₂/Δ¹⁵NH₂OH), and *Scalindua* sp. with 2.5 mM ¹⁵NH₂OH with and without acetylene (0.17 or 0.21 for Δ¹⁵NH₄⁺/Δ¹⁵NH₂OH). Batch incubations of *B. sinica* with 7.5 or 10 mM NH₂OH generally resulted in lower values for Δ¹⁵⁻¹⁵N₂/Δ¹⁵NH₂OH and Δ¹⁵NH₄⁺/Δ¹⁵NH₂OH, which were in the ranges of 0.14–0.19 and 0.09–0.19, respectively.

Cultivation of *B. sinica* with NH₂OH in up-flow column reactors

NH₂OH consumption and the abundance of the anammox bacterial 16S rRNA gene were examined in the 1) NH₂OH-, 2) NH₂OH and NH₄⁺-, and 3) NH₂OH and NO₂⁻-feeding up-flow column reactors. In all operated reactors, NH₂OH consumption markedly decreased after 7 d of operation, and halted after 15 d of operation (Fig. 3). NH₄⁺ concentrations in the effluents of the NH₂OH- and NH₂OH and NO₂⁻-feeding reactors were in the same range (Fig. 3a and c, respectively), and the consumption of NH₄⁺ did not occur in the NH₂OH and NH₄⁺-feeding reactor (Fig. 3b). The copy numbers of the anammox bacterial 16S rRNA gene decreased over time, and its abundance after 14 d of operation was an order of magnitude less than that after 1 d of operation. Copy numbers were not measured in the reactor fed with NH₂OH and NO₂⁻ (Fig. 3c).

Discussion

NH₂OH disproportionation was examined using phylogenetically different anammox bacteria, and the present study clearly indicated that NH₂OH disproportionation is a common nitrogen transformation process of anammox bacteria (Table 1). Although previous studies (van der Star *et al.*, 2008; Soler-Jofra *et al.*, 2020) reported anammox bacterial NH₂OH disproportionation, they did not examine the amount of N₂ gas produced. The present study performed sophisticated ¹⁵NH₂OH-tracing batch incubations, and revealed that anammox bacteria yielded both N₂ gas and NH₄⁺ from NH₂OH disproportionation. ¹⁵NH₂OH-tracing batch incubations enabled the stoichiometry of ¹⁵⁻¹⁵N₂ and ¹⁵NH₄⁺ production to ¹⁵NH₂OH consumption to be examined (Table 1), and the results obtained indicated that an increase in the initial concentration of NH₂OH resulted in a decrease in Δ¹⁵⁻¹⁵N₂/Δ¹⁵NH₂OH and Δ¹⁵NH₄⁺/Δ¹⁵NH₂OH for *B. sinica*. Furthermore, the addition of acetylene resulted in a decrease and increase in Δ¹⁵⁻¹⁵N₂/Δ¹⁵NH₂OH and Δ¹⁵NH₄⁺/Δ¹⁵NH₂OH, respectively. These variations in stoichiometry suggested that ¹⁵N₂ and/or ¹⁵NH₄⁺ were produced by multiple nitrogen transformation pathways other than NH₂OH disproportionation. Anammox bacterial hydroxylamine dehydrogenase oxidizes NH₂OH to NO (Maalcke *et al.*, 2014), and N₂ gas may be produced using the NO formed by the anammox process (the coupling of NH₄⁺ and NO) (Kartal *et al.*, 2013). Although the reduction of NH₂OH to NH₄⁺ by anammox bacterial cells has not yet been demonstrated, anammox bacteria are capable of dissimilatory nitrite reduction to ammonium (Kartal *et al.*, 2007).

N₂ and NH₄⁺-forming NH₂OH disproportionation has not

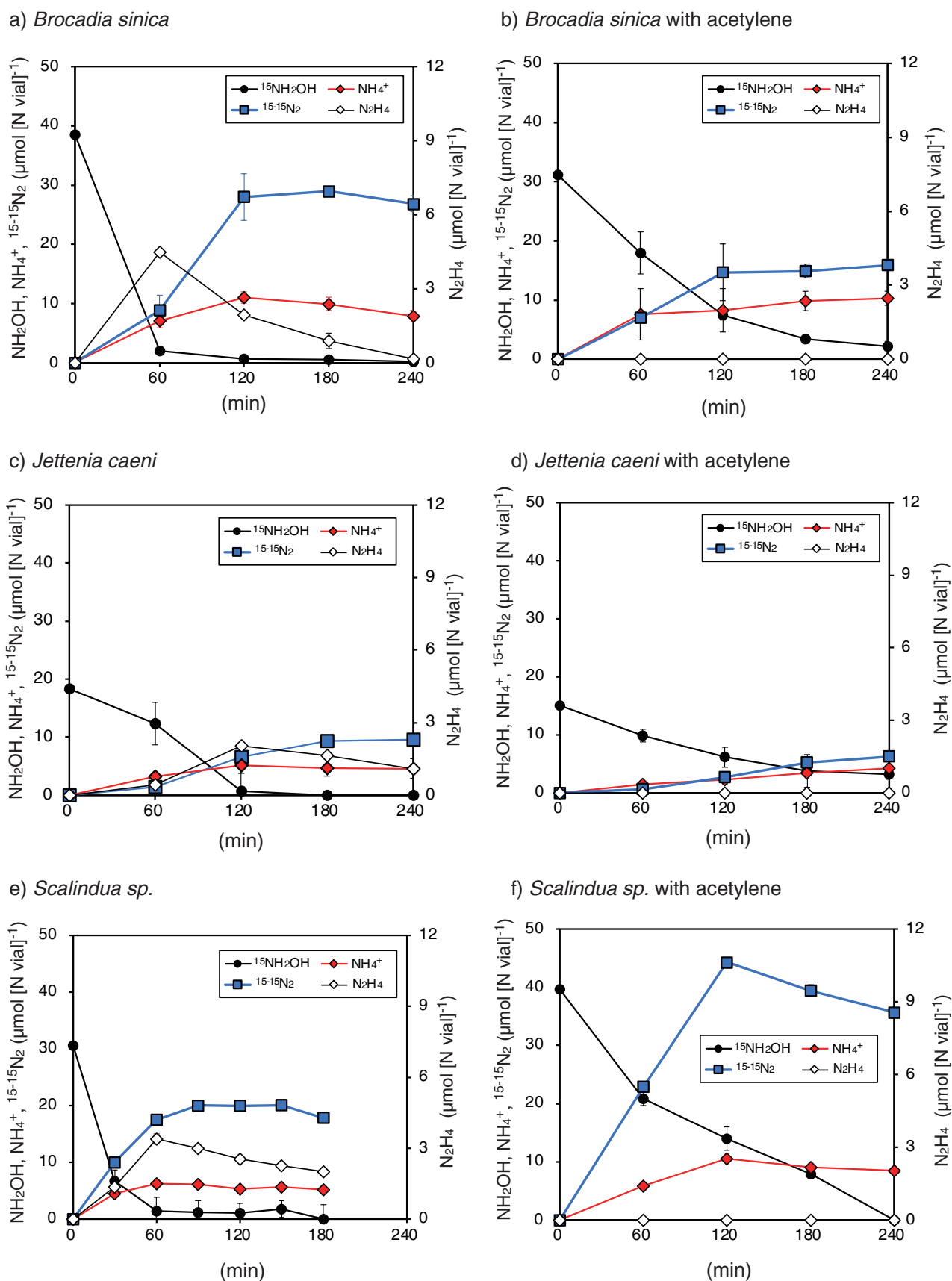


Fig. 1. $^{15}\text{NH}_2\text{OH}$ -tracing batch incubations to demonstrate anammox bacterial NH_2OH disproportionation. Twenty-five milliliters of *Brocadia sinica* (panel a and b), *Jettenia caeni* (panel c and d), and *Scalindua sp.* (panel e and f) cultures were incubated with the addition of 2.5 mM $^{15}\text{NH}_2\text{OH}$ in 70-mL glass vials. Incubations were repeated with the addition of 30 μM acetylene (panel b, d, and f). All incubations were performed in triplicate, and symbols and error bars represent mean values and the range of standard deviations, respectively. The standard deviations of data points are often within the symbols.

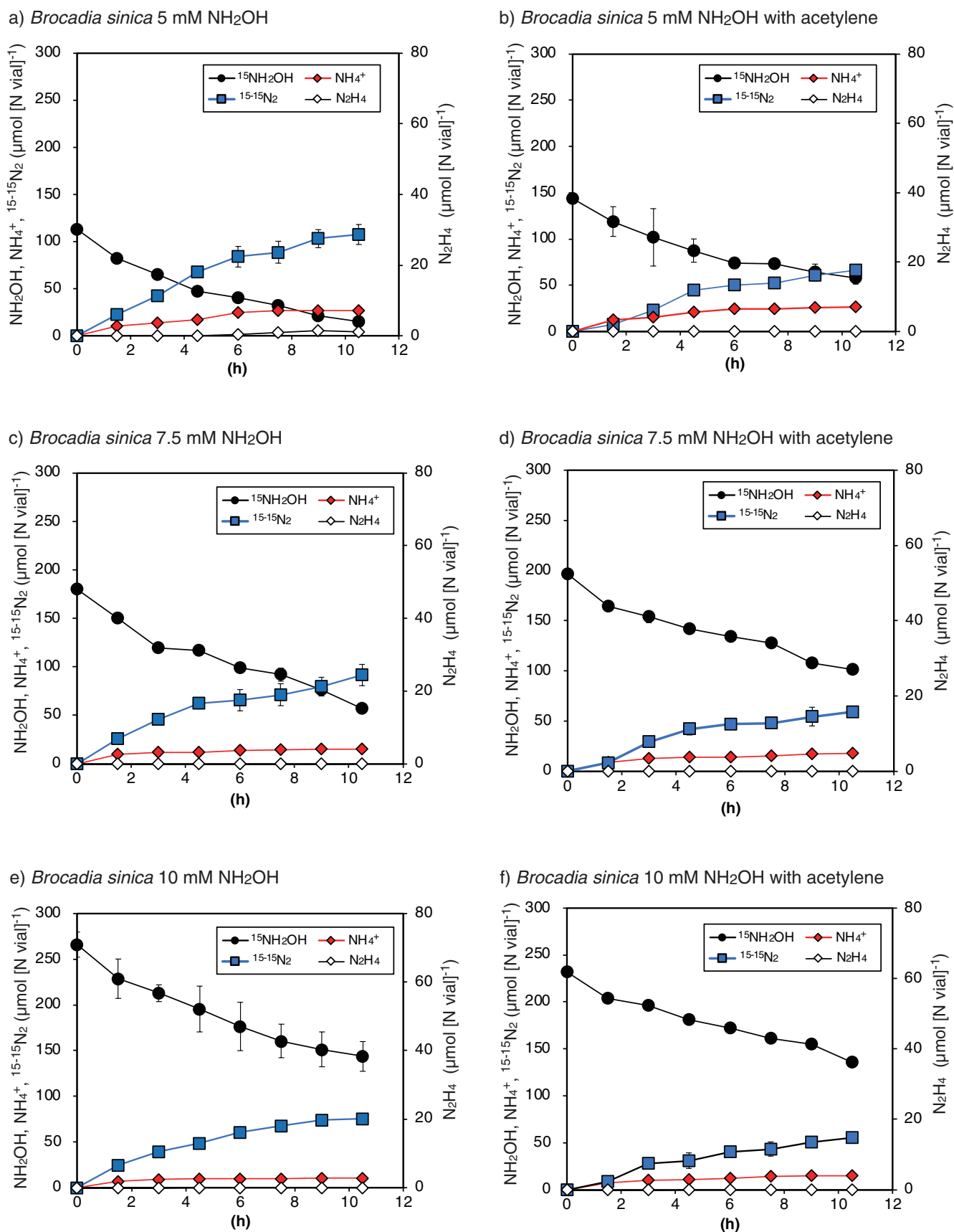


Fig. 2. Effects of the initial NH_2OH concentration on NH_2OH disproportionation by *Brocadia sinica*. Twenty-five milliliters of the *Brocadia sinica* culture was incubated with the addition of 5 mM (panel a and b), 7.5 mM (panel c and d), and 10 mM $^{15}\text{NH}_2\text{OH}$ (panel e and f) in 70-mL glass vials. Incubations were repeated with the addition of 30 μM acetylene (panel b, d, and f). All incubations were performed in triplicate, and symbols and error bars represent mean values and the range of standard deviations, respectively. The standard deviations of data points are often within the symbols.

Table 1. Stoichiometry of NH_2OH disproportionation mediated by anammox bacteria. The values obtained in the present study were mean values from triplicate biological replicates, and values were calculated from the initial and final concentrations during batch incubations. The N-mass balance (%) was calculated by dividing the total amounts of $^{15}\text{NH}_2\text{OH}$, $^{15}\text{NH}_4^+$, and $^{15-15}\text{N}_2$ at the end of the incubation ($\mu\text{mol} [\text{N vial}]^{-1}$) by the initial amounts of $^{15}\text{NH}_2\text{OH}$ ($\mu\text{mol} [\text{N vial}]^{-1}$).

Species	NH_2OH (mM)	Acetylene*	N-mass balance	$\Delta^{15-15}\text{N}_2/\Delta\text{NH}_2\text{OH}$ (mol/mol)	$\Delta^{15}\text{NH}_4^+/\Delta\text{NH}_2\text{OH}$ (mol/mol)	References
<i>B. sinica</i>	2.5	w/o	91%	0.35	0.20	This study
	5	w/o	85%	0.28	0.27	
	7.5	w/o	66%	0.19	0.12	
	10	w/o	72%	0.16	0.09	
	2	+	91%	0.27	0.35	
	5	+	81%	0.19	0.30	
	7.5	+	76%	0.16	0.19	
<i>J. caeni</i>	1	w/o	83%	0.26	0.25	
		+	91%	0.26	0.36	
<i>Scalindua sp.</i>	2	w/o	82%	0.29	0.17	
	2.5	+	111%	0.45	0.21	
<i>K. stuttgartiensis</i>	1.6–10	w/o	NA	ND	0.19–0.48	van der Star <i>et al.</i> , 2008 Soler-Jofra <i>et al.</i> , 2020
<i>B. flugida</i>	4	w/o	NA	ND	0.25	van der Star <i>et al.</i> , 2008

*; w/o and +: without and with the addition of 30 μM acetylene, respectively, NA: not available, ND: not determined.

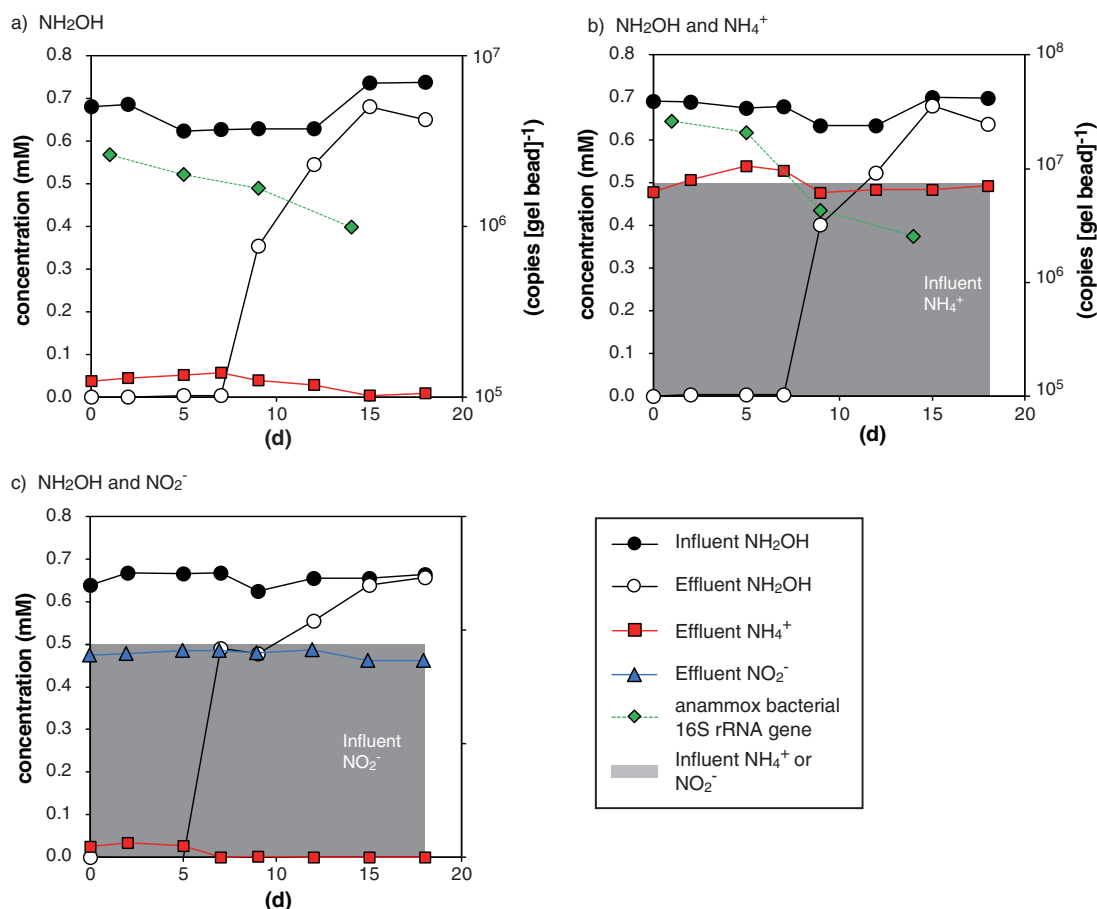


Fig. 3. NH_2OH consumption by *Brocadia sinica* in continuous up-flow column reactors. Up-flow column reactors were inoculated with PVA-SA gel beads immobilizing *B. sinica* cells and were operated with the continuous feeding of NH_2OH (panel a), NH_2OH and NH_4^+ (panel b), and NH_2OH and NO_2^- (panel c).

yet been reported for microorganisms other than anammox bacteria. It requires the formation of a nitrogen-nitrogen bond for N_2 gas, and only nitric oxide reductase and hydrazine synthase catalyze this reaction (Dietl *et al.*, 2015). This may be the reason why N_2 and NH_4^+ -forming NH_2OH dis-

proportionation has not yet been detected in microbial cultures other than anammox bacteria. Apart from N_2 and NH_4^+ -forming NH_2OH disproportionation, 1) NH_4^+ and NO_2^- , 2) NH_4^+ and NO_2^- , and 3) N_2O and NH_4^+ -forming NH_2OH disproportionation are thermodynamically favora-

ble (Pacheco *et al.*, 2011); however, limited information is currently available on their activities or involvement in the nitrogen transformation process in natural and man-made ecosystems.

The addition of acetylene did not induce the accumulation of N₂H₄, but reduced NH₂OH consumption (Fig. 1b, d, and f), which indicated that acetylene inhibited the enzymes involved in both NH₂OH consumption and N₂H₄ production reactions. *B. sinica* hydrazine synthase utilizes NH₂OH as a substrate for N₂H₄ synthesis (Oshiki *et al.*, 2016a); therefore, hydrazine synthase may be the enzyme that is inhibited by acetylene. The inhibition of anammox bacterial activity by acetylene has been reported (Jensen *et al.*, 2007); however, the underlying mechanism(s) remain unknown. Apart from hydrazine synthase, acetylene inhibited the NO₂⁻ reduction reaction of anammox bacteria (Kartal *et al.*, 2011; Oshiki *et al.*, 2016a), indicating that acetylene suppresses multiple nitrogen transformation reactions of anammox bacteria. Although the acetylene inhibition of copper-containing metalloproteins, such as ammonia monooxygenase and nitrous oxide reductase (Amo and Nos, respectively) has been described (Ensign *et al.*, 1993; Gilch *et al.*, 2009), the involvement of copper-containing metalloproteins in anammox bacterial metabolism, particularly N₂H₄ production, remains unclear. The binding site of acetylene to anammox bacterial enzymes is of interest for obtaining a more detailed understanding of the acetylene inhibition of anammox bacteria. The addition of 30 μM acetylene did not completely inhibit the production of ¹⁵⁻¹⁵N₂ gas or NH₄⁺ (Fig. 1 and 2). This result suggests the incomplete inhibition of anammox bacterial hydrazine synthase with the addition of 30 μM acetylene (Jensen *et al.*, 2007) and/or the production of ¹⁵⁻¹⁵N₂ gas and NH₄⁺, but not through N₂H₄. The corresponding mechanism has not yet been elucidated, and a further understanding of acetylene inhibition by anammox bacteria will provide novel insights.

Apart from the above acetylene inhibition, high NH₂OH concentrations (>0.1 mM NH₂OH in Fig 1a, c, and e, and >1.5 mM NH₂OH in Fig. 2a) did not induce the accumulation of N₂H₄. This behavior cannot simply be explained by the inhibition of anammox bacterial hydrazine dehydrogenase involved in N₂H₄ oxidation to N₂. The N₂H₄ oxidation activities of purified anammox bacterial hydrazine dehydrogenase were inhibited in the presence of 2.4 to 7.9 μM NH₂OH (Shimamura *et al.*, 2007; Maalcke *et al.*, 2016), and this inhibition provides an explanation for the accumulation of N₂H₄ during batch incubations, but not for the lack of its accumulation at high NH₂OH concentrations. On the other hand, anammox bacterial N₂H₄ accumulation may be explained by the balance between N₂H₄ production and consumption reactions (eq. 3 and 4, respectively), as reported in previous studies (van der Star *et al.*, 2008; Soler-Jofra *et al.*, 2020). N₂H₄ production and consumption reactions require 1 and 2 moles of NH₂OH, respectively, and higher NH₂OH concentrations increase N₂H₄ consumption rates more than N₂H₄ production rates; therefore, N₂H₄ does not accumulate at high NH₂OH concentrations. The affinity constants of eq. 3 and 4 for NH₂OH need to be examined in more detail in order to clarify the N₂H₄ accumulation behavior of anammox bacterial cells.

The results of the up-flow column reactor experiments revealed that *B. sinica* did not proliferate with NH₂OH disproportionation (Fig. 3), and this is the first experimental evidence to show that an anammox culture cannot be maintained with NH₂OH as the sole energy source. A 1 log reduction in the *B. sinica* 16S rRNA gene copy number clearly indicated that *B. sinica* did not proliferate in the operated reactors. *B. sinica* cells may have been compromised during reactor operation due to the high toxicity and mutagenesis of NH₂OH, which resulted in a decrease in the *B. sinica* 16S rRNA gene copy number in PVA-SA gel beads. We previously reported a log reduction in the anammox bacterial 16S rRNA gene copy number in PVA-SA gel beads under unfavorable cultivation conditions (Zhang *et al.*, 2017b). It is important to note that *B. sinica* cells preferentially performed NH₂OH disproportionation over anammox. Anammox using NO₂⁻ or NH₂OH did not occur in the NH₂OH and NO₂⁻ or NH₂OH and NH₄⁺-feeding reactors (Fig. 3c and b, respectively), which indicated that the anammox activities of *B. sinica* were inhibited in these reactors by NH₂OH. Therefore, low NH₂OH concentrations need to be maintained in order to avoid the inhibition of anammox activities and achieve the stable performance of nitrogen removal. Although the inhibitory effects of NH₂OH on nitrifying bacteria have been investigated (Kindaichi *et al.*, 2004; Soler-Jofra *et al.*, 2021), the IC₅₀ concentration of NH₂OH for anammox bacteria has not yet been systematically examined. In the present study, the sudden deterioration of NH₂OH consumption occurred after 7 d of operation; however, the concentration of NH₂OH in the influent was markedly lower than those in batch incubations in which the marked deterioration of NH₂OH consumption did not occur (*i.e.*, 0.7 and 2.5–10 mM, respectively). Therefore, it was not possible to approximate the IC₅₀ concentration of NH₂OH inhibition from short-term batch incubations, and further studies are warranted to assess the IC₅₀ concentration of the long-term inhibition of NH₂OH. NH₂OH may accumulate at the submicromolar range in natural aquatic environments (Fukumori *et al.*, 2003; Bikhulatova *et al.*, 2007) and at the submillimolar range in nitrifying cultures (Soler-Jofra *et al.*, 2021 and references therein); however, the impact of NH₂OH on nitrogen transformation reactions remains unclear. Further studies are needed to examine NH₂OH transformation, including anammox bacterial NH₂OH disproportionation, in natural and man-made ecosystems.

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References

- Ali, M., Oshiki, M., Rathnayake, L., Ishii, S., Satoh, H., and Okabe, S. (2015) Rapid and successful start-up of anammox process by immobilizing the minimal quantity of biomass in PVA-SA gel beads. *Water Res* 79: 147–157.

- Amano, T., Yoshinaga, I., Okada, K., Yamagishi, T., Ueda, S., Obuchi, A., *et al.* (2007) Detection of anammox activity and diversity of anammox bacteria-related 16S rRNA genes in coastal marine sediment in Japan. *Microbes Environ* **22**: 232–242.
- Bikbulatova, E.M., Stepanova, I.E., and Bikbulatov, E.S. (2007) Concentration and localization of hydroxylamine in the reservoirs and lakes in the territory of European Russia. *Water Resour* **34**: 554–562.
- Daims, H., Brühl, A., Amann, R., Schleifer, K.H., and Wagner, M. (1999) The domain-specific probe EUB338 is insufficient for the detection of all bacteria. Development and evaluation of a more comprehensive probe set. *Syst Appl Microbiol* **22**: 434–444.
- Dietl, A., Ferousi, C., Maalcke, W.J., Menzel, A., Vries, S. de, Keltjens, J.T., *et al.* (2015) The inner workings of the hydrazine synthase multiprotein complex. *Nature* **527**: 394–397.
- Egli, K., Bosshard, F., Werlen, C., Lais, P., Siegrist, H., Zehnder, A.J.B., and van der Meer, J.R. (2003) Microbial composition and structure of a rotating biological contactor biofilm treating ammonium-rich wastewater without organic carbon. *Microb Ecol* **45**: 419–432.
- Ensign, S.A., Hyman, M.R., and Arp, D.J. (1993) In vitro activation of ammonia monooxygenase from *Nitrosomonas europaea* by copper. *J Bacteriol* **175**: 1971–1980.
- Ferousi, C., Schmitz, R.A., Maalcke, W.J., Lindhoud, S., Versantvoort, W., Jetten, M.S.M., *et al.* (2021) Characterization of a nitrite-reducing octaheme hydroxylamine oxidoreductase that lacks the tyrosine cross-link. *J Biol Chem* **296**: 100476.
- Finster, K. (2008) Microbiological disproportionation of inorganic sulfur compounds. *J Sulfur Chem* **29**: 281–292.
- Frear, D.S., and Burrell, R.C. (1955) Spectrophotometric method for determining hydroxylamine reductase activity in higher plants. *Anal Chem* **27**: 1664–1665.
- Fukumori, R., Senga, Y., Okumura, M., Fujinaga, K., and Seike, Y. (2003) Pretreatment and pre concentration methods for hydroxylamine in environmental water samples using solid-phase extraction, followed by a spectrophotometric determination. *Bunseki Kagaku* **52**: 747–753 (in Japanese with an English abstract).
- Gilch, S., Vogel, M., Lorenz, M.W., Meyer, O., and Schmidt, I. (2009) Interaction of the mechanism-based inactivator acetylene with ammonia monooxygenase of *Nitrosomonas europaea*. *Microbiology* **155**: 279–284.
- Isobe, K., Koba, K., Ueda, S., Senoo, K., Harayama, S., and Suwa, Y. (2011a) A simple and rapid GC/MS method for the simultaneous determination of gaseous metabolites. *J Microbiol Methods* **84**: 46–51.
- Isobe, K., Suwa, Y., Ikutani, J., Kuroiwa, M., Makita, T., Takebayashi, Y., *et al.* (2011b) Analytical techniques for quantifying ¹⁵N/¹⁴N of nitrate, nitrite, total dissolved nitrogen and ammonium in environmental samples using a gas chromatograph equipped with a quadrupole mass spectrometer. *Microbes Environ* **26**: 46–53.
- Jensen, M.M., Thamdrup, B., and Dalsgaard, T. (2007) Effects of specific inhibitors on anammox and denitrification in marine sediments. *Appl Environ Microbiol* **73**: 3151–3158.
- Kartal, B., Kuypers, M.M.M., Lavik, G., Schalk, J., Op den Camp, H.J.M., Jetten, M.S.M., and Strous, M. (2007) Anammox bacteria disguised as denitrifiers: nitrate reduction to dinitrogen gas via nitrite and ammonium. *Environ Microbiol* **9**: 635–642.
- Kartal, B., Maalcke, W.J., de Almeida, N.M., Cirpus, I., Gloerich, J., Geerts, W., *et al.* (2011) Molecular mechanism of anaerobic ammonium oxidation. *Nature* **479**: 127–130.
- Kartal, B., de Almeida, N.M., Maalcke, W.J., Op den Camp, H.J.M., Jetten, M.S.M., and Keltjens, J.T. (2013) How to make a living from anaerobic ammonium oxidation. *FEMS Microbiol Rev* **37**: 428–461.
- Kindaichi, T., Okabe, S., Satoh, H., and Watanabe, Y. (2004) Effects of hydroxylamine on microbial community structure and function of autotrophic nitrifying biofilms determined by in situ hybridization and the use of microelectrodes. *Water Sci Technol* **49**: 61–68.
- Kindaichi, T., Awata, T., Suzuki, Y., Tanabe, K., Hatamoto, M., Ozaki, N., and Ohashi, A. (2011) Enrichment using an up-flow column reactor and community structure of marine anammox bacteria from coastal sediment. *Microbes Environ* **26**: 67–73.
- Kuypers, M.M.M., Slikers, A.O., Lavik, G., Schmid, M., Jørgensen, B.B., Kuenen, J.G., *et al.* (2003) Anaerobic ammonium oxidation by anammox bacteria in the Black Sea. *Nature* **422**: 608–611.
- Kuypers, M.M.M., Lavik, G., Woebken, D., Schmid, M., Fuchs, B.M., Amann, R., *et al.* (2005) Massive nitrogen loss from the Benguela upwelling system through anaerobic ammonium oxidation. *Proc Natl Acad Sci U S A* **102**: 6478–6483.
- Lotti, T., Kleerebezem, R., Lubello, C., and van Loosdrecht, M.C.M. (2014) Physiological and kinetic characterization of a suspended cell anammox culture. *Water Res* **60**: 1–14.
- Maalcke, W.J., Dietl, A., Marritt, S.J., Butt, J.N., Jetten, M.S.M., Keltjens, J.T., *et al.* (2014) Structural basis of biological NO generation by octaheme oxidoreductases. *J Biol Chem* **289**: 1228–1242.
- Maalcke, W.J., Reimann, J., de Vries, S., Butt, J.N., Dietl, A., Kip, N., *et al.* (2016) Characterization of anammox hydrazine dehydrogenase, a key N₂-producing enzyme in the global nitrogen cycle. *J Biol Chem* **291**: 17077–17092.
- Madigan, M.T., Bender, K.S., Buckley, D.H., Sattley, W.M., and Stahl, D.A. (2019) *Brock Biology of Microorganisms*, 15th edn. London: Pearson Education.
- Mulder, A., van de Graaf, A.A., Robertson, L.A., and Kuenen, J.G. (1995) Anaerobic ammonium oxidation discovered in a denitrifying fluidized bed reactor. *FEMS Microbiol Ecol* **16**: 177–183.
- Oshiki, M., Shimokawa, M., Fujii, N., Satoh, H., and Okabe, S. (2011) Physiological characteristics of the anaerobic ammonium-oxidizing bacterium “*Candidatus Brocadia sinica*.” *Microbiology* **157**: 1706–1713.
- Oshiki, M., Awata, T., Kindaichi, T., Satoh, H., and Okabe, S. (2013) Cultivation of planktonic anaerobic ammonium oxidation (anammox) bacteria by using membrane bioreactor. *Microbes Environ* **28**: 436–443.
- Oshiki, M., Ali, M., Shinyako-Hata, K., Satoh, H., and Okabe, S. (2016a) Hydroxylamine-dependent anaerobic ammonium oxidation (anammox) by “*Candidatus Brocadia sinica*.” *Environ Microbiol* **18**: 3133–3143.
- Oshiki, M., Satoh, H., and Okabe, S. (2016b) Ecology and physiology of anaerobic ammonium oxidizing (anammox) bacteria. *Environ Microbiol* **18**: 2784–2796.
- Pacheco, A.A., McGarry, J., Kostera, J., and Corona, A. (2011) Techniques for investigating hydroxylamine disproportionation by hydroxylamine oxidoreductases. *Methods Enzymol* **486**: 447–463.
- Quan, Z.X., Rhee, S.K., Zuo, J.E., Yang, Y., Bae, J.W., Park, J.R., *et al.* (2008) Diversity of ammonium-oxidizing bacteria in a granular sludge anaerobic ammonium-oxidizing (anammox) reactor. *Environ Microbiol* **10**: 3130–3139.
- Schmid, M., Schmitz-Esser, S., Jetten, M., and Wagner, M. (2001) 16S-23S rDNA intergenic spacer and 23S rDNA of anaerobic ammonium-oxidizing bacteria: Implications for phylogeny and in situ detection. *Environ Microbiol* **3**: 450–459.
- Shimamura, M., Nishiyama, T., Shigetomo, H., Toyomoto, T., Kawahara, Y., Furukawa, K., and Fujii, T. (2007) Isolation of a multiheme protein with features of a hydrazine-oxidizing enzyme from an anaerobic ammonium-oxidizing enrichment culture. *Appl Environ Microbiol* **73**: 1065–1072.
- Soler-Jofra, A., Laurenia, M., Warmerdama, M., Pérez, J., and van Loosdrecht, M.C.M. (2020) Hydroxylamine metabolism of *Ca. Kuenenia stuttgartiensis*. *Water Res* **184**: 116188.
- Soler-Jofra, A., Pérez, J., and van Loosdrecht, M.C.M. (2021) Hydroxylamine and the nitrogen cycle: A review. *Water Res* **190**: 116723.
- Strous, M., Fuenst, J., Kramer, E., Logemann, S., Muyzer, G., van de Pas-Schoonen, K., *et al.* (1999) Missing lithotroph identified as new planctomycete. *Nature* **400**: 446–449.
- Strous, M., Pelletier, E., Mangenot, S., Rattei, T., Lehner, A., Taylor, M., *et al.* (2006) Deciphering the evolution and metabolism of an anammox bacterium from a community genome. *Nature* **440**: 790–794.
- van de Graaf, A.A., de Bruijn, P., Robertson, L.A., Jetten, M.S.M., and Kuenen, J.G. (1996) Autotrophic growth of anaerobic ammonium-oxidizing micro-organisms in a fluidized bed reactor. *Microbiology* **142**: 2187–2196.
- van de Graaf, A.A., de Bruijn, P., Robertson, L.A., Jetten, M.S.M., and Kuenen, J.G. (1997) Metabolic pathway of anaerobic ammonium oxidation on the basis of ¹⁵N studies in a fluidized bed reactor. *Microbiology* **143**: 2415–2421.

- van der Star, W.R.L., van de Graaf, M.J., Kartal, B., Picoreanu, C., Jetten, M.S.M., and van Loosdrecht, M.C.M. (2008) Response of anaerobic ammonium-oxidizing bacteria to hydroxylamine. *Appl Environ Microbiol* **74**: 4417–4426.
- Watt, G.W., and Chrisp, J.D. (1952) A spectrophotometric method for the determination of hydrazine. *Anal Chem* **24**: 2006–2008.
- Yoshinaga, I., Amano, T., Yamagishi, T., Okada, K., Ueda, S., Sako, Y., and Suwa, Y. (2011) Distribution and diversity of anaerobic ammonium oxidation (anammox) bacteria in the sediment of a eutrophic freshwater lake, lake Kitaura, Japan. *Microbes Environ* **26**: 189–197.
- Zhang, L., and Okabe, S. (2017a) Rapid cultivation of free-living planktonic anammox cells. *Water Res* **127**: 204–210.
- Zhang, L., Narita, Y., Gao, L., Ali, M., Oshiki, M., and Okabe, S. (2017b) Maximum specific growth rate of anammox bacteria revisited. *Water Res* **116**: 296–303.
- Zhang, L., and Okabe, S. (2020) Ecological niche differentiation among anammox bacteria. *Water Res* **171**: 115468.