Halomonas zincidurans sp. nov., a heavy-metal-tolerant bacterium isolated from the deep-sea environment

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A Gram-stain-negative, aerobic, rod-like, motile by peritrichous flagella and moderately halophilic bacterium, designated strain B6¹, was isolated a deep-sea sediment collected from the South Atlantic Ocean. The isolate grew with 0.5–15 % (w/v) NaCl, at 4–37 °C and pH 5.0–8.5 and showed a high tolerance to zinc, manganese, cobalt and copper ions. The major fatty acids were C₁₆:₀, C₁₉:₀ cyclo ω8c, C₁₂:₀ 3-OH and C₁₂:₀. The predominant ubiquinone was Q-9. The genomic DNA G+C content was 61.1 mol%. Phylogenetic analysis based on 16S rRNA gene comparisons indicated that strain B6¹ belonged to the genus Halomonas, and the closest relative was Halomonas xinjiangensis TRM 0175⁵ (96.1 %). Based upon the phenotypic, chemotaxonomic and genetic data, strain B6¹ represents a novel species from the genus Halomonas, for which the name Halomonas zincidurans sp. nov. is proposed. The type strain is B6¹ (= CGMCC 1.12450° = JCM 18472°).

The genus Halomonas proposed by Vreeland et al. (1980) belongs to the family Halomonadaceae, which contains nine additional genera: Aidingtonimonas, Carninomonas, Chromohalobacter, Cobetia, Halotalea, Kushneria, Modicisalibacter, Salinicola and Zymobacter. At the time of writing, Halomonas was the largest genus within this family, comprised of 75 species with validly published names (http://www.bacterio.net/index.html.). Most of these were isolated from saline environments, such as salterns (Kim et al., 2007; Jeon et al., 2007; González-Domenech et al., 2008a; Arenas et al., 2009; Qu et al., 2011; Amjires et al., 2011; Wang et al., 2012), saline soils (Wang et al., 2007a, b, 2008b; González-Domenech et al., 2008b, 2009; Li et al., 2008; Llamas et al., 2011; Zhao et al., 2012; Luque et al., 2012; Poli et al., 2013), a saline well (Xu et al., 2007), a salt pool (Romano et al., 2006), saline lakes (Poli et al., 2007; Romano et al., 2007; Wu et al., 2008; Wang et al., 2008b; Guan et al., 2010; Guzmán et al., 2010; Menes et al., 2011), a fermented seafood (Kim et al., 2010b); marine animals (Chen et al., 2009); or a renal dialysis machine (Kim et al., 2010a). Here, we present a polyphasic study describing a novel strain of a member of the genus Halomonas isolated from a sediment sample collected from the deep-sea environment.

The deep-sea sediment samples were collected from the South Atlantic Mid-Ocean Ridge (13.60°S 14.52°W) at a depth of 2950 m by a TV grab bucket operated from the vessel Da Yang Yi Hao. Aboard the ship, an approximately 100 mg sediment subsample was incubated for 1 h in marine broth 2216 medium (MB; BD). The suspension was plated on marine agar 2216 (MA; BD) containing 20 mM NaCl, 50 μg mL⁻¹ of atpA, gyrB, rpoD and secA gene sequences of strain B6¹ and of Halomonas xinjiangensis TRM 0175⁵ are KC935333–KC935337 and KC967480 and KC967622–KC967625, respectively.

Three supplementary figures and three supplementary tables are available with the online version of this paper.

Abbreviations: EPS, exopolysaccharide; PHB, poly-β-hydroxybutyrate.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain B6¹ is JQ781698. The accession numbers for the 23S rRNA, atpA, gyrB, rpoD and secA gene sequences of strain B6¹ and of Halomonas xinjiangensis TRM 0175⁵ are KC935333–KC935337 and KC967480 and KC967622–KC967625, respectively.

The optimal conditions for growth were determined in HM medium with different NaCl concentrations (0, 0.5, 1, 2, 3, 5, 7.5, 10, 15 and 20 %, w/v) (Ventosa et al., 1982).
The HM medium contained (l−1): 178.0 g NaCl, 2.0 g KCl, 0.48 g MgSO4 (anhydrous), 0.27 g CaCl2, 0.23 g NaBr, 0.06 g NaHCO3, trace FeCl3, 5.0 g peptone (BD), 10.0 g yeast extract (BD) and 1.0 g glucose (pH 7.5). The pH range for growth was determined by adding MES (pH 4.5–6.0), PIPES (pH 6.5–7.5), Tricine (pH 8.0–8.5) and CAPSO (pH 9.0–10.0) to HM medium at a concentration of 25 mM. The temperature range for growth was determined by incubating at 4, 10, 15, 20, 25, 30, 35, 37, 42, 45 and 50 °C. Unless stated otherwise, the HM medium contained 5 % NaCl (w/v) and pH 7.0. Cell morphology and motility were examined by optical (DM 5000B; Leica), transmission electron (H-600; Hitachi) and scanning electron microscopy (S260; Cambridge).

Phenotypic tests were performed according to the methods of Mata et al. (2002) and Aralh et al. (2007). Oxidase activity was determined by oxidation of 1 % p-aminodi-methylaniline oxalate. Catalase activity was determined by bubble production in 3 % (v/v) H2O2 solution. Anaerobic growth was carried out with AnaeroPack (Mitsubishi) using nitrate, nitrite or fumarate as potential electron acceptors. Heavy metal tolerance was studied in HM medium supplemented with different concentrations of Mn2+ (0, 10, 20, 50, 100, 200 and 800 mM), Co2+ (0, 0.25, 0.5, 0.75, 1, 1.5, 2, 2.5 and 3 mM), Cu2+ (0, 0.25, 0.5, 0.75, 1, 1.5, 2, 2.5 and 3 mM) or Zn2+ (0, 0.25, 0.5, 0.75, 1, 1.5, 2, 10, 14, 16, 20 and 30 mM). Exopolysaccharide (EPS) and poly-β-hydroxybutyrate (PHB) production were investigated based on the methods of Poli et al. (2007), Stanier et al. (1966) and Wang et al. (1998). Hydrolysis of aesculin, casein, DNA, gelatin, starch and Tween 20 and 80; nitrate and nitrite reduction; growth on MacConkey and Cetrimide agar medium were tested as described by Mata et al. (2002). H2S production was tested in liquid medium supplemented with 0.5 % (w/v) thiosulfate. Single carbon source assimilation tests were performed by using HM medium without peptone, yeast extract and glucose; and the corresponding filter-sterilized sugars (0.2 %), alcohols (0.2 %), organic acids (0.1 %) or amino acids (0.1 %) was added into liquid medium. Acid production was tested by adding modified MOF medium supplemented with 0.5 % sugars or alcohols (Leifson, 1963; Xu et al., 2008). Susceptibility to antibiotics tests were performed with antibiotic disks on plate at 30 °C and observed 5 days after inoculation. Enzyme activity, acid production and additional phenotypic tests were performed by using API 20 E, 20 NE, 20 CH and ZYM miniaturized systems according to the instructions of the manufacturer (bioMérieux).

Isoprenoid quinones were analysed by reversed-phase HPLC (Komagata & Suzuki, 1987). Fatty acid methyl esters prepared from the lipids extracted from cells grown on HM medium (5 and 10 % NaCl, w/v) at 35 °C were analysed according to the instructions of the Microbial Identification System (MIDI; Microbial ID) (Kuykendall et al., 1988). Genomic DNA was obtained using the method described by Marmur (1961). The purified DNA was hydrolysed with P1 nuclease and the nucleotides dephosphorylated with calf intestine alkaline phosphatase (Mesbah & Whitman, 1989). The G+C content of the resulting deoxyribonucleosides was determined by reversed-phase HPLC and calculated from the ratio of deoxyguanosine (dG) and thymidine (dT) (Mesbah & Whitman, 1989).

The 16S rRNA gene was amplified and analysed as described previously (Xu et al., 2007). The sequence was compared with sequences of closely related reference organisms from the EzTaxon-e service (Kim et al., 2012). Phylogenetic trees were reconstructed by the neighbour-joining (Saitou & Nei, 1987), maximum-parsimony (Fitch, 1971) and maximum-likelihood (Felsenstein, 1981) methods with the MEGA 5 program package (Tamura et al., 2011). Evolutionary distances were calculated according to the algorithm of the Kimura two-parameter model (Kimura, 1980) for the neighbour-joining method. Multilocus sequence analysis was performed according to the methods described by de la Haba et al. (2012).

Cells of strain B6T stained Gram-negative and were rod-shaped, approximately 0.3–0.5 μm width and 0.7–1.4 μm length after cultivation for 24 h at 30 °C. Cells were motile by means of peritrichous flagella (Fig. S1, available in IJSEM Online). Colonies growing on HM agar at 30 °C were 1–2 mm in diameter, smooth, circular, elevated and cream after 2 days. Cells were oxidase- and catalase-positive. No growth was observed under anaerobic conditions on plates supplemented with nitrate (20 mM), nitrite (10 mM) or fumarate (20 mM). Strain B6T was able to grow in liquid containing high concentrations of heavy metals, such as Mn2+ (200 mM), Co2+ (1.0 mM), Cu2+ (2.5 mM) and Zn2+ (14 mM). Genomics data indicated that strain B6T contained some heavy-metal-resistance genes involved in copper homeostasis and tolerance, cobalt–zinc–cadmium resistance, mercuric reduction and arsenic resistance (data not shown). Zinc is highly toxic to moderate halophiles and its toxicity can be strikingly influenced by the inorganic anionic and cationic components of the medium as well as soluble organic matter (Nieto et al., 1989). The tolerance toward zinc was confirmed on HM, MB and SW-10 plates (Nieto et al., 1989) containing 5 % NaCl (w/v) and different concentrations of Zn2+ (0, 1, 10, 15, 20 and 30 mM). *Halomonas xinjiangensis* TRM 0175T, *Chromohalobacter israelensis* DSM 6768T and *Salinibacillus soisicus* DSM 19940T were used as controls. Strain B6T tolerated zinc concentrations up to 20 mM on HM and SW-10 plates and 30 mM on MB plates. None of the reference strains grew on plates containing more than 1 mM Zn2+. The major ubiquinone of strain B6T was Q-9 (98.0 %); a small amount of Q-10 (1.2 %) as well as Q-8 (0.8 %) was also detected. Detailed results of morphological and physiological characteristics, nutritional tests, biochemical tests and antibiotic sensitivity tests are given in the species description. Phenotypic characteristics that serve to differentiate strain B6T from its closest phylogenetic relative are listed in Table 1 as well as Table S1. The comparison of phenotypic features between

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Table 1. Differential characteristics of the novel isolate B6^T and its closest phylogenetic relative H. xinjiangensis as well as the type species of the genus, H. elongata

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
<th>2</th>
<th>3</th>
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<tbody>
<tr>
<td>Pigmentation</td>
<td>Cream</td>
<td>Brown–yellow</td>
<td>White</td>
</tr>
<tr>
<td>PHB production</td>
<td>–</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>NaCl range (%, w/v)</td>
<td>0.5–15</td>
<td>0–20</td>
<td>0–20*</td>
</tr>
<tr>
<td>NaCl optimum (%, w/v)</td>
<td>5</td>
<td>10–13</td>
<td>3–8*</td>
</tr>
<tr>
<td>pH range</td>
<td>5–8.5</td>
<td>6–9</td>
<td>5–10*</td>
</tr>
<tr>
<td>pH optimum</td>
<td>7</td>
<td>7</td>
<td>ND</td>
</tr>
<tr>
<td>Temperature range (°C)</td>
<td>4–37</td>
<td>15–50</td>
<td>4–45*</td>
</tr>
<tr>
<td>Temperature optimum (°C)</td>
<td>35</td>
<td>37</td>
<td>ND</td>
</tr>
<tr>
<td>Hydrolysis of casein</td>
<td>–</td>
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<tr>
<td>Methyl red test</td>
<td>+</td>
<td>+</td>
<td>–</td>
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<td>Utilization of:</td>
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<tr>
<td>Adonitol</td>
<td>+</td>
<td>–</td>
<td>+</td>
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<tr>
<td>L-Arabinose</td>
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<tr>
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<tr>
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<td>+</td>
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<td>D-Sorbitol</td>
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<td>Trehalose</td>
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<tr>
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<tr>
<td>Acid production from</td>
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<tr>
<td>Adonitol</td>
<td>+</td>
<td>–</td>
<td>+</td>
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<tr>
<td>Cellobiose</td>
<td>–</td>
<td>+</td>
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<tr>
<td>Ethanol</td>
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<td>–</td>
<td>–</td>
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<tr>
<td>Maltose</td>
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<td>+</td>
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<tr>
<td>L-Rhamnose</td>
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<td>–</td>
<td>+</td>
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<tr>
<td>D-Sorbitol</td>
<td>+</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>Trehalose</td>
<td>–</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>G + C content (mol%)</td>
<td>61.1</td>
<td>60.0†</td>
<td>60.5‡</td>
</tr>
</tbody>
</table>

*Data from Mata et al. (2002).
†Data from Guan et al. (2010).
‡Data from Vreeland et al. (1980); the value was 63.6 mol% from genome sequence.

The delineation of the family Halomonadaceae was mainly based on the phylogenetic relationship of 16S rRNA gene sequences (Arakal et al., 2002; Garrity et al., 2005). The phylogenetic trees reconstructed with all three treeing methods indicated that strain B6^T clustered with H. xinjiangensis TRM 0175^T with high bootstrap resampling values (Felsenstein, 1985) (97 % by the neighbour-joining method, 87 % by the maximum-likelihood method and 90 % by the maximum-parsimony method) (Figs 1, S2 and S3). Therefore, the steady phylogenetic topologies and the low sequence similarities strongly indicated that strain B6^T is a novel member of the genus Halomonas. The maximum-likelihood phylogenetic trees based on the individual gene sequences revealed that strain B6^T clustered with the members within the genus Halomonas (Halomonas muralis for 23S rRNA, rpoD and secA and Halomonas campaniensis for atpA) (Fig. S2). The maximum-likelihood phylogenetic trees based on the concatenated gene sequences showed that the species of the genus Chromohalobacter formed a monophyletic cluster and strain B6^T was placed outside of the Chromohalobacter group (Fig. S3).

Strain B6^T showed the highest sequence similarities to the type strain of H. xinjiangensis (96.1 %) and Halomonas korlensis (95.1 %) and less than 95.0 % sequence similarities with other species of the genus Halomonas with validly published names. The 16S rRNA gene sequence divergence values between strain B6^T and the type strains of the species of the genus Halomonas exceeded 3 %, a commonly accepted value for the distinction of different genomic species (Stackebrandt & Goebel, 1994). Contrary to a steady monophyletic clade between strain B6^T and H. xinjiangensis, H. korlensis clustered with H. muralis and Halomonas ilicica formed an independent clade, which was separate from strain B6^T in phylogenetic trees and was confirmed by all-species living tree (LTPs_108) (Yarza et al., 2010).

The fatty acids profile of strain B6^T was different from that of H. xinjiangensis TRM 0175^T (Table S3). The content of C16 : 0 of strain B6^T (25.3–32.0 %) was higher than that of H. xinjiangensis TRM 0175^T (9.7–9.8 %); whereas the content of C18 : 1 C7c (4.6–8.8 %) of the former was less than that of the latter (26.8–35.0 %). Strain B6^T and H. xinjiangensis TRM 0175^T could be differentiated from each other by different reactions in the tests for utilization of acetate, adonitol, L-arabinose, ethanol, L-glutamate, D-ribose, D-sorbitol, trehalose and D-xylose as sole carbon and energy sources. Further differences included tolerance to heavy metals, production of PHB, formation of acid from sugars and alcohols and the reactions in API miniaturized systems (Table 1 and Table S1).

On the basis of the phylogenetic and phenotypic data presented in this study, strain B6^T represents a novel species within the genus Halomonas, for which the name Halomonas zincidurans sp. nov. is proposed.
Description of Halomonas zincidurans sp. nov.

*Halomonas zincidurans* (zin.ci.du’rans. N.L. neut. n. zincum, zinc; L. part. adj. durans, enduring, being insensible; N.L. part. adj. zincidurans, zinc tolerating).

Cells stain Gram-negative and are rod-like (0.3–0.5 μm in width and 0.7–1.4 μm in length) and motile by means of peritrichous flagella. Colonies are 1–2 mm in diameter, smooth, circular, elevated and cream-coloured after 2 days. Moderately halophilic. Growth is observed at NaCl concentrations of 0.5–15.0 % (w/v) with optimum growth at 5.0 %. Zinc, cobalt and copper ions are tolerated in millimolar concentrations. The pH and temperature ranges for growth are pH 5.0–8.5 and 4–37 °C (optimum growth at pH 7.0 and 35 °C). Strictly aerobic. Growth is not observed on plates supplemented with nitrate, nitrite or fumarate under anaerobic condition. Oxidase- and catalase-positive. H₂S is produced from thiosulfate. Tween 20 is hydrolysed. Aesculin, agar casein, DNA, gelatin, starch and Tween 80 are not hydrolysed. Nitrate is reduced to nitrite, but nitrite is not reduced. Does not grow on MacConkey agar or Cetrimide agar. Positive for arginine dihydrolase, methyl red test and Voges–Proskauer test, but negative for EPS and PHB production, indole formation, lysine and ornithine decarboxylases, ONPG test, phenylalanine and tryptophan deaminases and urease. The following constitutive enzyme activities are detected in API ZYM tests: acid and alkaline phosphatases, esterase (C4), esterase lipase (C8) and leucine and valine arylamidases; but the species is negative for β-N-acetyl-b-glucosaminidase, a-chymotrypsin, cystine arylamidases, a-fucosidase, a- and b-galactosidases, b-glucuronidase, a- and b-glucosidases, lipase (C14), a-mannosidase, naphthol-AS-BI-phosphohydrolase and trypsin. The following compounds are used as sole carbon and energy sources: adonitol, L-arabinose, cellobiose, ethanol, D-fructose, D-glucose, glycerol, maltose, mannitol, D-mannose, N-acetyl-β-D-glucosaminidase, a-chymotrypsin, cystine arylamidases, a-fucosidase, a- and b-galactosidases, b-glucuronidase, a- and b-glucosidases, lipase (C14), a-mannosidase, naphthol-AS-BI-phosphohydrolase and trypsin.
The type strain is B6T (CGMCC 1.12450^T). The following compounds are not used as sole carbon and energy sources: aesculin, formate, fumarate, D-galactose, D-glucose, glycerol, mannitol, D-mannose, D-ribose, D-sorbitol and D-xylene, but not cellobiose, myo-inositol, z-lactose, maltose, melezitose, rhamnose, L-salinic acid, sorbose, sucrose and trehalose. The following compounds are used as sole carbon, nitrogen and energy sources: L-alanine, L-arginine, glycine, L-glutamate, L-lysine, L-ornithine and L-serine. Acids are produced from adonitol, L-arabinose, ethanol, D-fructose, D-galactose, glucose, glycerol, mannitol, D-mannose, D-ribose, D-sorbitol and D-xylene, but not cellobiose, myo-inositol, z-lactose, maltose, melezitose, raffinose, L-rhamnose, D-salicin, sorbose, sucrose and trehalose. According to the results from the API 50 CH test, acid is produced from: L-arabinose, D-fucose, D-galactose, D-glucose, glycerol, ribose and D-xylene; results are weakly positive for the production of acid from D-adonitol, D-arabinose, D-fructose, D-mannose and D-mannitol; but negative for N-acetylglucosamine, aesculin, amygdalin, D-arabitol, L-arabitol, arbutin, cellulbiose, dulcitol, erythritol, L-fucose, L-β-gentiobiose, glycogen, glyconate, inulin, inositol, 2-ketogluconate, 5-ketogluconate, lactose, maltose, melibiose, melezitose, methyl-α-D-glucoside, methyl-α-D-mannoside, methyl-β-D-xyllose, raffinose, L-rhamnose, D-salicin, L-sorbitose, starch, sucrose, D-tagatose, trehalose, turanose, xylitol, D-lyxose and L-xyllose. Acid production is negative from D-sorbitol in the API 50 CH test, but positive when tested according to the method of Leifson (1963). Susceptible to (μg per disc unless otherwise stated) amoxicillin (10), ampicillin (10), carbenicillin (100), cefotaxime (30), cephalothin (30), chloramphenicol (30), erythromycin (15), nalidixic acid (30), nitrofurantoin (30), chloramphenicol (30), tetracycline (30), stated amoxicillin (10), ampicillin (10), carbenicillin (100), novobiocin (30), penicillin (10), polymyxin B (300 IU), rifampicin (5), sulfamethoxazole (300) and tetracycline (30), but not susceptible to bacitracin (0.04 IU), kanamycin (30), nitrofurantoin (30), cefotaxime (30), cephalothin (30), chloramphenicol (30), tetracycline (30), stated amoxicillin (10), ampicillin (10), carbenicillin (100), novobiocin (30), penicillin (10), polymyxin B (300 IU), rifampicin (5), sulfamethoxazole (300) and tetracycline (30), but not susceptible to bacitracin (0.04 IU), kanamycin (30), and tobramycin (10). The predominant ubiquinone is Q-9. Major fatty acids (>10%) are C_{16:0}, C_{19:0} cyclo, C_{12:0} 3-0H, C_{12:0}. The type strain is B6^T (=CGMCC 1.12450^T=JCM 18472^T), isolated from a sediment sample collected from the South Atlantic Ocean. The DNA G+C content of the type strain is 61.1 mol% (by HPLC).

Acknowledgements

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