

This is the accepted manuscript version of the contribution published as:

Ding, C., Enyi, F.O., Adrian, L. (2018):

Anaerobic ammonium oxidation (anammox) with planktonic cells in a redox-stable semicontinuous stirred-tank reactor

Environ. Sci. Technol. **52** (10), 5671 - 5681

The publisher's version is available at:

<http://dx.doi.org/10.1021/acs.est.7b05979>

1 **Anaerobic ammonium oxidation (anammox) with planktonic cells**
2 **in a redox-stable semi-continuous stirred-tank reactor**

3 Chang Ding^{1,*}, Francis O. Enyi¹, Lorenz Adrian^{1,2}

4 ¹Helmholtz Centre for Environmental Research – UFZ, Isotope Biogeochemistry, Permoserstraße 15,
5 04318 Leipzig, Germany

6 ²Chair of Geobiotechnology, Technische Universität Berlin, Ackerstraße 76, 13355 Berlin, Germany

7

8 Running title: Planktonic anammox cultivation in semi-CSTR

9

10 *To whom correspondence should be addressed:

11 Chang Ding, Helmholtz Centre for Environmental Research – UFZ, Isotope Biogeochemistry,
12 Permoserstraße 15, 04318 Leipzig, Germany, Tel.: +49 (0) 341 235 1412, Fax: +49 (0) 341 235 1443,
13 E-Mail: chang.ding@ufz.de

14

15 Keywords: anammox, reactor design, semi-continuous stirred-tank reactor (semi-CSTR), “*Candidatus*
16 *Kuenenia stuttgartiensis*”, ammonium removal, anammox stoichiometry

17 Abstract

18 Anaerobic ammonium oxidizing (anammox) bacteria are routinely cultivated in mixed culture in
19 biomass-retaining bioreactors or as planktonic cells in membrane bioreactors. Here we demonstrate
20 that anammox bacteria can also be cultivated as planktonic cells in a semi-continuous stirred-tank
21 reactor (semi-CSTR) with a specific growth rate μ of 0.33 d^{-1} at 30°C . Redox potential inside the
22 reactor stabilized at around 10 mV ($\pm 15 \text{ mV}$) (vs standard hydrogen electrode) without gas purging.
23 Reactor headspace pressure was used as a sensitive and real-time indicator for nitrogen evolution and
24 anammox activity. The reactor was dominated by an organism closely related to “*Candidatus*
25 *Kuenenia stuttgartiensis*” (~87% abundance) as shown by Illumina amplicon sequencing and
26 fluorescence *in situ* hybridization. Epifluorescence microscopy demonstrated that all cells were in their
27 planktonic form. Mass balance analysis revealed a nitrite/ammonium ratio of 1.270, a
28 nitrate/ammonium ratio of 0.238, and a biomass yield of 1.97 g volatile suspended solids per mole of
29 consumed ammonium. Batch experiments with the reactor effluent showed that anammox activities
30 were sensitive to sulfide ($\text{IC}_{50} = 5 \text{ }\mu\text{M}$) and chloramphenicol ($\text{IC}_{50} = 19 \text{ mg L}^{-1}$), much lower than
31 reported for granular anammox biomass. This study shows that semi-CSTR is a powerful tool to study
32 anammox bacteria.

33 **Introduction**

34 Anaerobic ammonium oxidation (“anammox”) is a microbially catalyzed process of great importance
35 both in the natural nitrogen cycle and in technical applications for removal of fixed nitrogen. In this
36 process bacteria gain energy by oxidizing ammonium, channeling the electrons through an energy-
37 fixing electron transport chain and reducing nitrite to nitrogen gas. The overall reaction is driven by a
38 redox potential difference of about 400 mV (under standard conditions). In comparison with standard
39 nitrogen removal, anammox plants can save energy and co-substrates. To enable anammox, both
40 ammonium and nitrite must be present at the same time. Such conditions occur in natural redox
41 gradient, but in technical plants delicate control is necessary.

42 In spite of strong efforts, it has not yet been possible to obtain a pure bacterial anammox culture but
43 detailed studies in mixed cultures revealed the phylogenetic affiliation,¹ the morphology,²
44 physiology,^{1,3} and biochemistry^{4,5} of the catalyzing bacteria. Metagenomics approaches have revealed
45 partial genomic information.⁶⁻¹² In the context of our study it is important to emphasize i) that all
46 known anammox organisms cluster within the orders Brocadiales or Planctomycetales¹³ of the phylum
47 Planctomycetes,¹⁴ ii) that all anammox organisms described grow slowly, with specific growth rates μ
48 of 0.022 to 0.33 corresponding to doubling times t_d between 32 and 2.1 days,^{13,15} and iii) that
49 anammox cells contain an anammoxosome, a DNA-free compartment containing all directly-involved
50 enzymes.^{14,16}

51 One of the first described and best characterized anammox organisms is “*Candidatus* Kuenenia
52 stuttgartiensis”, which is a physiological generalist, also able to use iron and manganese as electron
53 acceptors and a wide variety of electron donors for respiration.¹¹ Growth rates are described to be
54 0.06-0.23 (doubling times of 3-11 days).^{17,18} Its first draft genome was sequenced in 2006,¹¹ and first
55 proteomic analyses with a focus on anammoxosome proteins were described.¹⁹ Genes for the
56 biosynthesis of flagella were found suggesting that it could express a flagellum enabling the bacteria
57 to freely swim e.g. within oxygen gradients.¹⁴

58 Due to the long doubling times, most research groups cultivated anammox bacteria in biomass-
59 retaining reactors such as upflow anaerobic sludge blanket, sequencing batch, or membrane
60 bioreactors to achieve high cell densities and high volumetric anammox reactivity.^{17,20,21} However, the
61 formation of sludge or granules can strongly influence physiological and biochemical characteristics
62 and only in membrane bioreactors was it possible to grow anammox cells in planktonic form.¹⁷

63 The goal of the current study was to establish active anammox bacteria in a simple continuous stirred-
64 tank reactor. By eliminating biomass retention we sacrificed high cell density in favor of culture
65 homogeneity, sub-cultivation reproducibility, long-term reactor stability and high growth rates. We
66 hypothesized that such a system is suitable to characterize physiological properties of the inhabiting
67 microorganisms and to optimize cultivation conditions in the lab. In addition, we hypothesized that we
68 can use the effluent as a stable and homogeneous source for batch cultivations, enrichments and
69 eventually isolation of anammox organisms. Within such batch cultivations we aimed at the
70 characterization of the inhibitory effects of various effectors such as salt, nitrite, sulfide, and phosphate
71 to compare IC_{50} values between free-living and granular anammox biomass. Chloramphenicol, a
72 potential inhibitor of denitrifying microbial populations and denitrification enzymatic activity,²² and
73 methylene blue, a redox indicator potentially useful for anammox cultivation, were specifically
74 evaluated in this study.

75 To achieve these goals, we here describe a semi-continuous stirred-tank reactor that is tightly
76 controlled especially in regard to redox-conditions, but also for pH, temperature, nutrients, electron
77 donors and electron acceptors and in which we use the headspace pressure as a key parameter for
78 reactor control. The reactor runs reproducibly with "*Ca. K. stuttgartiensis*" in planktonic form at high
79 growth rates. Batch cultivations with the effluent confirmed the success of the approach. Although the
80 main goal of this study was the description of reactor parameters at lab scale, our approach will be
81 extended to the description of reactors at pilot or full scale in the future.

82 **Material and Methods**

83 **Bacterial inoculum and media**

84 Anammox sludge granules from a sequencing batch reactor treating landfill leachate were kindly
85 provided by Prof. Yongzhen Peng (Beijing University of Technology) and were handled in an
86 anaerobic glovebox to provide strictly anoxic conditions.

87 Both, initial batch cultivation and reactor cultivation were done in an anoxic defined synthetic mineral
88 medium containing vitamins but no reducing agents. For initial batch cultivation in serum bottles,
89 cultures were inoculated with 10% vol/vol. To inoculate from granules, bottles were opened inside an
90 anaerobic glovebox and the inoculum was transferred with a sterile spatula. The reactor was semi-
91 continuously fed from three different solutions with ammonium, nitrite and mineral salts as the
92 principal components. All feeding solutions were degassed and purged with nitrogen to remove
93 oxygen. Details are described in the Supporting Information (SI) Methods.

94 **Reactor components and operation**

95 The reactor vessel was a “Widdelkolben”²³, an inverted 2.4 L Erlenmeyer flask with ports for medium
96 amendments, sampling and gas pressure measurements which were all done automatically and
97 controlled via a Raspberry Pi microprocessor (Figure 1 and SI Methods).

98 The reactor contained 2 L culture liquid and 400 mL headspace. Periodically, every 43-100 minutes,
99 depending on the chosen hydraulic retention time, 20 mL reactor suspension was pumped from the
100 reactor into the effluent bottle, and was replaced with 20 mL fresh medium (10 mL 40 mM nitrite
101 medium, 5 mL 120 mM ammonium medium and 5 mL salt medium). Details are given in the SI
102 Methods. Ammonium was always in excess to maintain a low redox potential and non-toxic nitrite
103 concentrations. The buildup of headspace pressure was continuously monitored and when it reached
104 7.71 kPa (sensor voltage output of 500 mV), a gas valve was opened for 30 s to release gas into the
105 gas collection bottle. This low threshold was set to minimize disturbance of the CO₂ layer in the
106 reactor headspace.

107 **Incubation of reactor effluent with inhibitory compounds**

108 In an anaerobic glovebox, 60 mL nitrogen-flushed glass bottles were filled with 50 mL reactor effluent
109 and closed with butyl rubber septa and aluminum crimp caps. Effectors were added within an
110 anaerobic glovebox with sterile syringes through the septa or directly added to the bottles as powder.
111 Except for the experiment in which nitrite was varied, 3 mM nitrite was added at time 0. Each bottle
112 was directly connected to a MPX5100DP pressure sensor via a 0.41 mm Luer Lock needle. All sensors
113 were electrically connected to a LabJack converter for data reading and storage. Pressure sensors were
114 read every 3 seconds. In total, twelve such bottles were set up for each experiment, allowing the
115 simultaneous testing of five different effector concentrations in duplicate plus two bottles as negative
116 controls without effector. Consistency of the obtained data between replicate bottles and correlation of
117 pressure build-up and effector concentration was demonstrated in an experiment where we tested the
118 effect of chloramphenicol on anammox activity (SI, Figure S1). In total, six effectors were tested in
119 this study: salt (NaCl, 30-940 mM), nitrite (3-35 mM), sulfide (Na₂S, 0-500 μM), phosphate (mixture
120 of K₂HPO₄ and KH₂PO₄, pH 7.2, 1.5-51.5 mM), chloramphenicol (0-1 g L⁻¹), and methylene blue (0-
121 10 mg L⁻¹).

122 Experiments were incubated for 24 hours after which 3 mL air was injected into each bottle for
123 calibration of the pressure sensor readings. Gas production rates were calculated as mL per day across
124 adjacent 1,000 consecutive data points (3,000 seconds). Maximum gas production was typically
125 reached after 10-14 hours. The same time frame was chosen for all twelve bottles in one experiment to
126 calculate anammox activities from the slopes.

127 **Analytical and microscopic techniques**

128 Ammonium concentrations were determined with a modified salicylate method.²⁴ In brief, samples
129 were diluted to an ammonium concentration below 0.15 mM, and 200 μL of these diluted samples
130 were sequentially mixed in a 96-well microplate with 50 μL bleach solution (120 mM NaOH, 0.15%
131 w/v sodium hypochlorite) and 50 μL catalyst solution (120 mM NaOH, 10% w/v sodium salicylate,
132 0.04% w/v sodium nitroferricyanide). Absorbance at 650 nm was measured on a Synergy 2 microplate

133 reader (Biotek, USA). This ammonium quantification method typically yielded a standard curve
134 linearity of >0.999 and a low standard deviation (<5%) among triplicates. Nitrate concentrations were
135 determined on a Dionex DS-120 ion chromatography with an IonPac AS4A-SC column and an eluent
136 containing 0.7 mM NaCO₃ and 0.7 mM NaHCO₃ at a flow rate of 1 mL min⁻¹. Due to tailing of the
137 chloride peak that immediately preceded the nitrite peak, nitrite could not be reliably quantified by ion
138 chromatography. Therefore, nitrite concentrations were determined separately with the Griess reagent
139 kit (Molecular Probes) according to the manufacturer's instructions. The detection limit of nitrite was
140 at ~0.05 mM.

141 To measure volatile suspended solids (VSS), 200 mL reactor effluent was filtered through 47-mm
142 diameter Whatman GF/F glass fiber filter (pore size 0.7 μm, GE Healthcare, USA) previously baked at
143 550°C for 1.5 h. After filtration the filter was dried overnight at 105°C and weighed to obtain the total
144 suspended solid (TSS) value. Then the filter was combusted at 550°C for 1.5 h to obtain the VSS value
145 from the difference of the weight. VSS analysis was done in triplicate.

146 Direct epifluorescence microscopic counting of SYBR-green stained cells on agarose-coated slides
147 and fluorescence *in situ* hybridization (FISH) of cells with 16S-rRNA-targeting probes are described
148 in the SI Methods.

149 **Microbial community analyses**

150 One milliliter of culture liquid was centrifuged at 10,000 g for 15 min at 4°C, and the resulting pellet
151 was used for extraction of genomic DNA using DNeasy Blood and Tissue kit (QIAGEN, Hilden,
152 Germany) according to manufacturer's instructions, except that 20 μL of lysozyme (100 mg mL⁻¹)
153 were added to facilitate cell lysis. Extracted DNA samples were stored at -20°C and used as template
154 for clone library construction and Illumina sequencing.

155 PCR amplification of 16S rRNA genes for clone library construction was done for 30 cycles using the
156 forward primer (338F 5'-ACT CCT ACG GGA GGC AGC AG-3' and 338F-AMX 5'-ACT CCT ACG
157 GGA GGC TGC AG-3', 0.05 μM each) and the reverse primer 1392R 5'-ACG GGC GGT GTG TRC-
158 3' (0.1 μM) with the annealing temperature of 55°C. Purified PCR products were ligated onto pGEM-

159 T vector (Promega) which was later transformed into *E. coli* competent cells. Clones were sequenced
160 by Sanger sequencing using the primers provided with the vector. Sequences have been deposited in
161 GenBank database under accession numbers MH040190 to MH040197.

162 For Illumina amplicon sequencing of the DNA from the initial batch culture, V3-V4 region of 16S
163 rRNA genes were amplified using the forward primer 338F 5'-ACT CCT ACG GGA GGC AGC AG-
164 3' and the reverse primer 806R 5'-GGA CTA CHV GGG TWT CTA AT-3'. Illumina MiSeq
165 sequencing (300 bp paired-end reads) was performed by BGI (Shenzhen, China). For Illumina
166 amplicon sequencing of the DNA from the reactor effluent, V3-V4 region of the 16S rRNA gene were
167 amplified using the forward primer 341F 5'-CCT ACG GGN GGC WGC AG-3' and the reverse primer
168 785R 5'-GAC TAC HVG GGT ATC TAA TCC-3'.²⁵ Illumina MiSeq sequencing (300 bp paired-end
169 reads) was performed by LGC Genomics (Berlin, Germany). All sequence reads were processed using
170 the NGS analysis pipeline of the SILVA rRNA gene database project (SILVAngs 1.3).²⁶ OTU
171 clustering threshold was 0.98 sequence identity. The classification was performed by a local
172 nucleotide BLAST search against the non-redundant version of the SILVA SSU Ref dataset (release
173 128). Classification threshold was 0.93 sequence similarity. Visualization of microbial population
174 abundance was done with Krona (www.krona.sourceforge.net).²⁷

175 The amplicon sequencing reads have been deposited under NCBI BioProject PRJNA437226, with
176 accession numbers SRX3778537 and SRX3778536 for the batch culture and the reactor effluent,
177 respectively.

178 **Results**

179 **Batch cultivation and microbial community analysis**

180 Suspended granules (30 mL) were obtained in August 2013 from an anammox reactor and stored
181 under nitrogen gas in a sealed 50-mL centrifuge tube at 4°C for almost one year because no
182 enrichment was planned at the time of sample receipt. The anammox enrichment process was started
183 in July 2014 using the stored sample, and 5 mL of the granules were transferred to 90 mL of batch

184 cultivation medium containing 3 mM nitrite and 4.6 mM ammonium. After two months of incubation,
185 nitrite was depleted in the bottle, and a 10% v/v inoculum was transferred to fresh medium. After
186 another two such transfers we obtained an active anammox culture free from granules and sludge. The
187 culture catalyzed conversion of 3 mM nitrite in ten days with concurrent decrease of ammonium
188 concentrations (Figure 2). A population analysis by sequencing clones from a 16S rRNA gene clone
189 library indicated that about a quarter of the detected 16S rRNA gene sequences (26.7%) were affiliated
190 with “*Ca. Kuenenia stuttgartiensis*”, whereas 56.7% were affiliated with the genus *Pseudomonas* (SI,
191 Table S1). With the same DNA sample, an Illumina amplicon sequencing was performed, confirming
192 that the culture was dominated by organisms described to catalyze the anammox process (“*Ca.*
193 *Kuenenia stuttgartiensis*”, 17.2% of the detected 16S rRNA gene sequences) and *Pseudomonas*
194 (70.3%), while the other OTUs were all at lower shares than 2% (Figure 3A).

195 To obtain sufficient culture liquid to inoculate the reactor, 100 mL of granule-free culture liquid was
196 transferred to 900 mL of medium containing 3 mM nitrite via nitrogen-flushed syringes and needles.
197 After 15 days of incubation the nitrite concentration was below the detection limit and the 1-L culture
198 was used for reactor inoculation.

199 **Reactor cultivation of “*Ca. Kuenenia stuttgartiensis*”**

200 A gas-tight semi-continuous stirred tank reactor (semi-CSTR) was constructed allowing strictly anoxic
201 reactor operation and real-time monitoring of pressure, redox potential, pH and temperature (Figure 1
202 and SI Methods). It allowed the amendment of nitrite and ammonium as the two main energy-
203 providing molecules from separate medium bottles. To start the reactor, the 1-L stem culture described
204 above was mixed with 1 L fresh batch cultivation medium containing 3 mM nitrite in the anaerobic
205 glovebox and transferred to the reactor. The reactor was started with a hydraulic retention time of 6.9
206 days, and influent nitrite and ammonium concentration of 20 mM and 30 mM, respectively. During
207 operation, the concentration of nitrite in the reactor effluent was constantly close to zero and gas was
208 produced continuously, demonstrating that the injected nitrogen compounds were used in the reactor.
209 When we decreased the hydraulic retention time by stepwise increase of the frequency of 1% medium

210 replacement, the effluent nitrite concentration stayed below 0.05 mM. In this way, the hydraulic
211 retention time was shortened to 3 days after 16 days of operation, corresponding to a dilution rate of
212 0.33 d^{-1} (SI, Figure S1). Note that in the well-mixed CSTR, the hydraulic retention time equals the
213 solid retention time, and therefore the dilution rate is the reciprocal of the hydraulic retention time at
214 steady state conditions. The chosen medium composition and reactor operation effected that the pH
215 was constantly between 7.3 and 7.6.

216 Previous studies on anammox bacteria showed that anammox activity depended on the redox potential
217 in the cultivation vessels,²⁸ and could be suppressed by nanomolar levels of oxygen.²⁹ We therefore
218 planned to provide a reducing agent to control the redox potential. However, long-time operation of
219 the reactor for over one year demonstrated that with the described reactor design, degassing of feeding
220 solutions and operation under exclusion of oxygen, no redox adjustment was necessary to maintain
221 redox potential inside the reactor, which stayed at around 10 mV (± 15 mV) vs the standard hydrogen
222 electrode (SHE). When the reactor flow was halted, the redox potential rose gradually to ~ 30 mV
223 within 26 h (SI, Figure S2). Once the reactor flow resumed, the redox potential instantly stopped rising
224 and slowly returned to the original level. After interrupting the reactor flow it took about 10 h for gas
225 production to completely cease, and another 5 h to regain full gas production rate after resuming the
226 reactor flow.

227 **Reactor recovery**

228 The reactor effluent was collected in nitrogen-flushed 2-L bottles and stored in the dark at 4°C to be
229 used later for inhibitor tests (see below) or as inoculum when the reactor collapsed. During one-year
230 operation under experimental conditions, the reactor collapsed three times under three different critical
231 conditions which were introduced unintentionally: 1) after the reactor was incubated for 24 h at 38.6°C
232 without feeding nitrite, 2) after we added a pulse of 0.2 mM Na_2S , and 3) after we added a pulse of 65
233 μM FeCl_2 from a separate FeCl_2 stock solution. The first two conditions led to complete loss of
234 anammox activity, while the third condition resulted in the formation of a thick precipitate in the
235 reactor which was presumably ferric oxides³⁰ and consequently stopped reactor operation. After such

236 reactor collapses, the reactor could be reproducibly reestablished with the stored eluent bottles. The
237 activity in the effluent bottles was recovered, as judged from pressure production rates, within only 2
238 days after a bottle was warmed up to room temperature, spiked with 3 mM nitrite and incubated at
239 30°C. Effluent could be stored at 4°C for at least three months without startup delay.

240 **Microbial community composition during reactor operation**

241 Under steady state conditions with a dilution rate of $\sim 0.33 \text{ d}^{-1}$ (hydraulic retention time of 3 days), no
242 granules developed in the reactor and the liquid changed to an orange color as has been described for
243 other anammox cultures.³¹ We performed FISH and Illumina amplicon sequencing after three-month
244 reactor operation at a dilution rate of $\sim 0.33 \text{ d}^{-1}$. The microbial cell density within the reactor was $7.6 \pm$
245 $1.3 \times 10^7 \text{ mL}^{-1}$. Direct microscopic analysis of SYBR Green stained cells also showed that the cells
246 were not assembling in aggregates, indicating that all cells in the reactor were in a planktonic form (SI,
247 Figure S3). The majority of the cells showed the typical morphology of anammox cells with a ring or
248 “c”-type shape indicating the presence of a DNA-free anammoxosome.¹⁹ The fluorescence intensity
249 was influenced by the concentration of SYBR Green dye applied and the incubation temperature (SI,
250 Figure S4).

251 To quantify the abundance of anammox-catalyzing organisms in the established reactor culture, FISH
252 was conducted using FAM-labeled EUB338-mix and cy5-labeled AMX820 probes for Eubacteria and
253 anammox bacteria, respectively, and DAPI as DNA-counterstain. Samples taken from the reactor
254 running steadily at a dilution rate of $\sim 0.33 \text{ d}^{-1}$ showed that the abundance of anammox organisms
255 increased to $\sim 85\%$ (Figure 4).

256 A second Illumina amplicon sequencing of the established reactor culture showed that the relative
257 share of “*Ca. Kuenenia*” 16S rRNA genes of the total detected 16S rRNA genes had increased to
258 around 75%, while bacteria of the genus *Pseudomonas* almost disappeared (0.007%) and were
259 replaced by heterotrophs such as *Methyloversatilis* (10.6%), *Azoarcus* (2.8%), *Melioribacter* (3.4%),
260 *Rubellimicrobium* (2.0%), and several genera within the *Lentimicrobiaceae* (1.5%) (Figure 3B). If the
261 genome of the “*Ca. Kuenenia stuttgartiensis*” strain in the reactor contains only one 16S rRNA gene

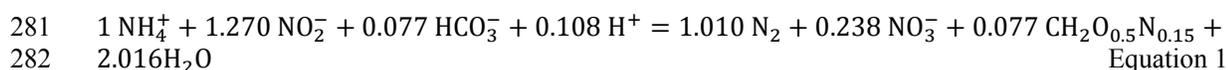
262 copy as described for the draft genome assembly of “*Ca. Kuenenia stuttgartiensis*”¹¹ and the other
263 detected strains in the reactor culture have the 16S rRNA gene copy numbers as given in *rrnDB*,³² the
264 adjusted anammox cell fraction in the reactor was around 87%.

265 **Stoichiometry of anaerobic ammonium oxidation in the reactor**

266 To calculate the stoichiometry of the anammox process, a correlation between the cell density and
267 VSS was first obtained. On day 30, the reactor effluent had a cell density of $8.5 \times 10^7 \text{ mL}^{-1}$ and a VSS
268 value of $48.1 (\pm 1.2) \text{ mg L}^{-1}$, giving a per cell weight of $5.65 \times 10^{-13} \text{ g VSS}$ which was used to convert
269 cell density to VSS in the nitrogen mass balance experiments below.

270 During a two-week monitoring period with a hydraulic retention time of 5.6 days, all nitrogen-
271 containing compounds flowing into and out of the reactor were measured (SI, Table S2) including
272 ammonium and nitrite in the reactor influent, ammonium, nitrite, nitrate and biomass in the reactor
273 effluent, and nitrogen gas evolution. The total cell density was converted to anammox cell density
274 using the anammox abundance observed above (87%). The elemental composition of the biomass was
275 assumed as $\text{CH}_2\text{O}_{0.5}\text{N}_{0.15}\text{S}_{0.05}$ according to published results for “*Ca. Brocadia*”³³. During the
276 monitoring period, 252.5 and 249.7 mmol of nitrogen flowed in and out of the reactor, respectively,
277 representing an almost closed mass balance (99.64%).

278 Data reconciliation³⁴ of the above measurements balancing nitrogen in- and output (SI, Table S2)
279 resulted in a balanced anammox stoichiometry as shown in Equation 1. Based on this stoichiometry,
280 biomass yield was 1.97 g VSS per mole of consumed ammonium.



283

284 **Incubations of the reactor effluent with various effectors**

285 An important advantage of the CSTR design was the homogeneity of the reactor effluent which can be
286 used for physiological characterization of anammox bacteria. For that we incubated the reactor
287 effluent in closed bottles and monitored the pressure build-up in the headspace over time (Figure 5).

288 For the six tested effectors, IC_{50} values were 183 mM (NaCl), 9.6 mM (nitrite), 5 μ M (sulfide), >51.5
289 mM (phosphate), 19 $mg L^{-1}$ (chloramphenicol), and 53 $\mu g L^{-1}$ (methylene blue). No apparent inhibition
290 was observed with salt concentrations up to 120 mM, while 270 mM caused 75% inhibition. Nitrite at
291 6 mM caused 24% inhibition. Sulfide severely inhibited anammox activity already at the very low
292 concentration of 5 μ M. Chloramphenicol induced 57% inhibition at a concentration of 30 $mg L^{-1}$. An
293 increase of anammox activity by 16% was observed when the phosphate concentration was increased
294 from 1.5 mM to 3.5 mM. At 6.5 mM phosphate, anammox activity was 11% higher than in the
295 controls at 1.5 mM. Therefore, a higher phosphate concentration may enhance anammox activity also
296 in the reactor. Still 65% of the anammox activity was preserved at the highest tested concentration of
297 51.5 mM phosphate. Whereas methylene blue caused no apparent inhibition of anammox activity at 10
298 $\mu g L^{-1}$, 100 $\mu g L^{-1}$ methylene blue caused 86% inhibition.

299 **Discussion**

300 **Semi-CSTR is a promising reactor design for anammox cultivation**

301 In this study, a semi-CSTR was successfully used for the cultivation of anammox cells in their
302 planktonic form. This and the previously described membrane bioreactors¹⁷ are the current two reactor
303 designs that produce planktonic anammox cells. Membrane bioreactors have been used to cultivate
304 “*Ca. Kuenenia stuttgartiensis*” ($\mu = 0.23 d^{-1}$), “*Ca. Brocadia sapporoensis*” ($\mu = 0.33 d^{-1}$), “*Ca.*
305 *Brocadia sinica*”, and “*Ca. Scalindua sp.*”.^{17,35,36} Our semi-CSTR was operating for more than three
306 months under a steady dilution rate of $\sim 0.33 d^{-1}$, indicating a specific growth rate (μ) of at least $0.33 d^{-1}$
307 for “*Ca. Kuenenia stuttgartiensis*”, which is higher than the previously reported value for this
308 species.¹⁷ The higher specific growth rate reported here is advantageous because it allows higher
309 dilution and nitrogen loading rates, thereby enabling a more efficient and stable anammox process.
310 Because we have not done a detailed analysis of the effect of the different cultivation parameters used
311 with our reactor, we cannot unambiguously connect any one parameter with this high growth rate.
312 Compared to membrane bioreactors, the basic design of our semi-CSTR is simpler and does not

313 require a sludge pump, a gas purging system, a water level sensor, or a membrane unit. Omission of
314 the membrane unit is especially advantageous as the membrane contributes significantly to the
315 investment and maintenance costs of membrane bioreactors, as the membrane unit needs to be
316 periodically cleaned after clogging or formation of biofilms on the membrane fibers.³¹ Our
317 microprocessor-controlled online-monitoring and controlling system introduces some complexity into
318 our system, however, the monitoring and controlling system is low-cost, flexible and implementable
319 without advanced programming knowledge.

320 When built as a laboratory-scale reactor, the CSTR design is very useful to precisely study the
321 microbiology, physiology and biochemistry of anammox bacteria due to its simple structure and
322 planktonic cell yield. Moreover, without the need for a gas supply system in our semi-CSTR, it is
323 possible to monitor headspace pressure change for rapid determination of anammox activity inside the
324 reactor (SI, Figure S2). The CSTR design may also be used in full scale wastewater treatment in the
325 future despite some apparent limitations. One of the limitations is that the dilution rate in CSTR
326 cannot be set above the growth rate of the anammox organisms, otherwise they will be diluted out of
327 the reactor. Membrane bioreactors, as well as other biomass-retaining reactors, decouple the solid
328 retention time from the hydraulic retention time, and therefore can be run with higher dilution rates.
329 Nevertheless, our semi-CSTR has already achieved a nitrogen removal rate of $0.21 \text{ kg-N m}^{-3} \text{ d}^{-1}$ when
330 operated at a dilution rate of 0.33 d^{-1} and an influent nitrite concentration of 20 mM. This value is only
331 slightly lower than the minimum nitrogen removal rate ($0.26 \text{ kg-N m}^{-3} \text{ d}^{-1}$) in existing full scale
332 anammox plants.³⁷ Another limitation of CSTR is that CSTR reactors are not able to provide biomass-
333 free effluent and therefore are more suitable in a side-stream process where the reactor effluent can be
334 directed to the mainstream process. With the above considerations, we believe the CSTR design has its
335 place in treating high-ammonium-content wastewater as a side-stream process and would be especially
336 attractive when a simple reactor design and low reactor maintenance are desired.

337 **Influence of oxygen and the redox potential on anammox**

338 Although anammox organisms can survive phases of oxic treatment in the lab, anammox activity is
339 extremely sensitive to oxygen.²⁹ On the other hand, anammox organisms are dependent on the
340 presence of nitrite, which is not available under strictly anoxic conditions. Therefore, anammox
341 bacteria are typical redox gradient organisms both in freshwater and marine habitats where they thrive
342 in so-called “oxygen minimum zones”.^{38,39} In a membrane bioreactor system, continuous bubbling
343 with 95% argon and 5% CO₂ was needed to maintain an oxygen-free environment.^{31,40} In contrast to
344 this intensive and expensive gas sparging, our CSTR design using degassed feeding solutions did not
345 require continuous gas purging to obtain stable growth of anammox cells.

346 In previous experiments oxygen also had a striking effect on the growth form of *Planctomycetes*: cells
347 of “*Ca. Brocadia sapporoensis*” started to aggregate in a membrane bioreactor when the oxygen
348 loading rate was $> 0.68 \mu\text{mol-O}_2 \text{ L}^{-1} \text{ d}^{-1}$.⁴⁰ In our semi-CSTR, cells of “*Ca. Kuenenia stuttgartiensis*”
349 were in their planktonic form throughout all reactor operations (Figure 4 and SI, Figure S3). Even after
350 exposure to air (21% oxygen) for 2 hours, no aggregates were formed in the reactor effluent as
351 observed by epifluorescence microscopy (images not shown). In summary, “*Ca. Brocadia*
352 *sapporoensis*” seems to aggregate more easily upon oxygen exposure than “*Ca. Kuenenia*
353 *stuttgartiensis*”.

354 Apart from dissolved oxygen, the redox potential is a parameter that greatly influences anammox
355 activities. Previous studies showed that anammox activities were maximal around 0 mV (vs SHE).^{28,41}
356 Indeed, the redox potential within our semi-CSTR stabilized at around 10 mV (± 15 mV) (vs SHE) as
357 long as the reactor was in operation (SI, Figure S2). The self-stabilization of the redox potential
358 without external manipulation such as reductant addition or gas purging is an interesting phenomenon,
359 and the underlying mechanism is worth further investigation. Currently we cannot attribute this redox
360 stabilization activity to either the anammox catalyzing population in the reactor or accompanying
361 populations.

362 **Growth rate and growth yield**

363 Since the demonstration of relatively fast growth of anammox bacteria in membrane bioreactors
364 anammox organisms have no longer been considered as slow-growing microorganisms.³⁶ So far, the
365 highest reported maximum growth rates for anammox bacteria were 0.33 d⁻¹ for “*Ca. Brocadia*”^{15,36}
366 and 0.18 d⁻¹ for “*Ca. Jettenia*”,¹⁵ corresponding to a steady state solid retention time of 3 days and 5.6
367 days, respectively. With our reactor design we gradually decreased the hydraulic retention time to 3
368 days within 16 days of reactor operation, corresponding to a dilution rate and bacterial specific growth
369 rate of $\mu = \sim 0.33 \text{ d}^{-1}$ at the steady state (SI, Figure S1). This was achieved without intensive
370 optimization of temperature, pH, or the medium recipe, and therefore there might be room for
371 improvement of the growth rate. For example, a relatively low iron concentration of 15 μM was used
372 in this study while a higher iron concentration may be beneficial.^{36,42} Also, adjusting the phosphate
373 concentration could enhance anammox activity as shown in the batch test (Figure 5D).

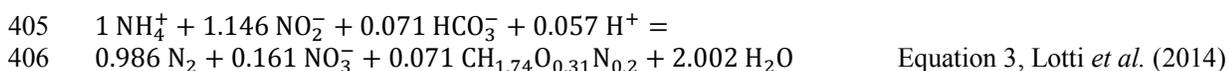
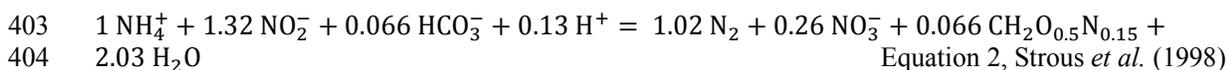
374 When the culture exhibited the highest growth rate, the specific anammox activity was 3.03 g NH₄ g⁻¹
375 VSS d⁻¹. This value is close to the one reported for “*Ca. Brocadia sapporoensis*” (3.38 g NH₄ g⁻¹ VSS
376 d⁻¹).³⁶ Given that these two species exhibited similar maximum growth rates and specific anammox
377 activity, these values may have approached the limit for freshwater anammox cells.

378 **Anammox stoichiometry**

379 The anammox stoichiometry for “*Ca. Kuenenia stuttgartiensis*” in our reactor was determined as given
380 in Equation 1 based on a two-week reactor operation and we compared this equation to two previously
381 determined equations for “*Ca. Brocadia anammoxidans*” (Equation 2)³³ and “*Ca. Brocadia*
382 *sapporoensis*” (Equation 3)⁴⁰ (Table 1). Our calculations are based on the two different biomass
383 formulae described by Strous *et al.* (1998) and Lotti *et al.* (2014), respectively. Two important values
384 in this calculation are the moles of consumed nitrite per mole of consumed ammonium (NO₂/NH₄) and
385 the moles of produced nitrate per mole of consumed ammonium (NO₃/NH₄). In such a comparison our
386 NO₂/NH₄ ratios of 1.270 and 1.249 for the two biomass formulae assumptions, respectively, are
387 between the NO₂/NH₄ ratio obtained by Strous *et al.* (1998) (1.320) and that obtained by Lotti *et al.*

388 (2014) (1.146). The NO_3/NH_4 ratio in our reactor (0.238 and 0.239 for the two biomass formula,
 389 respectively) is similar to that calculated by Strous *et al.* (1998) (0.258) but higher than the ratio
 390 calculated by Lotti *et al.* (2014) (0.161). Such a difference could be due to specific properties of the
 391 strains used. However, even the NO_3/NH_4 ratios for the two *Brocadia* strains differ strongly from each
 392 other. The NO_3/NH_4 ratio of 0.161 given by Lotti *et al.* (2014) contradicts their own stable
 393 measurements (Figure 5D in Lotti *et al.* (2014)) of 0.2 ± 0.01 for molar NO_2/NH_4 ratios and also
 394 contradicts the ratio of 0.210 obtained by us after recalculation and reconciliation of their original data
 395 (Supporting Table 2A in Lotti *et al.* (2014)) without constraints on the N-source (Table 1). This, the
 396 almost perfectly closed mass balance in our measurements and the very low errors between observed
 397 and calculated coefficients for our reactor support the precision of our formula. The cultivation in a
 398 homogeneous system with a highly enriched anammox culture contributes to this precision.

399 The biomass yield in our study with “*Ca. Kuenenia stuttgartiensis*” (1.97 g VSS per mole consumed
 400 ammonium) was higher than with the two “*Ca. Brocadia*” species (1.70 and 1.57, respectively),
 401 possibly due to intrinsic properties of the used “*Ca. Kuenenia*” species in comparison with “*Ca.*
 402 *Brocadia*” species.



407 **Microbial population changes during enrichment**

408 Bacteria of the genus *Pseudomonas*, which accounted for 70.3% of the total detected 16S rRNA genes
 409 in the batch cultures used as reactor inoculum, almost disappeared after three-months of reactor
 410 operation. This relative high abundance of *Pseudomonas* species in the batch cultures might be due to
 411 denitrifying activity making use of organic components as electron donors and nitrate/nitrite as
 412 electron acceptors. *Pseudomonas* species have previously been described as denitrifying bacteria, for
 413 example *Pseudomonas xiamenensis*.⁴³ *Pseudomonas bauzanensis* was described as a non-denitrifying
 414 bacterium,⁴⁴ but its genome (NCBI accession number JFHS00000000.1) contains the full set of
 415 denitrification genes suggesting that its denitrification activity might have not yet been discovered.

416 The disappearance of potentially denitrifying cells of the genus *Pseudomonas* in the reactor over time
417 might therefore be due to the fact that the dilution rate of the reactor exceeded their maximum growth
418 rate under reactor conditions and a competition for electron donors with other heterotrophs.

419 Several heterotrophs emerged during reactor operation, including *Methyloversatilis* which accounted
420 for more than 10% of the total detected 16S rRNA genes in the reactor after 3 months.
421 *Methyloversatilis* strains are facultative methylotrophs growing on a variety of organic compounds.⁴⁵
422 *Chloroflexi* were often reported to co-exist with anammox bacteria and scavenge organic compounds
423 derived from anammox bacterial cells.⁴⁶ However, in reactors with fast dilution rates and active
424 anammox populations, decayed anammox cells should be minimal. Indeed, in our reactor, *Chloroflexi*
425 accounted for only 0.019% of the total detected 16S rRNA genes.

426 Anammox abundance in our semi-CSTR reached around 87% as shown by Illumina amplicon
427 sequencing and FISH, lower than what membrane bioreactor systems usually achieved (>95%).³¹ This
428 is probably because the semi-CSTR was fed with only 20 mM nitrite while membrane bioreactor
429 influent typically contained 60 mM nitrite. A higher nitrite concentration can lead to higher cell
430 numbers of anammox organisms in the reactor whereas heterotrophs in the reactor are limited by trace
431 amounts of organics in the influent. The abundance of anammox bacteria is expected to increase when
432 influent nitrite is elevated and when the hydraulic retention time is further reduced but this was not the
433 goal in the current study.

434 **Effluent incubations**

435 The monitored effects in our incubations of reactor effluent with inhibitors are due to the combined
436 inhibitory effects on anammox enzymatic activity and on anammox cell growth. However, because the
437 incubation time was relatively short and only 3 mM nitrite was added (except for tests of nitrite effects)
438 compared to 20 mM nitrite in the reactor influent, cell growth during the experiment should be low.

439 Our results that salt concentrations of 120-270 mM start to inhibit anammox activity is consistent with
440 previous findings suggesting a salt tolerance range of between 50 and 200 mM.³ Slightly higher
441 sensitivity for nitrite and sulfide was found in the reactor effluent compared to the literature.³ While

442 we found that nitrite caused severe inhibition at 10 mM, previous reports described “*Ca. Kuenenia*
443 *stuttgartiensis*” to be tolerant to 13-25 mM nitrite.^{47,48} The observed inhibition by sulfide in our
444 experiments was even stronger than those reported with planktonic cells from membrane
445 bioreactors,^{49,50} and was orders of magnitude lower than values obtained with cell aggregates.⁵¹ “*Ca.*
446 *Kuenenia stuttgartiensis*” were found to be relatively insensitive to chloramphenicol when dispersed
447 anammox granules were used for anammox activity tests, with IC_{50} values of $\sim 400 \text{ mg L}^{-1}$ ⁵² or
448 even $>1 \text{ g L}^{-1}$ ⁴⁸. Interestingly, the study that observed an IC_{50} of $\sim 400 \text{ mg L}^{-1}$ on dispersed anammox
449 granules also showed that as low as 20 mg L^{-1} chloramphenicol caused a 25% drop in reactor
450 efficiency and a 75% drop in specific anammox activity after 4 days incubation in the same reactor
451 that provided anammox granules for activity tests.⁵² It is therefore possible that in these two studies the
452 relatively short incubation time of $\sim 6 \text{ h}$ in anammox activity tests was not sufficient to fully reveal the
453 inhibition effects by chloramphenicol, and the inhibition effects became prominent only after
454 prolonged incubation ($>4 \text{ d}$) in the reactor. In our study, 30 mg L^{-1} chloramphenicol caused 57%
455 inhibition within 10.4 h of incubation (SI, Figure S5). These results suggest that the planktonic cells in
456 our study were more readily accessible for the effector and inhibition was observable within a shorter
457 incubation time. However, we cannot exclude that the previously investigated “*Ca. Kuenenia*” strains
458 display undescribed antibiotic resistance.

459 **Associated Content**

460 **Supporting Information**

461 The Supporting Information is available free of charge on the ACS Publications website at DOI: ...

462 Population composition of the initial anammox culture (Table S1); data-set used for
463 stoichiometry calculation (Table S2); hydraulic retention time in the reactor during start-up
464 (Figure S1); gas pressure and redox changes over time in the reactor after discontinuing medium
465 amendments (Figure S2); epifluorescence microscopic image of the SYBR Green-stained
466 reactor culture (Figure S3); influencing parameters on cell counting by epifluorescence

467 microscopy (Figure S4); gas production in cultures with reactor effluent amended with different
468 chloramphenicol concentrations (Figure S5); supporting methods

469 **Author Information**

470 **Corresponding Author**

471 *E-mails: chang.ding@ufz.de

472 **ORCID**

473 Chang Ding: 0000-0001-5550-4685

474 Lorenz Adrian: 0000-0001-8205-0842

475 **Notes**

476 The authors declare no competing financial interest.

477 **Acknowledgements**

478 C.D. was supported by Humboldt Research Fellowship for Postdoctoral Researchers from the
479 Alexander von Humboldt Foundation, Germany. We thank Prof. Dr. Jianzhong He (National
480 University of Singapore) for providing data from Illumina MiSeq sequencing of the 16S rRNA genes
481 in the batch culture. We thank Florin Musat and Songcan Chen (Helmholtz Centre for Environmental
482 Research – UFZ) for Illumina MiSeq sequencing of the 16S rRNA genes in the reactor effluent. We
483 appreciate the help of Niculina Musat (Helmholtz Centre for Environmental Research – UFZ) in
484 establishing the FISH method and microscopic FISH images were taken on instruments of the ProVIS
485 platform at UFZ.

486 **References**

- 487 (1) van Niftrik, L.; Jetten, M. S. M., Anaerobic ammonium-oxidizing bacteria: Unique
488 microorganisms with exceptional properties. *Microbiol. Mol. Biol. Rev.* **2012**, *76* (3), 585-596.
- 489 (2) van Teeseling, M. C. F.; Maresch, D.; Rath, C. B., et al., The S-layer protein of the anammox
490 bacterium *Kuenenia stuttgartiensis* is heavily o-glycosylated. *Front. Microbiol.* **2016**, *7*, 1721.
- 491 (3) Oshiki, M.; Satoh, H.; Okabe, S., Ecology and physiology of anaerobic ammonium oxidizing
492 bacteria. *Environ. Microbiol.* **2016**, *18* (9), 2784-2796.
- 493 (4) Kartal, B.; Keltjens, J. T., Anammox biochemistry: A tale of heme *c* proteins. *Trends*
494 *Biochem.Sci.* **2016**, *41* (12), 998-1011.
- 495 (5) de Almeida, N. M.; Wessels, H. J. C. T.; de Graaf, R. M.; Ferousi, C.; Jetten, M. S. M.;
496 Keltjens, J. T.; Kartal, B., Membrane-bound electron transport systems of an anammox bacterium: A
497 complexome analysis. *Biochim. Biophys. Acta - Bioenergetics* **2016**, *1857* (10), 1694-1704.
- 498 (6) Speth, D. R.; Lagkouvardos, I.; Wang, Y.; Qian, P.-Y.; Dutilh, B. E.; Jetten, M. S. M., Draft
499 genome of *Scalindua rubra*, obtained from the interface above the discovery deep brine in the red sea,
500 sheds light on potential salt adaptation strategies in anammox bacteria. *Microbiol. Ecol.* **2017**, *74* (1),
501 1-5.
- 502 (7) Speth, D. R.; in 't Zandt, M. H.; Guerrero-Cruz, S.; Dutilh, B. E.; Jetten, M. S. M., Genome-
503 based microbial ecology of anammox granules in a full-scale wastewater treatment system. *Nat.*
504 *Commun.* **2016**, *7*, 11172.
- 505 (8) Ali, M.; Haroon, M. F.; Narita, Y.; Zhang, L.; Rangel Shaw, D.; Okabe, S.; Saikaly, P. E.,
506 Draft genome sequence of the anaerobic ammonium-oxidizing bacterium “*Candidatus Brocadia* sp.
507 40”. *Genome Announ.* **2016**, *4* (6), e01377-16.
- 508 (9) Oshiki, M.; Shinyako-Hata, K.; Satoh, H.; Okabe, S., Draft genome sequence of an anaerobic
509 ammonium-oxidizing bacterium, “*Candidatus Brocadia sinica*”. *Genome Announ.* **2015**, *3* (2),
510 e00267-15.
- 511 (10) van de Vossenberg, J.; Woebken, D.; Maalcke, W. J., et al., The metagenome of the marine
512 anammox bacterium ‘*Candidatus Scalindua profunda*’ illustrates the versatility of this globally
513 important nitrogen cycle bacterium. *Environ. Microbiol.* **2013**, *15* (5), 1275-1289.
- 514 (11) Strous, M.; Pelletier, E.; Mangenot, S., et al., Deciphering the evolution and metabolism of an
515 anammox bacterium from a community genome. *Nature* **2006**, *440* (7085), 790-794.
- 516 (12) Speth, D. R.; Hu, B.; Bosch, N.; Keltjens, J. T.; Stunnenberg, H. G.; Jetten, M. S. M.,
517 Comparative genomics of two independently enriched “*candidatus Kuenenia stuttgartiensis*”
518 anammox bacteria. *Front. Microbiol.* **2012**, *3*, 307.
- 519 (13) Khramenkov, S. V.; Kozlov, M. N.; Kevbrina, M. V., et al., A novel bacterium carrying out
520 anaerobic ammonium oxidation in a reactor for biological treatment of the filtrate of wastewater
521 fermented sludge. *Microbiol.* **2013**, *82* (5), 628-636.
- 522 (14) van Teeseling, M. C. F.; Neumann, S.; van Niftrik, L., The anammoxosome organelle is
523 crucial for the energy metabolism of anaerobic ammonium oxidizing bacteria. *J. Mol. Microbiol.*
524 *Biotechnol.* **2013**, *23* (1-2), 104-117.
- 525 (15) Zhang, L.; Narita, Y.; Gao, L.; Ali, M.; Oshiki, M.; Okabe, S., Maximum specific growth rate
526 of anammox bacteria revisited. *Water Res.* **2017**, *116* (1), 296-303.
- 527 (16) van Niftrik, L. A.; Fuerst, J. A.; Damsté, J. S. S.; Kuenen, J. G.; Jetten, M. S. M.; Strous, M.,
528 The anammoxosome: an intracytoplasmic compartment in anammox bacteria. *FEMS Microbiol. Lett.*
529 **2004**, *233* (1), 7-13.
- 530 (17) van der Star, W. R. L.; Miclea, A. I.; van Dongen, U. G. J. M.; Muyzer, G.; Picioreanu, C.;
531 van Loosdrecht, M. C. M., The membrane bioreactor: A novel tool to grow anammox bacteria as free
532 cells. *Biotechnol. Bioeng.* **2008**, *101* (2), 286-294.
- 533 (18) Kartal, B.; van Niftrik, L.; Keltjens, J. T.; Op den Camp, H. J. M.; Jetten, M. S. M., Chapter 3
534 - anammox—growth physiology, cell biology, and metabolism. In *Adv. Microb. Physiol.*, Robert, K.
535 P., Ed. Academic Press: 2012; Vol. Volume 60, pp 211-262.

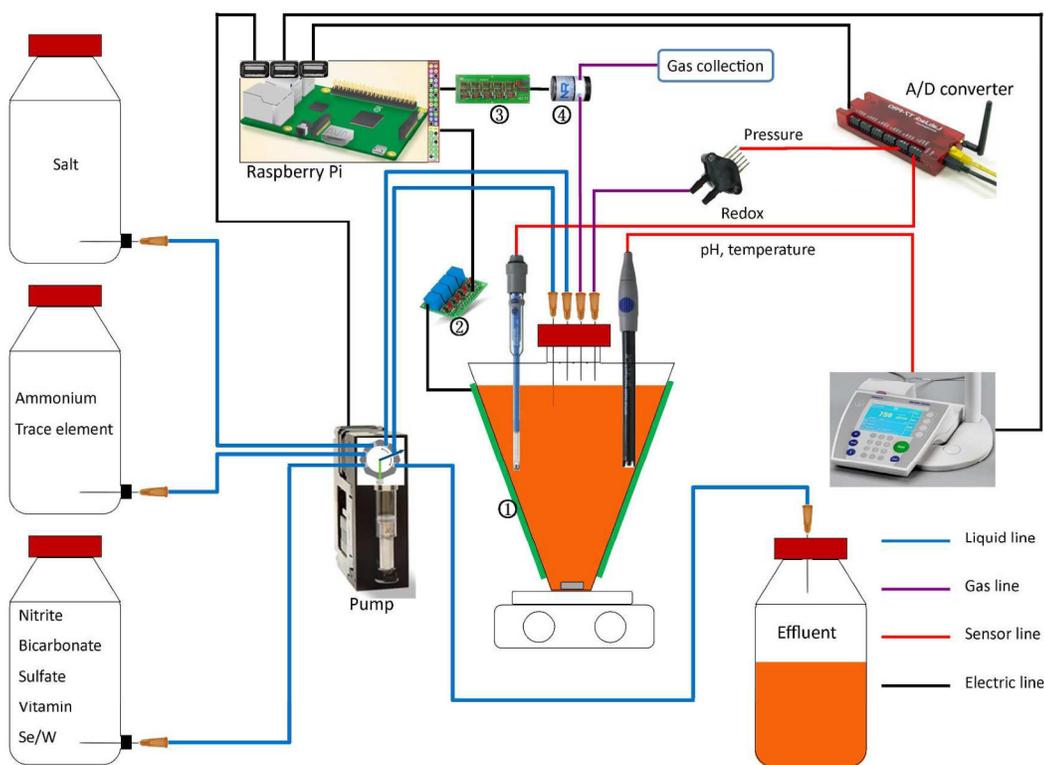
- 536 (19) Neumann, S.; Wessels, H. J. C. T.; Rijpstra, W. I. C.; Sinninghe Damsté, J. S.; Kartal, B.;
537 Jetten, M. S. M.; van Niftrik, L., Isolation and characterization of a prokaryotic cell organelle from the
538 anammox bacterium *Kuenenia stuttgartiensis*. *Mol. Microbiol.* **2014**, *94* (4), 794-802.
- 539 (20) Okamoto, H.; Kawamura, K.; Nishiyama, T.; Fujii, T.; Furukawa, K., Development of a fixed-
540 bed anammox reactor with high treatment potential. *Biodegradation* **2013**, *24* (1), 99-110.
- 541 (21) Trigo, C.; Campos, J. L.; Garrido, J. M.; Méndez, R., Start-up of the Anammox process in a
542 membrane bioreactor. *J. Biotechnol.* **2006**, *126* (4), 475-487.
- 543 (22) Brooks, M. H.; Smith, R. L.; Macalady, D. L., Inhibition of existing denitrification enzyme
544 activity by chloramphenicol. *Appl. Environ. Microbiol.* **1992**, *58* (5), 1746-1753.
- 545 (23) Widdel, F., Anaerober Abbau von Fettsäuren und Benzoesäure durch neu isolierte Arten
546 Sulfat-reduzierender Bakterien. *Ph.D.Thesis, Universität Göttingen* **1980**, doi.
- 547 (24) Kandeler, E.; Gerber, H., Short-term assay of soil urease activity using colorimetric
548 determination of ammonium. *Biol. Fertil. Soils* **1988**, *6* (1), 68-72.
- 549 (25) Klindworth, A.; Pruesse, E.; Schweer, T.; Peplies, J.; Quast, C.; Horn, M.; Glöckner, F. O.,
550 Evaluation of general 16S ribosomal RNA gene PCR primers for classical and next-generation
551 sequencing-based diversity studies. *Nucleic Acids Res.* **2013**, *41* (1), e1.
- 552 (26) Quast, C.; Pruesse, E.; Yilmaz, P., et al., The SILVA ribosomal RNA gene database project:
553 improved data processing and web-based tools. *Nucleic Acids Res.* **2013**, *41* (Database issue), D590-
554 D596.
- 555 (27) Ondov, B. D.; Bergman, N. H.; Phillippy, A. M., Interactive metagenomic visualization in a
556 Web browser. *BMC Bioinformatics* **2011**, *12* (1), 385.
- 557 (28) Yang, J.; Trela, J.; Plaza, E.; Wahlberg, O.; Levlin, E., Oxidation-reduction potential (ORP) as
558 a control parameter in a single-stage partial nitritation/anammox process treating reject water. *J.*
559 *Chem. Technol. Biotechnol.* **2015**, *91* (10), 2582-2589.
- 560 (29) Dalsgaard, T.; Stewart, F. J.; Thamdrup, B., et al., Oxygen at nanomolar levels reversibly
561 suppresses process rates and gene expression in anammox and denitrification in the oxygen minimum
562 zone off northern Chile. *mBio* **2014**, *5* (6), e01966-14.
- 563 (30) Ferousi, C.; Lindhoud, S.; Baymann, F.; Kartal, B.; Jetten, M. S. M.; Reimann, J., Iron
564 assimilation and utilization in anaerobic ammonium oxidizing bacteria. *Curr. Opin. Chem. Biol.* **2017**,
565 *37*, 129-136.
- 566 (31) Kartal, B.; Geerts, W.; Jetten, M. S. M., Chapter four - cultivation, detection, and
567 ecophysiology of anaerobic ammonium-oxidizing bacteria. In *Methods Enzymol.*, Martin, G. K., Ed.
568 Academic Press: 2011; Vol. Volume 486, pp 89-108.
- 569 (32) Lee, Z. M. P.; Bussema, C.; Schmidt, T. M., *rrnDB*: documenting the number of rRNA and
570 tRNA genes in bacteria and archaea. *Nucleic Acids Res.* **2009**, *37* (Database issue), D489-D493.
- 571 (33) Strous, M.; Heijnen, J. J.; Kuenen, J. G.; Jetten, M. S. M., The sequencing batch reactor as a
572 powerful tool for the study of slowly growing anaerobic ammonium-oxidizing microorganisms. *Appl.*
573 *Microbiol. Biotechnol.* **1998**, *50* (5), 589-596.
- 574 (34) van der Heijden, R.; Heijnen, J.; Hellinga, C.; Romein, B.; Luyben, K., Linear constraint
575 relations in biochemical reaction systems: I. Classification of the calculability and the balanceability of
576 conversion rates. *Biotechnol. Bioeng.* **1994**, *43* (1), 3-10.
- 577 (35) Oshiki, M.; Awata, T.; Kindaichi, T.; Satoh, H.; Okabe, S., Cultivation of planktonic
578 anaerobic ammonium oxidation (anammox) bacteria using membrane bioreactor. *Microbes Environ.*
579 **2013**, *28* (4), 436-443.
- 580 (36) Lotti, T.; Kleerebezem, R.; Abelleira-Pereira, J. M.; Abbas, B.; van Loosdrecht, M. C. M.,
581 Faster through training: The anammox case. *Water Res.* **2015**, *81*, 261-268.
- 582 (37) Mao, N.; Ren, H.; Geng, J.; Ding, L.; Xu, K., Engineering application of anaerobic ammonium
583 oxidation process in wastewater treatment. *World J. Microbiol. Biotechnol.* **2017**, *33* (8), 153.
- 584 (38) Kalvelage, T.; Jensen, M. M.; Contreras, S., et al., Oxygen sensitivity of anammox and
585 coupled N-cycle processes in oxygen minimum zones. *PLoS One* **2011**, *6* (12), e29299.
- 586 (39) Pitcher, A.; Villanueva, L.; Hopmans, E. C.; Schouten, S.; Reichart, G.-J.; Sinninghe Damsté,
587 J. S., Niche segregation of ammonia-oxidizing archaea and anammox bacteria in the Arabian Sea
588 oxygen minimum zone. *The ISME Journal* **2011**, *5* (12), 1896-1904.

- 589 (40) Lotti, T.; Kleerebezem, R.; Lubello, C.; van Loosdrecht, M. C. M., Physiological and kinetic
590 characterization of a suspended cell anammox culture. *Water Res.* **2014**, *60*, 1-14.
- 591 (41) Lackner, S.; Lindenblatt, C.; Horn, H., 'Swinging ORP' as operation strategy for stable reject
592 water treatment by nitrification-anammox in sequencing batch reactors. *Chem. Eng. J.* **2012**, *180*, 190-
593 196.
- 594 (42) Liu, Y.; Ni, B.-J., Appropriate Fe(II) addition significantly enhances anaerobic ammonium
595 oxidation (anammox) activity through improving the bacterial growth rate. *Sci. Rep.* **2015**, *5*, 8204.
- 596 (43) Lai, Q.; Shao, Z., *Pseudomonas xiamenensis* sp. nov., a denitrifying bacterium isolated from
597 activated sludge. *Int. J. Sys. Evol. Microbiol.* **2008**, *58* (8), 1911-1915.
- 598 (44) Zhang, D.-C.; Liu, H.-C.; Zhou, Y.-G.; Schinner, F.; Margesin, R., *Pseudomonas bauzanensis*
599 sp. nov., isolated from soil. *Int. J. Sys. Evol. Microbiol.* **2011**, *61* (10), 2333-2337.
- 600 (45) Kalyuzhnaya, M. G.; De Marco, P.; Bowerman, S.; Pacheco, C. C.; Lara, J. C.; Lidstrom, M.
601 E.; Chistoserdova, L., *Methyloversatilis universalis* gen. nov., sp. nov., a novel taxon within the
602 *Betaproteobacteria* represented by three methylotrophic isolates. *Int. J. Sys. Evol. Microbiol.* **2006**, *56*
603 (11), 2517-2522.
- 604 (46) Kindaichi, T.; Yuri, S.; Ozaki, N.; Ohashi, A., Ecophysiological role and function of
605 uncultured Chloroflexi in an anammox reactor. *Water Sci. Technol.* **2012**, *66* (12), 2556-2561.
- 606 (47) Egli, K.; Fanger, U.; Alvarez, P. J. J.; Siegrist, H.; van der Meer, J. R.; Zehnder, A. J. B.,
607 Enrichment and characterization of an anammox bacterium from a rotating biological contactor
608 treating ammonium-rich leachate. *Arch. Microbiol.* **2001**, *175* (3), 198-207.
- 609 (48) Dapena-Mora, A.; Fernández, I.; Campos, J. L.; Mosquera-Corral, A.; Méndez, R.; Jetten, M.
610 S. M., Evaluation of activity and inhibition effects on Anammox process by batch tests based on the
611 nitrogen gas production. *Enzyme Microbiol. Technol.* **2007**, *40* (4), 859-865.
- 612 (49) Russ, L.; Speth, D. R.; Jetten, M. S. M.; Op den Camp, H. J. M.; Kartal, B., Interactions
613 between anaerobic ammonium and sulfur-oxidizing bacteria in a laboratory scale model system.
614 *Environ. Microbiol.* **2014**, *16* (11), 3487-3498.
- 615 (50) Carvajal-Arroyo, J. M.; Sun, W.; Sierra-Alvarez, R.; Field, J. A., Inhibition of anaerobic
616 ammonium oxidizing (anammox) enrichment cultures by substrates, metabolites and common
617 wastewater constituents. *Chemosphere* **2013**, *91* (1), 22-27.
- 618 (51) Jin, R.-C.; Yang, G.-F.; Zhang, Q.-Q.; Ma, C.; Yu, J.-J.; Xing, B.-S., The effect of sulfide
619 inhibition on the ANAMMOX process. *Water Res.* **2013**, *47* (3), 1459-1469.
- 620 (52) Fernández, I.; Mosquera-Corral, A.; Campos, J. L.; Méndez, R., Operation of an anammox
621 SBR in the presence of two broad-spectrum antibiotics. *Process Biochemistry* **2009**, *44* (4), 494-498.
- 622

623 **Tables**624 Table 1: Comparison of anammox stoichiometry coefficients for “*Ca. Kuenenia*” and two “*Ca.*
625 *Brocadia*” species.

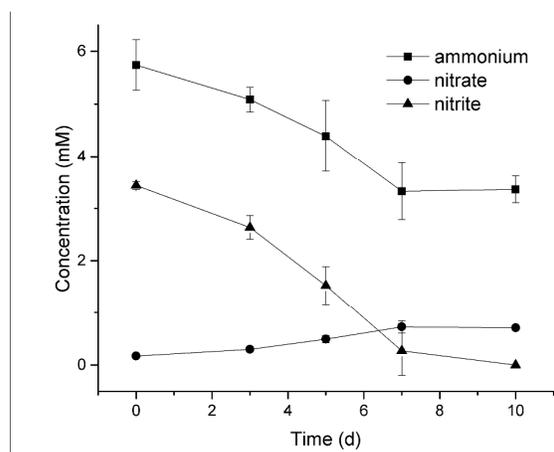
Species	Coefficient in stoichiometric equations											
	“ <i>Ca. Kuenenia stuttgartiensis</i> ”				“ <i>Ca. Brocadia anammoxidans</i> ”				“ <i>Ca. Brocadia sapporoensis</i> ”			
Reference of input data	This study				Strous <i>et al.</i> (1998) ³³				Lotti <i>et al.</i> (2014) ⁴⁰			
Biomass formula	CH ₂ O _{0.5} N _{0.15} S _{0.05}		CH _{1.74} O _{0.31} N _{0.2} S _{0.01} P _{0.01}		CH ₂ O _{0.5} N _{0.15} S _{0.05}		CH _{1.74} O _{0.31} N _{0.2} S _{0.01} P _{0.01}					
Constraint	No N-source constraints						NH ₄ as N-source		No N-source constraints			
Measured biomass yield ^a	-						0.071 C-mol NH ₄ -mol ⁻¹				0.059 C-mol NH ₄ -mol ⁻¹	
Compound	Value	Diff ^b %	Value	Diff %	Value	Diff %	Value	Diff %	Value	Diff %	Value	Diff %
NH ₄ ⁺	1	-0.4	1	1.1	1	-5.5	1	6.6	1	1.0	1	-1.4
NO ₂ ⁻	1.270	-0.1	1.249	-0.3	1.320	3.0	1.146	0.7	1.225	0.0	1.250	1.6
HCO ₃ ⁻	0.077	-	0.087	-	0.066	-3.7	0.071	-	0.073		0.061	-
H ⁺	0.108	-	0.097	-	0.128	-	0.057	-	0.088 ^c		0.099	-
N ₂	1.010	0.3	0.996	0.4	1.026	-0.9	0.986	-	1.000		1.013	-
NO ₃ ⁻	0.238	0.6	0.239	2.2	0.258	-4.1	0.161	-17.9	0.210	0.4	0.212	-0.0
Biomass	0.077	-0.4	0.087	-3.4	0.066	5.0	0.071	6.6	0.073	3.2	0.061	0.9
H ₂ O	2.016	-	2.016	-	2.031	-	2.002	-	1.950	-	2.027	-
Yield ^d	1.97		1.93		1.70		1.57		1.62		1.34	

626 ^a Lotti *et al.* (2014) gave conflicting biomass yield values (in C-mol NH₄-mol⁻¹) of 0.071 as given
627 directly in their text and 0.059 as calculated from data in Table 2A in their supporting online material.628 ^b “Diff”: difference in percent between the measured conversion rates and the calculated balanced
629 conversion rates according to the corresponding coefficients.630 ^c The coefficient for proton 0.024 as given in Table 3 by Lotti *et al.* (2014) caused imbalance in charge
631 and element. Here we give the inferred value of 0.088 based on charge and element balance.632 ^d Biomass yield calculated based on the stoichiometry, unit: g VSS per mole of consumed ammonium.
633

634 **Figures**

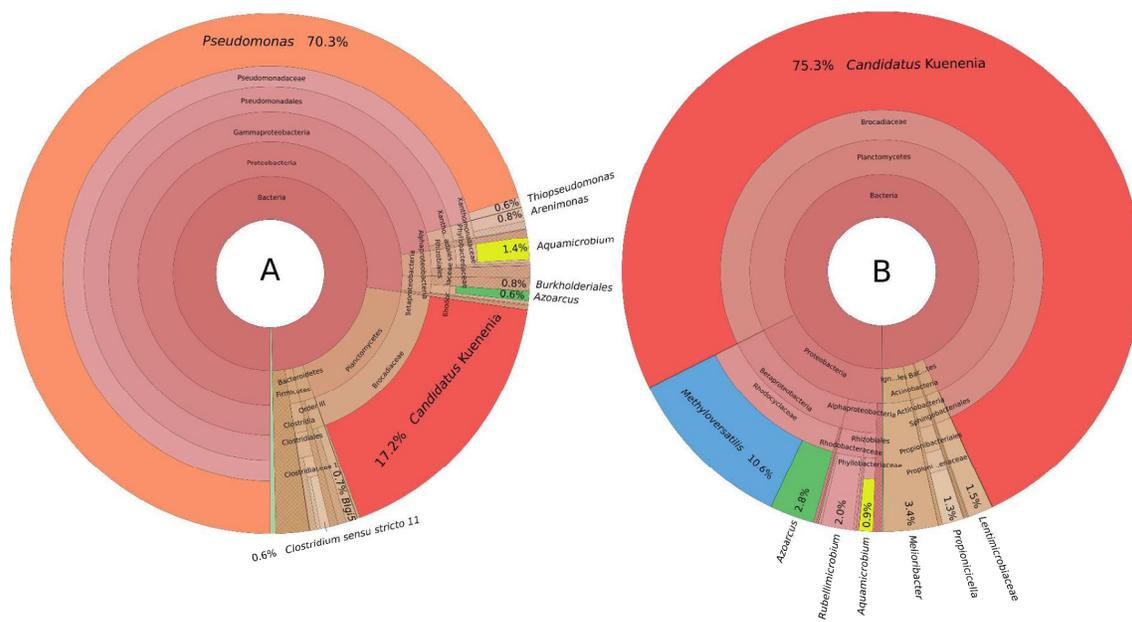
635

636 Figure 1: Schematic layout of the semi-continuous stirred-tank reactor. Labels: (1) Heating blanket, (2)
 637 Relay for heating blanket, (3) Relay for gas valve, (4) Gas valve. All medium bottles and the effluent
 638 bottle were pressurized with a gas mixture of 80% N₂ and 20% CO₂ at 10 kPa (not shown in the
 639 figure).



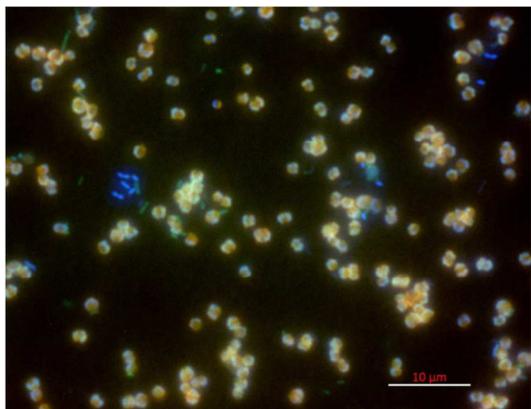
640

641 Figure 2: Anammox activity in a sludge- and granule-free planktonic batch cultures after three
642 transfers. Shown are means \pm SD of triplicate cultures. Nitrogen evolution and cell growth were not
643 measured here.



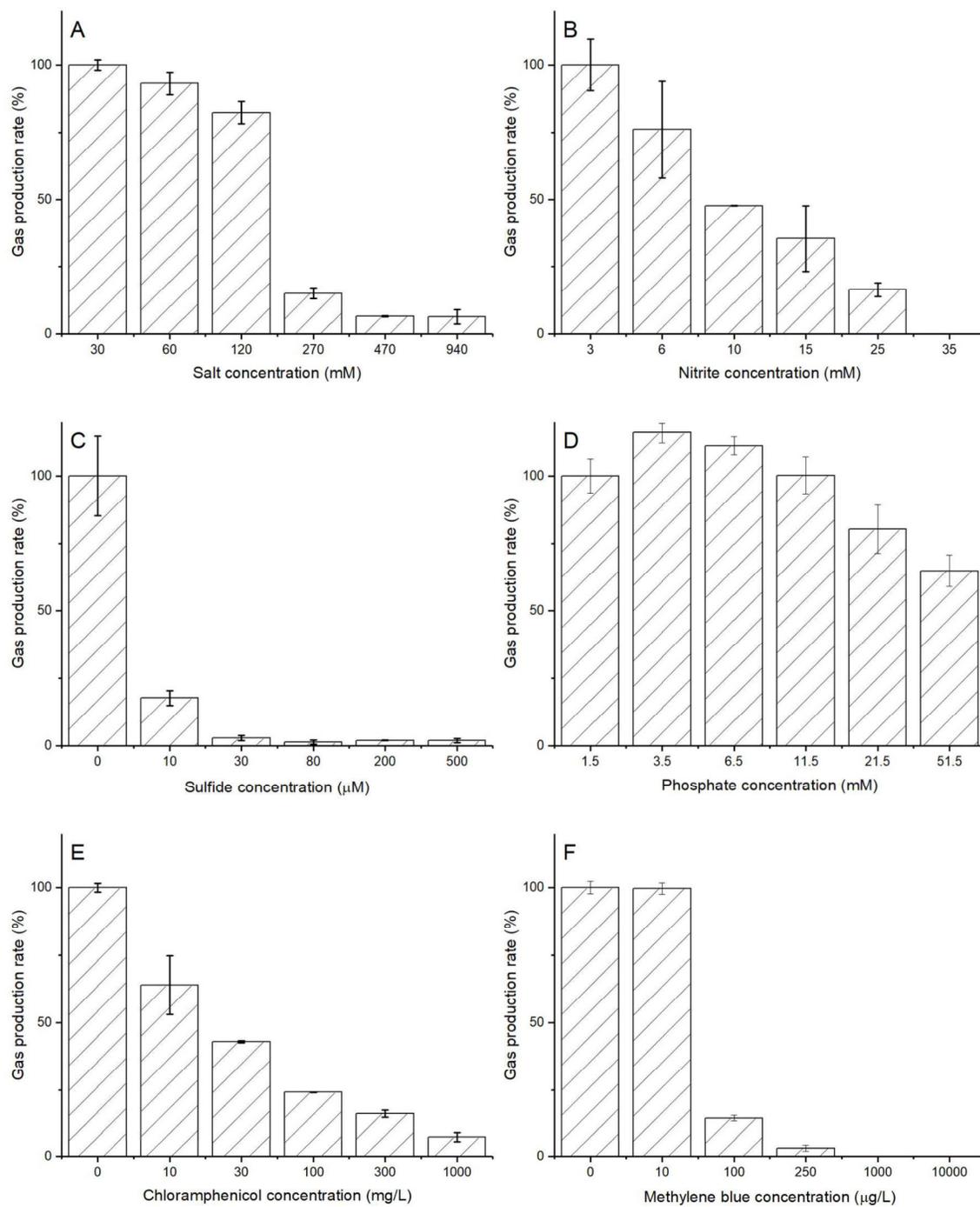
644

645 Figure 3: Illumina amplicon sequencing analyses of the microbial communities (A) in the granule-free
 646 batch culture after three transfers and (B) in the reactor after three months of operation. Common and
 647 unique abundant (>10%) populations are labeled. Shown are data based on the absolute numbers of
 648 detected 16S rRNA genes not taking into account different copy numbers of 16S rRNA genes per
 649 genome in the respective populations.



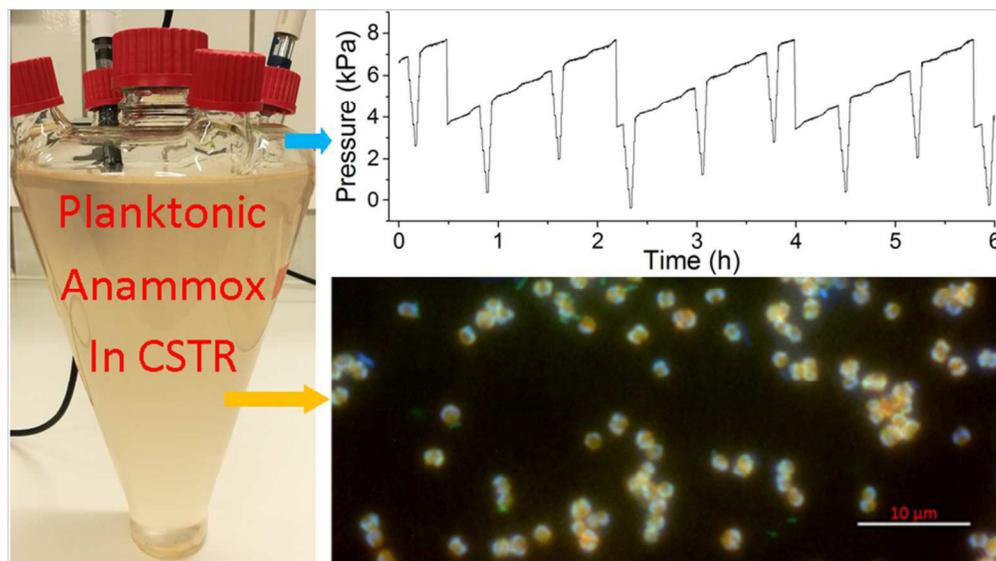
650

651 Figure 4: Fluorescence *in situ* hybridization of the reactor culture with FAM-labeled Eub338-mix
652 (green), cy5-labeled AMX820 (red) and counter stained with DAPI (blue). Anammox cells are light
653 blue on the edges due to DAPI-stained high DNA content in the cytoplasm ('riboplasm' in
654 Planctomyetes); the center of the anammox organisms ('anammoxosome') is DNA-free and stains
655 orange/brown due to three overlapping weak signals from the two FISH probes and DAPI from the
656 over/underlying riboplasm. Cells that do not hybridize with AMX820 are blue or green.



657

658 Figure 5: Influence of different effectors on anammox activity of reactor effluent. (A) Salt (NaCl); (B)
 659 Nitrite (NaNO_2); (C) Sulfide (Na_2S); (D) Phosphate (mixture of K_2HPO_4 and KH_2PO_4 , pH 7.2); (E)
 660 Chloramphenicol; (F) Methylene blue. Gas production rates were normalized against positive controls
 661 with no effectors and 3 mM nitrite which produced $70\text{-}120 \text{ mL N}_2 \text{ L}^{-1} \text{ d}^{-1}$ at 30°C .



TOC-Graphic

84x47mm (300 x 300 DPI)