

**Nautilia abyssi sp. nov., a thermophilic,  
chemolithoautotrophic, sulfur-reducing bacterium  
isolated from an East Pacific Rise hydrothermal vent**

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Prieur

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1 *Nautilia abyssi* sp. nov.,

2 **a novel thermophilic, chemolithoautotrophic, sulfur-reducing bacterium isolated from an East Pacific**  
3 **Rise hydrothermal vent**

4  
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15  
16 Running title: *Nautilia abyssi* sp. nov.

17  
18 Category: New taxa, *Proteobacteria*

19  
20 Footnote: The GenBank/EMBL/DDBJ accession number for the 16S rDNA sequence of *Nautilia*  
21 *abyssi* PH1209<sup>T</sup> is AM937002.

22 Scanning electron micrographs of cells of strain PH1209<sup>T</sup> (*Nautilia abyssi* sp. nov.) (Fig S1)  
23 and a graph showing the maximum growth rate of strain PH1209<sup>T</sup> at varying temperatures,  
24 pH and NaCl concentrations (Fig. S2) are available in IJSEM online.  
25

26 **A novel, strictly anaerobic, thermophilic, sulfur-reducing bacterium designated PH1209<sup>T</sup>, was**  
27 **isolated from an East Pacific Rise hydrothermal vent (13°N) sample and subjected to a polyphasic**  
28 **taxonomic analysis. The cells were Gram-negative motile rods (approximately 1.60 x 0.40 μm) with a**  
29 **single polar flagellum. Strain PH1209<sup>T</sup> grew at temperatures between 33 and 65°C (optimum 60°C),**  
30 **from pH 5.0 to 8.0 (optimum 6.0-6.5) and between 2 and 4% (w/v) NaCl (optimum 3%). Cells grew**

31 chemolithoautotrophically with H<sub>2</sub> as an energy source, S<sup>o</sup> as an electron acceptor and CO<sub>2</sub> as a  
32 carbon source. Alternatively, strain PH1209<sup>T</sup> was able to use peptone and yeast extract as carbon  
33 sources. The G+C content of the genomic DNA was 35 mol%.

34 Phylogenetic analyses based on 16S rRNA gene sequencing showed that strain PH1209<sup>T</sup> fell within the  
35 order *Nautiliales*, in the class *Epsilonproteobacteria*. Comparative 16S rRNA gene sequence analysis  
36 indicated that strain PH1209<sup>T</sup> belonged to the genus *Nautilia*, and shared, respectively, 97.2 and  
37 98.7% 16S rRNA gene sequence identity with *Nautilia lithotrophica* and *Nautilia profundicola*. It is  
38 proposed, from the polyphasic evidence, that the strain should be placed into a novel species, *Nautilia*  
39 *abyssi* sp. nov. The type strain is PH1209<sup>T</sup> (= DSM 21157<sup>T</sup> = JCM 15390<sup>T</sup>).

40  
41 *Epsilonproteobacteria* are widely distributed in marine and terrestrial ecosystems (Campbell *et al.*, 2006).  
42 They are particularly common and abundant in 30-70°C areas of deep sea hydrothermal vents, as indicated  
43 by their prevalence in the clone libraries (Polz & Cavanaugh, 1995; Longnecker & Reysenbach, 2001;  
44 Lopez-Garcia, 2002; Alain *et al.*, 2004), the results of fluorescence *in situ* hybridization (Moussard *et al.*,  
45 2006) and the isolation of several representatives (Alain *et al.*, 2002; Miroshnichenko *et al.*, 2002; Inagaki *et*  
46 *al.*, 2003; Takai *et al.*, 2003, 2005, 2006; Voordeckers *et al.*, 2005). Within this singular ecosystem,  
47 *Epsilonproteobacteria* are retrieved in various habitats, thriving (i) as free-living organisms on chimney  
48 structures, within vent plumes and in sediments, (ii) as epi- or endosymbionts of hydrothermal invertebrates,  
49 or (iii) embedded in mats on the surfaces of chimney rocks or animals. Cultured isolates from deep-sea vents  
50 are all mesophilic to thermophilic chemolithoautotrophs coupling the oxidation of hydrogen or sulfur  
51 compounds to the reduction of nitrate, sulfur compounds or oxygen (Takai *et al.*, 2003; Campbell *et al.*,  
52 2006). Because of their abundance and metabolic abilities, *Epsilonproteobacteria* are likely to be key  
53 players of the carbon, sulfur and nitrogen biogeochemical cycling at deep-sea vents.

54 Two orders are currently described within the class *Epsilonproteobacteria* Garrity *et al.* 2006 (Validation  
55 List n°107, Garrity *et al.*, 2005), namely the *Nautiliales* (Miroshnichenko *et al.*, 2004) and the  
56 *Campylobacterales* Garrity *et al.* 2006 (Validation List n°107, Garrity *et al.*, 2005). The order *Nautiliales*  
57 comprises the genera *Nautilia* (Miroshnichenko *et al.*, 2002), *Caminibacter* (Alain *et al.*, 2002) and  
58 *Lebetimonas* (Takai *et al.*, 2005) which are exclusively composed of thermophilic strains isolated from

59 deep-sea hydrothermal vents and which have been found in association with invertebrates or with chimney  
60 edifices. At present, the genus *Nautilia* is composed of two species, *Nautilia lithotrophica* (Miroshnichenko  
61 *et al.*, 2002) and *Nautilia profundicola* (Smith *et al.*, 2008). Both strains are strictly anaerobic sulfur-  
62 reducing mixotrophs able to grow on hydrogen and carbon dioxide, or alternatively on formate.

63 In this study, a novel marine bacterium belonging to the genus *Nautilia* is described. Based on the results of  
64 a polyphasic taxonomic analysis, the strain PH1209<sup>T</sup> represents a novel species, *Nautilia abyssi* sp. nov.

65

66 In April-May 2002, during the PHARE oceanographic cruise, fragments of active hydrothermal chimney  
67 rocks covered with colonies of the tubeworm polychaete *Alvinella* spp. were collected from 2620m depth at  
68 the Elsa vent field, on the East Pacific Rise 13°N (12°48'N, 103°56'W). Sample collection, subsampling and  
69 storage procedures were as described elsewhere (Alain *et al.*, 2004). One subsample collected on the Ph01  
70 chimney was used to inoculate series of media, including KA22 medium (Alain *et al.*, 2002), and incubated  
71 at 60°C under a gas phase of H<sub>2</sub>/CO<sub>2</sub> (80/20; 200 kPa). After 24h incubation, dense populations of short,  
72 rod-shaped, motile cells were observed and purified by repeated dilution to extinction series. One isolate,  
73 referenced as strain PH1209<sup>T</sup>, is described in this publication. Purity of this isolate was confirmed routinely  
74 by microscopic examination and by repeated partial sequencing of the 16S rRNA gene using several  
75 primers. Stock cultures were stored at -80°C in KA22 medium supplemented with 5% (v/v) DMSO.

76

77 Morphological characteristics of the cells were determined by light microscopy (Olympus CX40) and by  
78 scanning electron microscopy (FEI Quanta 200). Cells of strain PH1209<sup>T</sup> were Gram-negative, straight rods  
79 of 1.05-2.21 μm in length (mean 1.63μm ± 0.34, n=11) and 0.30-0.51 μm in width (mean 0.39 ± 0.05, n=11)  
80 in the mid-exponential phase of growth (see Supplementary Fig. S1 in IJSEM online). They occurred mainly  
81 singly and were highly motile by a polar flagellum (Fig. S1A). Division was by constriction (Fig. S1B).  
82 Formation of spores was never observed.

83

84 The physiological characterization of the novel isolate was carried out in a basal medium referenced as  
85 “NPKsalts” and containing (per liter): 0.33 g NH<sub>4</sub>Cl, 0.33 g KCl, 0.33 g CaCl<sub>2</sub>·2H<sub>2</sub>O, 0.33 g MgCl<sub>2</sub>·6H<sub>2</sub>O,  
86 25 g NaCl, 1.0 g NaNO<sub>3</sub>, 1.95 g MES buffer (Sigma) and 1 mg resazurin (Sigma). Its pH was adjusted to

87 6.0. Once prepared, this medium was autoclaved and then cooled to room temperature under a stream of O<sub>2</sub>-  
88 free N<sub>2</sub> gas. Concentrated anaerobic filter-sterilized solutions of vitamins and trace elements were added to  
89 the medium after autoclaving. Then, just before inoculation, Na<sub>2</sub>S·9H<sub>2</sub>O, KH<sub>2</sub>PO<sub>4</sub> and elemental sulfur were  
90 provided from sterile stocks, to final concentrations of 0.04% (w/v), 20 mM and 1.2% (w/v), respectively.  
91 Unless stated otherwise, the experiments were carried out anaerobically, under a gas phase of H<sub>2</sub>/CO<sub>2</sub>  
92 (80/20; 200 kPa), and incubation were done in the dark and under agitation. Growth was routinely  
93 monitored by direct cell counting using a modified Thoma chamber (depth 10 μm), or by counting after  
94 fixation with 1% (v/v) glutaraldehyde and storage at -20°C. Growth rates were calculated using linear  
95 regression analysis of four to nine points along the logarithmic portions of the resulting growth curves. The  
96 determination of the temperature range for growth was tested over the range 30-80°C (i.e. 30, 33, 37, 45, 50,  
97 55, 60, 65, 70, 75, 80°C). No growth was observed at 30°C, 70°C and above. The novel isolate grew from 33  
98 to 65°C, with an optimum growth rate at 60°C (see Supplementary Fig. S2A in IJSEM online). The pH  
99 range for growth was tested at 60°C in basal medium buffered and adjusted to the required initial pH as  
100 described elsewhere (Alain *et al.*, 2002). Growth was observed from pH 5.0 to pH 8.0, the optimum being  
101 around pH 6.0-6.5 (Fig. S2B). No growth was observed at pH 4.0 and pH 8.5. Salt tolerance was tested at  
102 60°C in NPKsalts medium prepared with various concentrations of NaCl (0, 0.5, 1, 2, 3, 4, 5, 6, 8 and 10%  
103 w/v). Growth was observed at salt concentrations ranging from 2 to 4% (w/v) NaCl, the optimum salinity  
104 being around 3% (Fig. S2C). No growth was observed at 1 and 5% (w/v) NaCl. Under optimal growth  
105 conditions, the generation time of strain PH1209<sup>T</sup> was around 120 minutes.

106

107 Strain PH1209<sup>T</sup> was a strictly anaerobic, chemolithoautotrophic bacterium that used sulfur, hydrogen and  
108 carbon dioxide as respective primary electron acceptor, electron donor and carbon source. Its ability to use  
109 alternative electron acceptors was tested by adding colloidal sulfur (Sigma Aldrich) (5 g l<sup>-1</sup>), L-cystine (12 g  
110 l<sup>-1</sup>), sulfite (1 mM), thiosulfate (20 mM), sulfate (20 mM), nitrate (10 mM), nitrite (1 mM) and oxygen (1%  
111 v/v) to nitrate and sulfur-depleted media, under an atmosphere of H<sub>2</sub>/CO<sub>2</sub> (80/20; 200 kPa). Quantitative  
112 determination of hydrogen sulfide was as described elsewhere (Cord-Ruwisch, 1985). The novel isolate was  
113 found to grow with elemental sulfur and colloidal sulfur, with concomitant production of H<sub>2</sub>S, but did not  
114 grow when L-cystine, sulfite, thiosulfate, sulfate, nitrate, nitrite and oxygen were used as electron acceptors.

115 To examine possible carbon sources other than CO<sub>2</sub>, a variety of organic carbon sources were tested in the  
116 presence of sulfur, under an atmosphere of H<sub>2</sub> 100% (200 kPa). Formate (10 mM), acetate (10 mM),  
117 butyrate (10 mM), propionate (10 mM), methanol (0.5% v/v), pyruvate (10 mM), lactate (0.5% v/v),  
118 fumarate (10 mM), glucose (10 mM), peptone (2 g l<sup>-1</sup>) and yeast extract (2 g l<sup>-1</sup>) were tested as potential  
119 substrates. Heterotrophic growth (with concomitant H<sub>2</sub>S production) was observed exclusively with yeast  
120 extract and peptone and was probably the result of the decarboxylation of amino acids. The growth rates  
121 with yeast extract and peptone were in the same order of magnitude than the one measured with carbon  
122 dioxide as carbon source. To test for the capability of the strain to use electron donors other than molecular  
123 hydrogen, the strain was cultivated under a gas phase of N<sub>2</sub>/CO<sub>2</sub> (80/20, 200 kPa) in the presence of formate  
124 (20 mM), acetate (20 mM), methanol 0.5% (v/v) and yeast extract (2 g l<sup>-1</sup>), and with sulfur as a terminal  
125 electron acceptor. No growth was observed with the alternative energy sources, indicating that strain  
126 PH1209<sup>T</sup> was a strict hydrogen-oxidizer. The nitrogen sources for growth were also examined in a nitrogen-  
127 depleted medium. The novel isolate was found to grow on organic and inorganic nitrogen sources.  
128 Significant growth was observed when NH<sub>4</sub>Cl (20 mM), glutamate (10 mM), yeast extract (0.2 g l<sup>-1</sup>),  
129 tryptone (0.2 g l<sup>-1</sup>), gelatin (0.05% v/v) and urea (0.05% v/v) were provided as sole nitrogen source.

130

131 Antibiotic resistance was tested in the presence of a variety of antibiotics from different chemical nature and  
132 with different targets and mechanisms. The resistance to vancomycin, streptomycin, chloramphenicol,  
133 kanamycin, rifampicin, penicillin, ampicillin and tetracycline was investigated at concentrations of 10, 25,  
134 50 and 100 µg ml<sup>-1</sup>. When the antibiotic was diluted in ethanol (chloramphenicol) or DMSO (rifampicin),  
135 the same volume of solvent was added to control cultures. All antibiotics were added aseptically before  
136 inoculation and the cultures were incubated at 60°C for one week. Strain PH1209<sup>T</sup> was found to be sensitive  
137 to vancomycin, streptomycin, chloramphenicol, penicillin, ampicillin and tetracycline, all at 10 µg ml<sup>-1</sup>. It  
138 grew in the presence of 10 µg ml<sup>-1</sup> rifampicin and 25 µg ml<sup>-1</sup> kanamycin, but was sensitive to higher  
139 concentrations of these two antibiotics.

140

141 The genomic DNA G+C content was determined, by the Identification Service of the DSMZ (Deutsche  
142 Sammlung von Mikroorganismen und Zellkulturen GmbH, Braunschweig,

143 Germany), by HPLC analysis of deoxyribonucleosides as described by Mesbah *et al.* (1989). The G+C  
144 content of strain PH1209<sup>T</sup> was 35 mol%.

145

146 The almost complete 16S rRNA gene (1369 bp) of the strain was double-strand sequenced, as described  
147 elsewhere (Alain *et al.*, 2002). This sequence was compared to those in available databases by use of the  
148 BLAST program (Altschul *et al.*, 1990) and then aligned to its nearest neighbours using the CLUSTALX  
149 program (Thompson *et al.*, 1997). Alignments were refined manually using the SEAVIEW program (Galtier  
150 *et al.*, 1996). Distance matrixes were calculated with the Lasergene 6 version software. Phylogenetic trees  
151 were constructed by the PHYLIP (PHYlogeny Inference Package) version 3.63 software  
152 (<http://evolution.genetics.washington.edu/phylip/getme.html>) on the basis of evolutionary distance  
153 (neighbour-joining method with Jukes and Cantor corrections) (Saitou and Nei, 1987) and maximum  
154 likelihood (Felsenstein, 1981). The robustness of the inferred topologies was assessed by bootstrap analyses  
155 based on 1000 bootstrap resamplings for the neighbour-joining and 100 replications for the maximum  
156 likelihood method (Felsenstein, 1985). Comparison of the 16S rRNA gene sequence with sequences of  
157 *Bacteria* indicated that the novel isolate belonged to the class *Epsilonproteobacteria* Garrity *et al.* 2006  
158 (Validation List n°107, Garrity *et al.*, 2005) and more especially to the order *Nautiliales* (Miroshnichenko *et*  
159 *al.*, 2004). Within this lineage that is composed exclusively of taxa from deep-sea hydrothermal vents, the  
160 novel isolate was found to be most closely related to a group of moderately thermophilic sulfur reducers, all  
161 isolated from the EPR 13°N like PH1209<sup>T</sup> (Fig. 1). The novel isolate shared 98.7% 16S rRNA gene  
162 sequence identity with *Nautilia profundicola* strain AmH<sup>T</sup> (Smith *et al.*, 2008), 97.2% 16S rRNA gene  
163 sequence identity with *Nautilia lithotrophica* strain 525<sup>T</sup> (Miroshnichenko *et al.*, 2002) and 97.4% 16S  
164 rRNA gene sequence identity with strain Ex-18.2, a third isolate not formerly described (Campbell *et al.*,  
165 2001). These three closest relatives were all isolated from tubes of the worm *Alvinella pompejana* and  
166 belonged to the genus *Nautilia*. Otherwise, the novel isolate was most distantly related to members of the  
167 genera *Lebetimonas* and *Caminibacter*, sharing 91.9% to 93.2% 16S rRNA gene sequence identity with  
168 representative species of these genera (Table 1). Based on the sequence similarity and phylogenetic  
169 analyses, the novel isolate could be assigned to the genus *Nautilia*. The level of 16S rDNA sequence

170 dissimilarity with *N. profundicola* and *N. lithotrophica* suggests that the novel isolate belongs to a novel  
171 species (Stackebrandt and Ebers, 2006).

172

173 The phenotypic and genotypic properties of the novel isolate described herein generally met the minimal  
174 characteristics described for the order *Nautiliales* (Miroshnichenko *et al.*, 2004). Indeed, strain PH1209<sup>T</sup> is a  
175 marine thermophilic sulfur-reducing bacterium growing chemolithoautotrophically from H<sub>2</sub> oxidation. It  
176 unambiguously branches with other *Nautiliales*. Nevertheless, strain PH1209<sup>T</sup> can be easily distinguished  
177 from other *Nautiliales* species in terms of a number of phylogenetic, genotypic and physiological features.  
178 These distinctive criteria are detailed in Table 1. In brief, in addition to the phylogenetic distance, the novel  
179 taxon differs from its closest relatives by its temperature, NaCl and pH ranges for growth. Its generation  
180 time under optimal growth condition is also slightly different from the ones of its relatives. Furthermore,  
181 differences in the utilization profiles of carbon sources, electron donors and electron acceptors are also  
182 observed. In contrast to its congeners *N. lithotrophica* and *N. profundicola* which are able to use formate as  
183 energy and carbon source, the novel isolate is unable. Finally, another distinctive criterion is the DNA G+C  
184 content. In conclusion, in view of all the above-mentioned distinctive features, we propose that the isolate  
185 PH1209<sup>T</sup> should be assigned as the type strain of a novel species, for which the name *Nautilia abyssi* sp.  
186 nov. is proposed.

187

#### 188 **Description of *Nautilia abyssi* sp. nov.**

189 *Nautilia abyssi* (a.bys'si. L. gen. n. *abyssi*, of an abyss, of the great deep).

190 Cells are Gram-negative motile rods, approximately 1.6 µm in length and 0.4 µm in width, with a single polar flagellum.  
191 Optimal growth occurs at 60°C, with a growth range from 33 to 65°C. The pH and NaCl ranges are 5.0-8.0 (optimum  
192 6.0-6.5) and 2-4% (w/v) (optimum, 3% w/v NaCl), respectively. Growth occurs under strictly anaerobic conditions  
193 using H<sub>2</sub> as an electron donor, elemental sulfur (or colloidal sulfur) as a terminal electron acceptor and CO<sub>2</sub> as a carbon  
194 source. Yeast extract and peptone can be used as alternative carbon sources, but formate, acetate, methanol, lactate,  
195 propionate, fumarate, malate, citrate, pyruvate, glucose and glycogen can not. The following are not utilized as electron  
196 acceptors: L-cystine, thiosulfate, sulfate, sulfite, nitrate, nitrite, oxygen. The following are not used as electron donors:  
197 formate, acetate, methanol and yeast extract. Sensitive to 10 µg ml<sup>-1</sup> of the following antibiotics: vancomycin,



198 streptomycin, chloramphenicol, penicillin, ampicillin, tetracycline; sensitive to 25 µg ml<sup>-1</sup> rifampicin and 50 µg ml<sup>-1</sup>  
199 kanamycin. Genomic DNA G+C content of the type strain PH1209<sup>T</sup> is 35 mol%.

200 The type strain, PH1209<sup>T</sup> (DSM 21157<sup>T</sup>, JCM 15390<sup>T</sup>) was isolated from the walls of an active deep-sea hydrothermal  
201 chimney colonized with alvinellid worms, on the East Pacific Rise (103°56'W, 12°48'N). It is also available under  
202 request at the "Souchothèque de Bretagne" (catalogue LMBE) culture collection (<http://www.ifremer.fr/souchotheque/>).

203

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211

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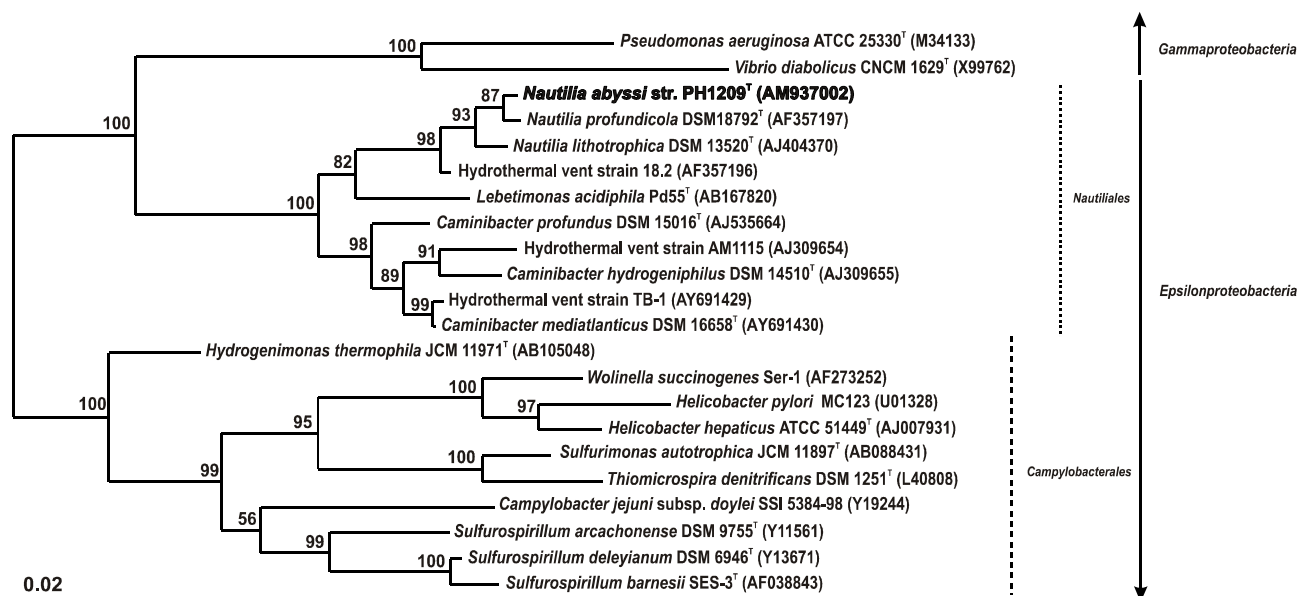
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290 **TABLES and FIGURES**

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292

293 **Fig. 1. Phylogenetic tree based on 16S rRNA gene sequences of strain PH1209<sup>T</sup> and representative**  
 294 **members of related genera within the class Epsilonproteobacteria.** Sequence data of reference strains  
 295 were obtained from the GenBank/EMBL and/or RDP databases. Two species from the  
 296 *Gammaproteobacteria* were chosen as outgroups. Accession numbers are indicated in parentheses. The  
 297 topology shown corresponds to an unrooted tree obtained by the maximum likelihood algorithm, established  
 298 using the PHYLIP package. Bootstrap values (from 100 replicates) are indicated at the branch nodes. The  
 299 positioning of the novel isolate was confirmed by the neighbour-joining method. The scale bar indicates 2 nt  
 300 substitutions per 100 nt.

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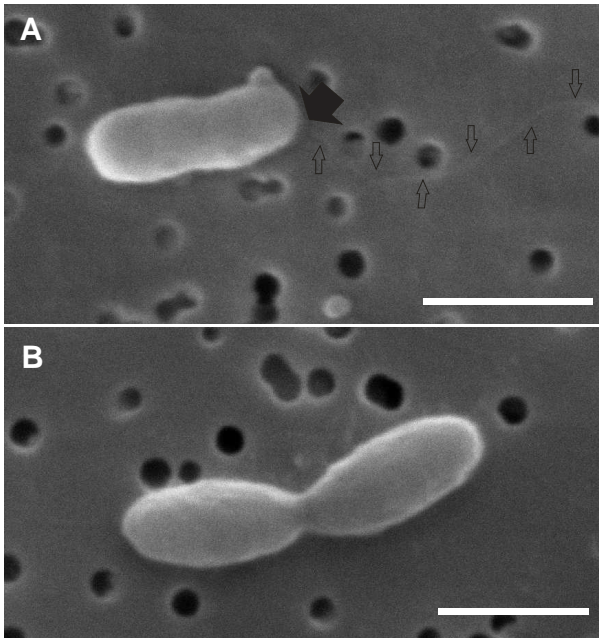
302 **Table 1. Characteristics differentiating strain PH1209<sup>T</sup> from related species of the order Nautiliales.**  
 303 Species: 1, *Nautilia abyssii* PH1209<sup>T</sup> (this study); 2, *Nautilia profundicola* AmH<sup>T</sup> (Smith *et al.*, 2008); 3,  
 304 *Nautilia lithotrophica* 525<sup>T</sup> (Miroshnichenko *et al.*, 2002); 4, *Caminibacter hydrogeniphilus* AM1116<sup>T</sup>  
 305 (Alain *et al.*, 2002); 5, *Caminibacter profundus* CR<sup>T</sup> (Miroshnichenko *et al.*, 2004); 6, *Caminibacter*  
 306 *mediatlanticus* TB-2<sup>T</sup> (Voordeckers *et al.*, 2005); 7, *Lebetimonas acidiphila* Pd55<sup>T</sup> (Takai *et al.*, 2005).  
 307 Legend: +, positive; -, negative; w, weak growth; ND, not determined. The percentage of 16S rRNA gene  
 308 sequence identity is calculated in reference to the 16S rRNA gene sequence of the novel isolate PH1209<sup>T</sup>.

309

<b>Characteristic</b>	<b>1</b>	<b>2</b>	<b>3</b>	<b>4</b>	<b>5</b>	<b>6</b>	<b>7</b>
<b>Temperature range for growth (°C) [optimum]</b>	33-65 [60]	30-55[40]	37-68 [53]	50-70 [60]	45-65 [55]	45-70 [55]	30-68 [50]
<b>pH range for growth [optimum]</b>	5.0-8.0 [6.0-6.5]	6.0-9.0 [7.0]	6.4-7.4 [6.8-7.0]	5.5-7.5 [5.5-6.0]	6.5-7.4 [6.9-7.0]	4.5-7.5 [5.5]	4.2-7.0 [5.2]
<b>NaCl concentration range for growth (%) [optimum]</b>	2.0-4.0 [3.0]	2.0-5.0 [3.0]	0.8-5.0 [3.0]	1.0-4.0 [2.0-2.5]	0.5-5.0 [3.0]	1.0-4.0 [3.0]	0.6-5.0 [2.0]
<b>Generation time (min.)</b>	120	360	140	90	40	50	120
<b>Utilization of C source other than CO<sub>2</sub></b>							
<b>Formate</b>	—	+	+	—	—	—	—
<b>Complex organic substrates</b>	+	ND	ND	+	ND	ND	—
<b>Utilization of electron donor other than H<sub>2</sub></b>							
<b>Formate</b>	—	+	+	—	—	—	—
<b>Utilization of electron acceptor other than S<sup>0</sup></b>							
<b>Oxygen</b>	—	—	—	—	+	—	—
<b>Nitrate</b>	—	—	—	+	+	+	—
<b>Sulfite</b>	—	ND	w	ND	—	—	—
<b>Colloidal sulfur</b>	+	ND	w	ND	ND	ND	ND
<b>DNA G+C content (mol%)</b>	35.0	33.5	34.7	29±1	32.1	25.6	34.0
<b>16S rRNA gene sequence identity (%)</b>	100	98.7	97.2	92.8	92.4	93.2	91.9

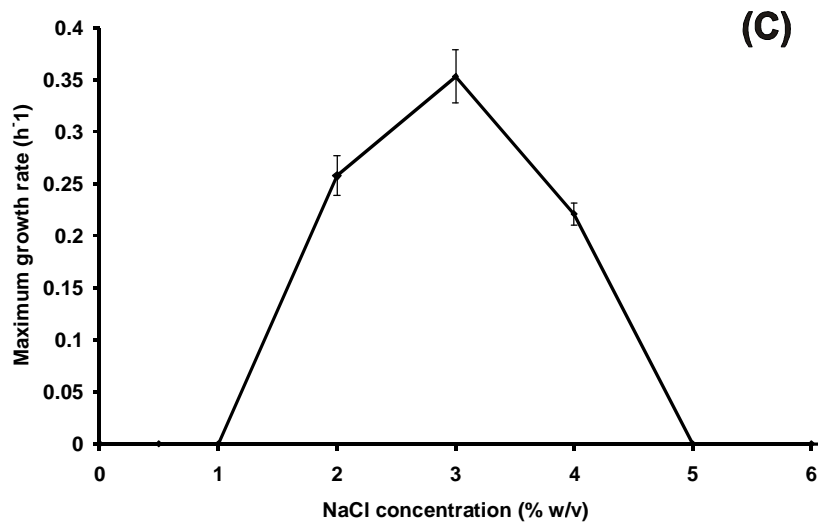
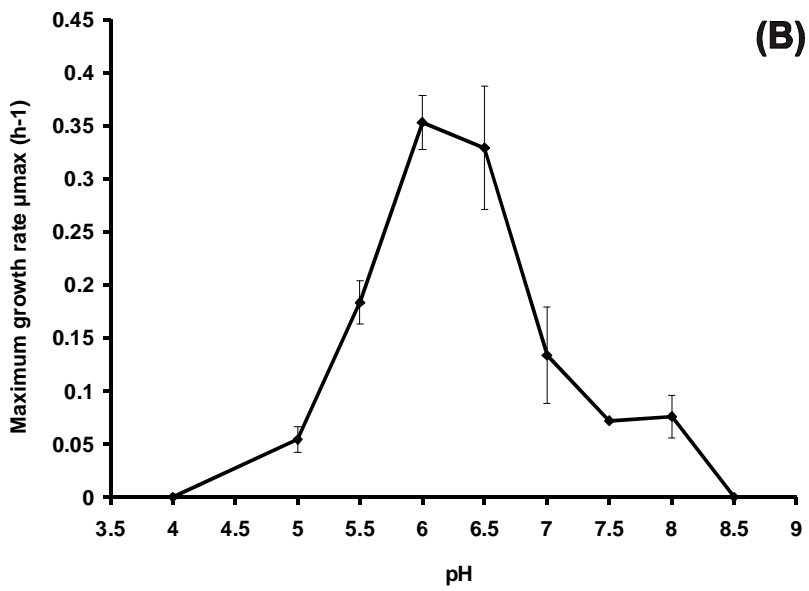
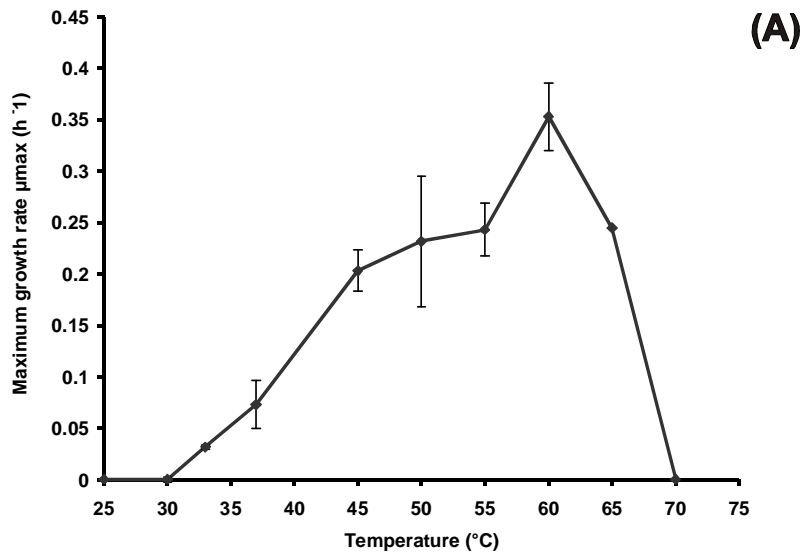
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313 **Fig. S1. Scanning electron micrographs of cells of strain PH1209<sup>T</sup> in the mid-exponential phase of**  
314 **growth, showing the polar flagellum (A) and division by constriction (B). Bar, 1.0  $\mu$ m.**



316

317 **Fig. S2. Maximum growth rate ( $\text{h}^{-1}$ ) of strain PH1209<sup>T</sup> (*Nautilia abyssi* sp. nov.) at varying**  
318 **temperatures (A), pH (B) and NaCl concentrations (C). Bars indicate confidence intervals.**

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