Aureibacillus halotolerans gen. nov., sp. nov.,
isolated from marine sediment

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A Gram-staining-positive, strictly aerobic, spore-forming and rod-shaped motile bacterium with
peritrichous flagellae, designated strain S1203T, was isolated from the sediment of the northern
Okinawa Trough. Phylogenetic analysis based on 16S rRNA gene sequences indicated that
strain S1203T formed a lineage within the family Bacillaceae that was distinct from the most
closely related genera Bacillus, Bhargavaea, Planomicrobium and Virgibacillus with gene
sequence similarities ranging from 86.2 to 93.76 %. Optimal growth occurred in the presence
of 4–8 % (w/v) NaCl, at pH 7.0–8.0 and 25–32 °C. The cell-wall peptidoglycan was based on
meso-diaminopimelic acid and unsaturated menaquinone with seven isoprene units (MK-7) as
the predominant respiratory quinone. The major fatty acids (>10 % of total fatty acids) were
anteiso-C₁₅ : 0, iso-C₁₅ : 0 and C₁₆ : 0. The polar lipids were phosphatidylglycerol,
diphosphatidylglycerol, an unidentified glycolipid and an unidentified phospholipid. The DNA
G + C content of strain S1203T was 47.7 mol%. On the basis of polyphasic analysis,
strain S1203T was considered to represent a novel species in a new genus of the family
Bacillaceae, for which the name Aureibacillus halotolerans gen. nov., sp. nov. is proposed; the
type strain of Aureibacillus halotolerans is S1203T (=DSM 28697T=JCM 30067T=MCCC
1K00259T).

Since the first strain was renamed as Bacillus subtilis (‘Vibrio
subtilis’, Ehrenberg 1835) by Cohn in 1872, many novel taxa
within the family Bacillaceae have been described and, at the
time of writing, this family comprises more than 50 genera.
As a result of adaptation to their environment, bacteria can
be subdivided into two groups: halotolerant species, which
are able to grow in the absence as well as in the presence
of salt and halophilic species, which require salt for growth
(Margesin & Schinner, 2001). In Bacillaceae, Bacillus mari-
nus was first described as a halophilic species isolated from
Later, even more halophilic or halotolerant bacillus-related
bacteria belonging to the genera Marinibacillus, Virgibacillus,
Oceanobacillus and Ornithinibacillus have been isolated from
marine environments including salterns, hypersaline soils,
lakes (Yoon et al., 2004b; Waine et al., 1999) and sediments
(Lu et al., 2001; Yu et al., 2014; Yoon et al., 2010; Yin et al.,
2015). These investigations expanded our knowledge of the
biodiversity of halophilic and halotolerant bacteria from
Bacillaceae.

In the course of a study on bacterial diversity in marine
sediments, we investigated a halotolerant bacillus-like bac-
terial strain, designated S1203T, which was isolated from the
surface sediment at a water depth of 864.9 m in the
northern Okinawa Trough at station 12 (29° 36.88’ N,
127° 52.87’ E) during an expedition on the R/V Kexue
No. 1 in August 2013. The aim of this study was to deter-
mine the exact taxonomic position of strain S1203T using a
polyphasic characterization that included the determi-
nation of chemotaxonomic and other phenotypic proper-
ties and detailed phylogenetic investigation based on 16S
rRNA gene sequences.

Strain S1203T was isolated by the standard dilution plating technique on marine agar 2216 (MA; Becton Dickinson) at
4 °C for 3 months or 28 °C for up to 2 weeks. After pri-
mary isolation and purification, working cultures were
routinely maintained on MA at 28 °C and stocks were pre-
served as a suspension in sterile 0.85 % (w/v) saline sup-
plemented with 15 % (w/v) glycerol at −80 °C.

Genomic DNA extraction, PCR amplification, cloning and
sequencing of the 16S rRNA gene were performed accord-
ing to Yu et al. (2013). The almost complete 16S rRNA gene
sequence (1519 nt) was manually checked and submitted to
GenBank. Pairwise similarity values between strain
S1203T and closely related type strains were calculated
using the EzTaxon-e server (http://eztaxon-e.ezbiocloud.
net; Kim et al., 2012). The 16S rRNA gene sequence was

†These authors contributed equally to this paper.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA
gene sequence of Aureibacillus halotolerans S1203T is KJ620986.

Four figures and one table are available with the online Supplementary
Material.
aligned with closely related sequences belonging to members of the genera *Bacillus*, *Bhargavaea*, *Planomicrobium* and *Virgibacillus* using CLUSTAL_X (Thompson et al., 1997). Phylogenetic trees with gaps completely deleted were reconstructed based on the neighbour-joining maximum-likelihood and maximum-parsimony algorithms using MEGA version 5.0 (Tamura et al., 2011). The neighbour-joining tree was reconstructed with the distance calculated by the Kimura two-parameter model (Kimura, 1980). For the maximum-likelihood analysis, nearest-neighbour interchange was used as a heuristic method based on the Kimura two-parameter model (Kimura, 1980). Initial trees for the heuristic search were obtained automatically. Phylogenetic analysis by maximum-parsimony was done using the close-neighbour-interchange algorithm on random trees (Tamura & Nei, 1993) with search level 1. Initial trees were obtained through the random addition of sequences (10 replicates). The topology of the phylogenetic trees was evaluated by the bootstrap resampling method of Felsenstein (1981) with 1000 replicates for all methods.

The neighbour-joining tree, showing the phylogenetic relationship between strain S1203^T^ and selected type strains of species in the closest families, is presented in Fig. 1. Strain S1203^T^ formed a distinct lineage within the clade of family *Bacillaceae*, including the genera *Bacillus*, *Virgibacillus* and *Ornithinibacillus*, which separated it from the clade composed of the genera *Bhargavaea* and *Planomicrobium* belonging to family *Planococcaceae*. The branch pattern of these clades was identical to that in phylogenetic trees obtained by the maximum-likelihood and maximum-parsimony algorithm (Figs S1 and S2, available in the online Supplementary Material).

Cell morphology of strain S1203^T^ was determined by transmission electron microscopy (JEOL; JEM-1200EX) after cells in the exponential phase had been negatively stained with 1 % (w/v) phosphotungstic acid. Gram staining and flagellum staining were performed according to Beveridge et al. (2007). Salinity and pH ranges supporting growth were investigated in 96-well microplates by measuring the optical
densities (wavelength, 590 nm). In the salinity experiment, artificial seawater (Lyman & Fleming, 1940) with Na+ replaced by appropriate K+ and distilled water were used to prepare synthetic marine ZoBell broth (5 g peptone, 1 g yeast extract and 0.1 g FePO4 in 1 l water). Concentrations of NaCl were adjusted to 0–20.0 % (w/v, at intervals of 1.0 %). Growth was evaluated at 0, 4, 10, 16, 24, 28, 32, 37, 42 and 46 °C on MA and at pH 2.0–11.0 (at intervals of 1 pH unit) in marine broth using the following buffer systems: Na2HPO4/citric acid (pH 2.0–7.0), Tris/HCl (pH 8.0–9.0) and Na2CO3/NaHCO3 (pH 10.0–11.0). To test for anaerobic growth, strain S1203T was cultured at 28 °C for one month on MA with resazurin (0.02 %, w/v) added as an indicator of anaerobic condition. Inoculated plates were incubated in an anaerobic jar filled with nitrogen and a bag of AnerPack-Anaero (Mitsubishi Gas Chemical). Various phenotypic characteristics of strain S1203T and related reference strains were tested according to standard approaches (Tindall et al., 2007) with sterile seawater substituted for distilled water: activities of catalase, oxidase (method 2, Tindall et al., 2007) and hydrolysis of starch, casein, gelatin and Tweens 20, 40 and 80 (method 2, Tindall et al., 2007). DNase agar (Qingdao 96 Hope Bio-technology) prepared with sterile seawater was used to detect the DNase activity. Chitin (1 %, w/v) and sodium alginate (2 %, w/v) were added to MA plates for the determination of degradation by observing the formation of clear zones around colonies directly or after flooding with appropriate solutions (Teather & Wood, 1982). Activities of constitutive enzymes, the fermentation–oxidation profile, acid production and substrate utilization as sole carbon and energy source were analysed using API 20E, API 20NE, API 50CH, API ZYM strips and the GP2 MicroPlate kit according to the manufacturers’ instructions, except that sterile seawater was used to prepare the cell mass. The morphological, physiological and biochemical characteristics of strain S1203T are given in Table 1, Fig. S3 and the species description.

For cellular fatty acid analysis, strain S1203T and the related reference strains were grown on MA at 28 °C for 48 h when the bacterial communities reached the late exponential stage of growth according to the four-quadrant streak method (Sasser, 1990). Fatty acid methyl esters were prepared and analysed according to the standard protocol of MIDI (Sherlock Microbial Identification System, version 6.10), and identified by the TSBA6.0 database of the Microbial Identification System (Sasser, 1990). For analysis of the peptidoglycan, respiratory quinones and polar lipids, cells were harvested from marine broth after incubation at 28 °C for 48 h and freeze-dried. Polar lipids were extracted according to Minnikin et al. (1984), separated by two-dimensional TLC on silica gel 60 F254 plates (Merck) and identified by spraying with the appropriate detection reagents (Komagata & Suzuki, 1987). The respiratory quinones of strain S1203T were extracted with chloroform/methanol (2:1, v/v) and identified by HPLC as described by Xie & Yokota (2003). The peptidoglycan was analysed by the Identification Service of the DSMZ according to Protocol 1 of Schumann (2011). The genomic DNA of strain S1203T was extracted according to Moore et al. (1999) and the G+C content was determined by reversed-phase HPLC according to Mesbah et al. (1989).

The most predominant cellular fatty acids (>10 % of total fatty acids) of strain S1203T were anteiso-C15 : 0, iso-C15 : 0 and C16 : 0. The proportion of fatty acid C16 : 0 was significantly higher than that observed in members of other related genera but that of anteiso-C17 : 0 was observably lower. Other quantitative differences in the fatty acid composition that might serve to differentiate the novel isolate from these related genera are listed in Table S1. The predominant isoprenoid quinone detected in strain S1203T was unsaturated menaquinone with seven isoprene units (MK-7), and the cell-wall peptidoglycan was based on meso-diaminopimelic acid; these results were consistent with the strain's placement in the family Bacillaceae. The major polar lipids detected in S1203T were phosphatidylglycerol, diphosphatidylglycerol, an unidentified glycolipid and an unidentified phospholipid (Fig. S4). The DNA G+C content of S1203T was 47.7 mol%.

Strain S1203T showed the highest 16S rRNA gene sequence similarities with members of the genus Bacillus (86.2–93.76 %) in the family Bacillaceae, with similarities to the genus Virgibacillus (93.15–93.75 %) in the family Planococcaceae, the genus Planomicrobium (90.6–93.47 %) in the family Planococcaceae and the genus Virgibacillus (91.78–93.28 %) in the family Bacillaceae, indicating that the genera Bacillus, Virgibacillus, Planomicrobium and Virgibacillus were the nearest phylogenetic neighbours to the novel isolate. Phylogenetic analysis based on neighbour-joining (Fig. 1), maximum-likelihood (Fig. S1) and maximum-parsimony (Fig. S2) algorithms showed that the strain S1203T formed a deeply rooted lineage within the clade of the genera Bacillus, Virgibacillus and Ornithinibacillus, which separated it from the clade composed of the genera Phragmataea and Planomicrobium. Thus, considering the branch patterns from phylogenetic trees along with low-level sequence similarity to the other type species, strain S1203T should be assigned to a novel genus in the family Bacillaceae.

Further evidence in support of genus status for strain S1203T came from an analysis based on a comparison of the 16S rRNA gene sequences. This indicated that strain S1203T exhibited a difference of 122, 124, 132 and 129 nt with the genera Bacillus, Bhargavaea, Planomicrobium and Virgibacillus, respectively, in the highly variable region of the 16S rRNA gene.

Along with the above genotypic and phylogenetic differences, strain S1203T was distinguished from genera Phragmataea and Planomicrobium in the family Planococcaceae with respect to sporulation, motility, type of flagella, halotolerant phenotype, the composition of menaquinones and peptidoglycan type, in that strain S1203T was spore-forming, motile by peritrichous flagella, grew in 15 % (w/v) NaCl and was composed of MK-7 and meso-diaminopimelic acid (Table 1). Furthermore, strain S1203T was distinguishable from the members of genera Bacillus, Virgibacillus and Ornithinibacillus in terms of the composition of polar
Table 1. Characteristics that differentiate strain S1203T from members of related genera

Taxa: 1, strain S1203T (data from this study); 2, *Bacillus* [*B. subtilis subsp. subtilis* DSM 10T (data from this study; Claus & Berkeley, 1986; Nazina et al., 2001); *B. acidocaldarius* 10S-1T (data from this study; Claus & Berkeley, 1986; Nazina et al., 2001); 3, *Bacillus kimae* 3S-1T (data from this study; Claus & Berkeley, 1986; Nazina et al., 2001); 4, *Bacillus stearothermophilus* LMG 21831T (Heyman et al., 2004); 5, *B. lactofermenti* LMG 18435T (Logan et al., 2004); 6, *Bacillus licheniformis* LMG 18435T (Logan et al., 2004); 7, *Bacillus sphaericus* LMG 18435T (Logan et al., 2004); 8, *B. subterraneus* COOI3BT (Kanso et al., 2002); 9, *Bhargavaea* [*B. cecembensis* DSE10T (Manorama et al., 2009), *B. ginsengi* DSM 19038T (Qiu et al., 2009; Verma et al., 2012), *B. indica* KJW98T (Verma et al., 2013), *B. beijingensis* DSM 19038T (Qiu et al., 2009; Verma et al., 2012), *B. beijingensis* DSM 19038T (Qiu et al., 2009; Verma et al., 2012); 10, *Planomicrobium* [*P. koreense* JG07T (Yoon et al., 2001), *P. chinense* DX3-12T (Dai et al., 2005), *P. glaciei* 0423T (Zhang et al., 2009); 11, *Virgibacillus* [*V. pantothenticus* ATCC 14576T (Heyndrickx et al., 1998; Heyndrickx et al., 1999; Heyrman et al., 2003), *V. halodenitrificans* DSM 10037T (Denariaz et al., 1989; Yoon et al., 2004b, c), *V. sediminis* YIM kkny3T (Chen et al., 2009), *V. tartaricicus* DSM 10037T (Denariaz et al., 1989); 12, *Ornithinibacillus* [*O. bavariensis* WSBC 24001T (Mayr et al., 2006), *O. contaminans* CCUG 53201T (Kämper et al., 2010). +, Positive; –, negative; NO, not observed; NR, not reported or data are not available for the type strain; V, varies between species and/or strains; W, weak reaction.

DPG, Diphosphatidylglycerol; GL, unidentified glycolipid; m-DAP, meso-diaminopimelic acid; PE, phosphatidylethanolamine; PG, phosphatidylglycerol.

<table>
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<th>Characteristic</th>
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<td>orange/yellow</td>
<td>Cream/white/yellow</td>
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<td>Rods</td>
<td>Rods or short rods</td>
<td>Coci, short rods or rods</td>
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<td>Rods</td>
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<td>+</td>
<td>v</td>
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<td>Growth in:</td>
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<td>+</td>
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<td>10</td>
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<td>+</td>
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<td>–/NR</td>
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<td>–/NR</td>
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<td>–/NR</td>
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Table 1. cont.

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<td>Major cellular fatty acids</td>
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<td>anteiso-C15:0, iso-C15:0, anteiso-C16:0, iso-C16:0</td>
<td>anteiso-C15:0, iso-C15:0, anteiso-C16:0, iso-C16:0</td>
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<td>anteiso-C15:0, iso-C15:0, anteiso-C16:0, iso-C16:0</td>
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<td>Major peptidoglycan type</td>
<td>PG, DPG, PE</td>
<td>PG, DPG, PE</td>
<td>PG, DPG, PE</td>
<td>PG, DPG, PE</td>
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<td>45.4</td>
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Further, strain S1203T, as a marine species, was characterized as a halotolerant bacterium in this study. Many more halophilic or halotolerant bacteria have been isolated from marine environments, especially sediments (Lu et al., 2001; Yu et al., 2014; Yoon et al., 2010; Yin et al., 2015), rather than just salterns, hypersaline soils and lakes (Garabito et al., 1998; Yoon et al., 2004b; Wainø et al., 1999), indicating that the deep sea is a promising environment to find novel halophilic or halotolerant bacteria. Strain S1203T shared common characteristics with other halophilic or halotolerant species in a marine bacillus-related group: peritrichous flagella, strictly aerobic, MK-7 as the predominant menaquinones, anteiso-C15:0 as the common and major fatty acid and the relatively low G+C content (<50 mol%) (Table 2). However, strain S1203T showed significant differences from other halophilic or halotolerant species in the growth pattern in terms of salinity and temperature. For example, members of the genera Jeotgalibacillus, Virgibacillus and Halobacillus showed a moderate or extremely halophilic phenotype, but no growth occurred in the absence of salt, in contrast with strain S1203T. Species of genus Oceanobacillus had the ability to grow without salt, although they could be cultured only at temperatures above 15 °C, while the minimum growth temperature for strain S1203T was much lower (Table 2).

The conclusion drawn from phylogenetic analysis that strain S1203T represents a novel genus of the family Bacillaceae was
Table 2. Differential characteristics between strain S1203T and other halophilic or halotolerant species

Strains: 1, strain S1203T; 2, Oceanobacillus iheyensis HTE831T (Lu et al., 2001); 3, Oceanobacillus pacificus XH204T (Yu et al., 2014); 4, Jeotgalibacillus marinus (Rüger & Richter, 1979; Rüger 1983; Yoon et al., 2010); 5, Virgibacillus oceani (Yin et al., 2015); 6, Halobacillus profundi (Hua et al., 2007); 7, Halobacillus kuroshimensis (Hua et al., 2007). +, Positive; −, negative; w, weakly positive reaction; nr, not reported; no, not observed. All strains showed MK-7 as the major isoprenoid quinone.

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
</tr>
</thead>
<tbody>
<tr>
<td>Flagella</td>
<td>Peritrichous</td>
<td>Peritrichous</td>
<td>Peritrichous</td>
<td>Peritrichous</td>
<td>Peritrichous</td>
<td>NO</td>
<td>NO</td>
</tr>
<tr>
<td>Anaerobic growth</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>w</td>
<td>w</td>
</tr>
<tr>
<td>Growth temperature (°C)</td>
<td>4–42</td>
<td>15–42</td>
<td>15–42</td>
<td>5–30</td>
<td>15–45</td>
<td>9–47</td>
<td>9–48</td>
</tr>
<tr>
<td>Growth at 0 % NaCl</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>Maximum growth salinity (‰)</td>
<td>15</td>
<td>22</td>
<td>14</td>
<td>10</td>
<td>18</td>
<td>30</td>
<td>25</td>
</tr>
<tr>
<td>pH range for growth</td>
<td>7–10.0</td>
<td>6.5–10.0</td>
<td>7.0–10.0</td>
<td>NR</td>
<td>6.0–10.0</td>
<td>5.5–10.0</td>
<td>5.5–10.0</td>
</tr>
<tr>
<td>Major cellular fatty acids</td>
<td>anteiso-C15 : 0, iso-C15 : 0, iso-C16 : 0</td>
<td>anteiso-C15 : 0, iso-C14 : 0, iso-C16 : 0</td>
<td>anteiso-C15 : 0, iso-C14 : 0, iso-C16 : 0</td>
<td>anteiso-C15 : 0, iso-C14 : 0, iso-C16 : 0</td>
<td>anteiso-C15 : 0, iso-C14 : 0, iso-C16 : 0</td>
<td>C16 : 0, C16 : 1o7c alcohol, C18 : 1o7c, C19 : 6 cyc</td>
<td>C16 : 1o7c alcohol, C18 : 1o7c, C19 : 6 cyc</td>
</tr>
<tr>
<td>G+C content (mol%)</td>
<td>47.7</td>
<td>35.8</td>
<td>38.8</td>
<td>37–42</td>
<td>34.2</td>
<td>43.3</td>
<td>42.1</td>
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</tbody>
</table>
supported by morphological and physiological characteristics that distinguished it from other genera. Phylogenetically, strain S1203T shared low-level sequence similarity with the nearest phylogenetic neighbours and formed a deeply rooted distinct lineage in phylogenetic trees. Based on analyses of morphological and physiological characteristics, strain S1203T showed significant differences from other genera. (i) Cellular fatty acids, as an important criterion for discriminating different genera, clearly proved that strain S1203T were distinct from other genera and represented a novel genus. The proportion of fatty acid C_{16:0} obtained from strain S1203T was significantly higher but that of anteiso-C_{17:0} was observably lower relative to other related genera. (ii) As a halotolerant bacteria, strain S1203T had a relatively higher salt tolerance and could grow on media without added salt, which was another distinguishable feature. (iii) The presence of peritrichous flagellae further proved that strain S1203T differed from most members of other related genera. In addition to the characteristics that propose the novel genus, strain S1203T could also be distinguished from bacillus-group species by the following characteristics: (1) based on phenotypic data, strain S1203T showed the ability to grow at a relatively low temperature, for example 4 °C; (2) unlike other species, strain S1203T could not produce acid from D-glucose or maltose; (3) except for phosphatidylglycerol and diphosphatidylglycerol as major polar lipids detected in strain S1203T and bacillus-group species, an unidentified glycolipid and phosphatidylethanolamine were present as another major polar lipid of strain S1203T and Bacillus-group species, respectively. Other characteristics that differentiate strain S1203T from members of related genera are shown in Table 1 and Table S1.

By combining phenotypic, phylogenetic and genetic data, strain S1203T was assigned as the type species of a new genus in the family Bacillaceae, for which the name *Aureibacillus halotolerans* gen. nov., sp. nov. is proposed.

**Description of *Aureibacillus halotolerans* gen. nov.**

*Aureibacillus* (Au.re.i.ba.cil’lus. L. adj. aureus golden; L. masc. n. bacillus rod; N.L. masc. n. *Aureibacillus* golden rod).

Cells with ellipsoidal spores and peritrichous flagellae are Gram-staining-positive and strictly aerobic rods. Oxidase- and catalase-positive. Starch, Tween 20 and DNA are hydrolysed, Tween 40, 80 and gelatin are weakly hydrolysed, but casein, chitin and alginate are not hydrolysed. The major respiratory quinone is MK-7 and cell-wall peptidoglycan is based on meso-diaminopimelic acid. Predominant cellular fatty acids are anteiso-C_{15:0}, iso-C_{15:0} and C_{16:0}. The major polar lipids are phosphatidylglycerol, diphosphatidylglycerol, an unidentified glycolipid and an unidentified phospholipid. Phylogenetically, the genus belongs to the family *Bacillaceae* in the class *Bacilli*. The type species is *Aureibacillus halotolerans*.

**Description of *Aureibacillus halotolerans* sp. nov.**

*Aureibacillus halotolerans* (ha.lo.to’le.rans. Gr. n. halos, halos salt; L. part. tolerans tolerating; N.L. part. adj. halotolerans referring to the ability to tolerate high salt concentrations).

In addition to the characteristics listed for the genus, the following features are characteristic of *Aureibacillus halotolerans*. Cells are rods, 0.5–0.7 μm in width by 2.0–2.3 μm in length. Growth occurs on MA and R2A medium. Colonies on MA are light orange, regular, opaque and smooth with an entire margin of 0.5–1.5 mm in diameter after incubation for 3 days at 28 °C. Growth occurs at 4–42 °C with an optimum temperature of 24–32 °C. The pH range for growth is 7.0–10.0 (optimum 7.0–8.0). The NaCl range for growth is 0–15 % (optimum 4–8 %). In the API 20E and 20NE strips, there are positive results for aesculin hydrolysis; and negative results for β-galactosidase, arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase, phenylalanine deaminase, H$_2$S production, nitrate reduction to nitrite, citrate utilization, urea hydrolysis, indole production and acetoin production. In the API ZYM strip test, alkaline phosphatase, esterase (C4), esterase lipase (C8), leucine arylamidase, acid phosphatase, naphthol-AS-BI-phosphohydrolase, β-galactosidase and β-glucosidase activities are absent; lipase (C14), valine arylamidase, cystine arylamidase, trypsin, α-chymotrypsin, α-galactosidase, α-galactosidase, α-galactosidase, β-glucuronidase, β-mannosidase, β-fucosidase and N-acetyl-β-glucosaminidase activities are present. According to the API 50CH strip test, acid is produced from none of the substrates except aesculin and ferric citrate. In the Biolog GN2 MicroPlate system, there are positive results for Tween 80, glycerol, α-D-glucose, D-fructose, D-mannitol, trehalose, D-sorbitol, arbutin, gentiobiose, maltose, salcin, N-acetyl-D-galactosamine and β-ketovaleric acid; weakly positive results for turanose, acetic acid, succinic acid mono-methyl ester and pyruvic acid; and negative results for other substrates.

The type strain, S1203T (=DSM 28697T =JCM 30067T =MCCC 1K00259T), was isolated from sediment of the northern Okinawa Trough. The DNA G+C content of the type strain is 47.7 mol%.

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Aureibacillus halotolerans gen. nov., sp. nov.


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Y. Liu and others


