Shewanella canadensis sp. nov. and Shewanella atlantica sp. nov., manganese dioxide- and hexahydro-1,3,5-trinitro-1,3,5-triazine-reducing, psychrophilic marine bacteria

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Two strains belonging to the genus Shewanella, HAW-EB2T and HAW-EB5T, were isolated previously from marine sediment sampled from the Atlantic Ocean, near Halifax harbour in Canada, for their potential to degrade explosive hexahydro-1,3,5-trinitro-1,3,5-triazine (RDX). In the present study, strains HAW-EB2T and HAW-EB5T were found to display high 16S rRNA gene sequence similarity (90–99.5 %) to species of Shewanella, but their gyrB sequences were significantly different from each other and from species of Shewanella (79–87.6 %). Furthermore, DNA–DNA hybridization showed that the genomic DNA of the two strains was only 22 % related and showed less than 41 % relatedness to closely related species of Shewanella. In comparison to other species of Shewanella, strains HAW-EB2T and HAW-EB5T were also unique in some phenotypic properties such as activities of β-galactosidase and tyrosine arylamidase and the ability to metabolize certain organic acids and sugars. Both strains HAW-EB2T and HAW-EB5T utilize malate, valerate, peptone and yeast extract as sole carbon and energy sources. The major membrane fatty acids of the two strains were C14 : 0, iso-C15 : 0, C16 : 0, C16 : 1 v 7, C18 : 1 v 7 and C20 : 5 v 3 and their major quinones were Q-7, Q-8 and MK-7. On the basis of these results, strain HAW-EB2T (NCIMB 14238T = CCUG 54553T) is proposed as the type strain of Shewanella canadensis sp. nov. and strain HAW-EB5T (NCIMB 14239T = CCUG 54554T) is proposed as the type strain of Shewanella atlantica sp. nov.

Abbreviations: RDX, hexahydro-1,3,5-trinitro-1,3,5-triazine; TMAO, trimethylamine N-oxide.

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of strains HAW-EB2T and HAW-EB5T are AY579749 and AY579752 and those for the gyrB gene sequences of strains HAW-EB2T and HAW-EB5T are AY842129 and AY842132.

A comparison of the fatty acid compositions of strains HAW-EB2T and HAW-EB5T and related species is available as supplementary material with the online version of this paper.

Members of the genus Shewanella are Gram-negative, oxidase-positive, rod-shaped, aquatic bacteria whose genomic DNA contains 38–54 mol% G+C (Bowman, 2005). At the time of writing, there are 38 species of Shewanella with validly published names (http://www.bacterio.cict.fr/s/shewanella.html), mostly isolated from marine environments, with a few isolated from freshwater sediment, industrial wastewater, clinical specimen and spoiled foods.

Members of Shewanella can grow aerobically or anaerobically by reducing alternative electron acceptors such as trimethylamine N-oxide (TMAO) and nitrate (Bowman, 2005). Species of Shewanella also require or tolerate NaCl (1–4 %) and low temperatures for growth (Zhao et al., 2005). Some species isolated from cold and deep-sea environments, such as Shewanella hanedai, S. gelidimarina, S. violacea and S. benthica, are known for production of polyunsaturated fatty acids (Kato & Nogi, 2001; Russell & Nichols, 1999; Bowman et al., 1997). Species such as Shewanella oneidensis and S. putrefaciens have been reported to be able to reduce heavy-metal oxides (Myers & Nealson, 1988; Roh et al., 2006) and chlorinated pollutants (Petrovskis et al., 1994) and for their potential to generate electricity (Ringseis et al., 2006; Park & Zeikus, 2002).

Previously, we reported the isolation of several psychrophilic strains of Shewanella, including strains HAW-EB2T and HAW-EB5T, for their ability to degrade...
hexahydro-1,3,5-trinitro-1,3,5-triazine (RDX) in sediment from an undersea unexploded ordnance dumping site at Emerald Basin, in the Atlantic Ocean, that is 215 m deep and 50 nautical miles (93 km) from Halifax harbour, Canada (Zhao et al., 2004a, b). In the present study, we provide genetic, chemotaxonomic and phenotypic evidence to propose each of the isolates as the type strain of a novel species of *Shewanella*.

As described previously, strains HAW-EB2\textsuperscript{T} and HAW-EB5\textsuperscript{T} are Gram-negative, psychrophilic bacteria with an optimal temperature of 10 °C for growth (Zhao et al., 2004a). The two strains grew well in marine medium 2216 (liquid or agar; Becton Dickinson) or Brewer anaerobic agar (Becton Dickinson) supplemented with either sea salts (Sigma; 4 %) or 2 % NaCl. The biomass had a pinkish colour, typical of *Shewanella* (Bowman, 2005; Venkateswaran et al., 1999).

Cells of strain HAW-EB2\textsuperscript{T} and HAW-EB5\textsuperscript{T} harvested after 3 days of aerobic growth in marine broth 2216 were used for transmission (TEM; Hitachi H7500) and scanning (SEM; Hitachi S3000N) electron micrographic imaging analyses under previously described experimental conditions (Zhao et al., 2006). Both strains showed cellular morphology similar to other members of *Shewanella*: straight or slightly curved rods (1–5 μm long and 0.55–0.7 μm in diameter) with a single flagellum in a polar position (Fig. 1).

To determine the phylogenetic affiliation of the two bacteria, genomic DNA (1–5 mg) was purified using Marmur’s method (Johnson, 1994) from the present isolates and *Shewanella woodyi* ATCC 51908\textsuperscript{T} and *S. hanedai* ATCC 33224\textsuperscript{T}, purchased from the American Type Culture Collection. Genes were amplified using primers generated in this study by the Genetool software (Biotools Inc.) and known sequences published in GenBank, and the experiments were conducted using standard protocols (Sambrook & Russell, 2001). The forward and reverse primers used to amplify 16S rRNA genes were 5′- AAGCCACGGCTAACTACG and 5′-GTGTGTACAAGNGCCCGGAA, respectively. The forward and reverse primers used to amplify *gyrB* (encoding the β subunit of DNA topoisomerase II) were 5′- MGGYGTTCTGCAGCGGT and 5′-GTGCCAGATTGC7TGGT, respectively. The resulting 16S rRNA (1282–1295 bases) and *gyrB* (939–1013 bases) gene PCR products were subsequently sequenced and compared with published sequences using BLAST and aligned with those of closely related species using CLUSTAL\_X (1.81). The neighbour-joining method (Saitou & Nei, 1987) included in the MEGA3 package (Kumar et al., 2004), based on pairwise nucleotide distances from Kimura’s two-parameter method (complete deletion) (Kimura, 1980), was used to build phylogenetic trees (Figs 2 and 3). The number of bootstrap repetitions was 4000.

Strains HAW-EB2\textsuperscript{T} and HAW-EB5\textsuperscript{T} were 98.9 % similar to each other in their 16S rRNA gene sequences. Phylogenetic analyses based on 16S rRNA gene sequences showed that both strains were members of *Shewanella*, 90–99.5 % similar to members of all 38 recognized species of the genus (Fig. 2). The 16S rRNA genes of strain HAW-EB2\textsuperscript{T} and strain HAW-EB5\textsuperscript{T} formed a solid cluster (with a bootstrap value of 82 %) with three intermediate-sea species of *Shewanella* (95.7–99.5 % similar), including two bioluminescent isolates (*S. woodyi* ATCC 51908\textsuperscript{T}, *S. hanedai* ATCC 33224\textsuperscript{T}) and another Halifax isolate, *Shewanella sediminis* DSM 17055\textsuperscript{T} (Fig. 2). The 16S rRNA genes of both strain HAW-EB2\textsuperscript{T} and strain HAW-EB5\textsuperscript{T} displayed the highest similarity to *S. sediminis* DSM 17055\textsuperscript{T} (HAW-EB2\textsuperscript{T}, 99.5 %; HAW-EB5\textsuperscript{T}, 98.6 %), a bacterium that was previously isolated from this site (Zhao et al., 2005). Two barophilic and deep-sea species of *Shewanella*, *S. benthica* and *S. violacea*, also showed 96.8–97.3 % 16S rRNA gene sequence similarity to strains HAW-EB2\textsuperscript{T} and HAW-EB5\textsuperscript{T}.

However, these two species, isolated from the intestine of a sea animal and sediment of deep Atlantic or Pacific Trenches (Deming et al., 1984; Nogi et al., 1998), appeared
to belong to a lineage different from the one including the three intermediate-sea species *S. woodyi*, *S. hanedai* and *S. sediminis*, as shown in Fig. 2.

Strains HAW-EB2<sup>T</sup> and HAW-EB5<sup>T</sup> were 87.6 % similar in the sequences of their *gyrB* genes. This similarity value is lower than the 90 % species cut-off value proposed for *Shewanella* by Venkateswaran *et al.* (1999), thus the two strains appeared to belong to different species of *Shewanella*. The *gyrB* gene sequences of strains HAW-EB2<sup>T</sup> and HAW-EB5<sup>T</sup> were also found to be less than 90 % similar (79–86.5 %) to known species of *Shewanella* including *S. violacea*, *S. hanedai*, *S. baltica*, and *S. benthica* (see Supplementary Table S1 in IJSEM Online). Since the relatedness values are below the 70 % species cut-off value recommended for bacteria (Wayne *et al.*, 1987; Stackebrandt & Goebel, 1994), strains HAW-EB2<sup>T</sup> and HAW-EB5<sup>T</sup> likely represent two novel species of *Shewanella*.

To provide chemotaxonomic evidence for the affiliation of the two strains to *Shewanella*, we characterized their quinone content as described by Collins (1985, 1994), Akagawa-Matsushita *et al.* (1992) and Nishijima *et al.* (1997) and analysed their fatty acid compositions using the protocol described by Bowman (2001) and Fay & Richli (1991) under experimental and instrumental conditions described previously (Zhao *et al.*, 2005). Strains HAW-EB2<sup>T</sup> and HAW-EB5<sup>T</sup> contained ubiquinones (Q-7, Q-8) and menaquinones (MK-7 and/or MMK-7) (details in the species descriptions) that are commonly found in *Shewanella* (Bowman, 2005).

To determine the relatedness between total genomic DNA of strains HAW-EB2<sup>T</sup> and HAW-EB5<sup>T</sup> and related species of *Shewanella*, we conducted genomic DNA–DNA hybridization tests using the spectrophotometric method as described by Johnson (1985b) and Bowman *et al.* (1998). As shown in Table 1, genomic DNA of strains HAW-EB2<sup>T</sup> and HAW-EB5<sup>T</sup> showed only 22 % (*n* = 3) relatedness to each other and less than 41 % (*n* = 3) relatedness to the type strains of three closely related species of *Shewanella*, *S. woodyi*, *S. hanedai* and *S. sediminis*. Since the relatedness values are below the 70 % species cut-off value recommended for bacteria (Wayne *et al.*, 1987; Stackebrandt & Goebel, 1994), strains HAW-EB2<sup>T</sup> and HAW-EB5<sup>T</sup> likely represent two novel species of *Shewanella*.
4.0, 6.0 or 8.0 % (w/v) NaCl (aerobic growth conditions). Growth in the absence of Na\(^+\) was tested in a Na\(^+\)-free agar that contained 0.3 % Bacto beef extract and 0.5 % Bacto peptone. The two strains required a minimum of 1 % (w/v) NaCl for growth and both showed optimal growth in the presence of 1.5–3 % NaCl, similar to many species of Shewanella. Strain HAW-EB5\(^T\) appeared to be more halo-tolerant than HAW-EB2\(^T\) because, at 4 % (w/v) NaCl, strain HAW-EB5\(^T\) showed good growth whereas strain HAW-EB2\(^T\) did not grow.

To compare the phenotypic properties of strains HAW-EB2\(^T\) and HAW-EB5\(^T\) with known species of Shewanella further, we used previously described protocols (Bowman, 2001; Smibert & Krieg, 1994) to test the following biochemical and physiological properties: spore formation, H\(_2\)S formation from thiosulfate, acid production from various sugars (1 % w/v in Leifson modified O-F medium), activities of catalase, oxidase and DNase (in BBL DNA agar, supplemented with 4 % w/v sea salts; Becton Dickinson), hydrolysis of casein (50 % w/v skimmed milk), gelatin (1 %, w/v), Tween\(_s\) 20, 40 and 80 (1 % w/v), olive oil (1 % w/v), lecithin (5 % w/v egg yolk), pure chitin (0.3 % w/v), alginate (1 % w/v) and starch (1 % w/v) using marine broth 2216 as a basal medium. Aerobic utilization of substrates (0.1 % w/v) as sole carbon and energy sources was tested in basic marine salts medium (pH 7.0) containing 0.1 % (w/v) NH\(_4\)Cl as the nitrogen source (Zhao et al., 2005). Reduction of electron acceptors was tested on Brewer anaerobic agar supplemented with 2 % (w/v) NaCl (in anaerobic jars) and one of the following compounds: manganese dioxide (MnO\(_2\), 40 mM), ferric citrate (40 mM), amorphous iron oxide (FeOOH, 40 mM), TMAO (5 mM), nitrate (5 mM), nitrite (5 mM) and elemental sulfur (40 mM). Clear zones around colonies were used to indicate reduction of Fe(III), Mn(IV) and sulfur (Myers & Nealson, 1988). Enhanced growth of strains in the presence of electron acceptors was used as an indicator of dissimilatory reduction. Bacterial growth on agar was estimated by multiplying the average area of colonies and the total number of colony-forming units (Zhao et al., 2005). Additional enzyme activities and utilization of substrates were tested by API Rapid 20E and ID32A (bioMe´rieux) test kits and GN2 microplates (Biolog) (using a cell suspension in sea-salts medium with an OD\(_{600}\) of 0.9; 10 days incubation). Results were determined by colour change as instructed by the manufacturers: no colour change, negative; faint colour change, yellow; yellow–red; red; deep red.

### Table 1. Similarity of 16S rRNA and gyrB gene sequences and total genomic DNA–DNA relatedness between the novel isolates and type strains of related species of Shewanella

<table>
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<th>Strain</th>
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<td>1</td>
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<tr>
<td>1. HAW-EB2(^T)</td>
<td>–</td>
<td>98.9/87.6</td>
<td>99.5/85.5</td>
<td>97.8/83.0</td>
<td>97.8/83.0</td>
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<td>2. HAW-EB5(^T)</td>
<td>22</td>
<td>–</td>
<td>98.6/86.5</td>
<td>97.8/84.5</td>
<td>97.1/80.6</td>
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<tr>
<td>3. <em>S. sediminis</em> HAW-EB3(^T)</td>
<td>41</td>
<td>40</td>
<td>–</td>
<td>ND</td>
<td>ND</td>
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<tr>
<td>4. <em>S. woodyi</em> ATCC 51908(^T)</td>
<td>9</td>
<td>14</td>
<td>ND</td>
<td>–</td>
<td>ND</td>
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<tr>
<td>5. <em>S. hanedai</em> ATCC 33224(^T)</td>
<td>20</td>
<td>15</td>
<td>ND</td>
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negative for API Rapid 20E and ID32A and weakly positive for Biol og tests; strong colour change, positive. For comparison, S. sediminis HAW-EB3T, S. woodyi ATCC 51908T, S. halendai ATCC 33224T and S. bentic a ATCC 43991 were tested for reduction of MnO2, H2S production from thi osulfate, activity of cata lase and other enzymes using ID32A and metabolism of Biol og (GN2) substrates under the conditions used for strains HAW-EB2T and HAW-EB5T. All of the above physiological properties were tested in triplicate at 10 °C unless noted otherwise.

The two strains, like all species of Shewanella, were positive for oxidase activity and for reduction of TMAO and nitrate. Cluster analyses of phenotypic properties, conducted as described previously (Zhao et al., 2005), of the two strains and all species of Shewanella showed that strains HAW-EB5T and HAW-EB2T were close to the intermediate-sea species S. sediminis and S. woodyi, consistent with the earlier observation made from 16S rRNA and gyrB gene sequencing. Like S. sediminis, S. woodyi and S. benthica, the two strains reduced MnO2, a common sediment component in the marine environment. As shown in Table 2, strains HAW-EB5T and HAW-EB2T exhibited significant differences from each other and from related species (S. sediminis, S. woodyi, S. halendai, S. violacea and S. benthica) in several phenotypic properties such as bioluminescence, requirements for temperature, NaCl and pressure and metabolism of certain sugars and acids.

All of the genetic (Figs 2 and 3; Table 1), chemotaxonomic (Supplementary Table S1) and phenotypic (Table 2) data presented above demonstrate that strains HAW-EB2T and HAW-EB5T represent novel species of Shewanella, named Shewanella canadensis sp. nov. and Shewanella atlantica sp. nov., respectively.

**Description of Shewanella canadensis sp. nov.**

*Shewanella canadensis* (ca.na.den’sis. N.L. fem. adj. canadensis from Canada, the country nearest to the sediment sampling site, Emerald Basin, where the type strain was isolated).

Cells are Gram-negative, non-sporing, straight or slightly curved rods, 1.5–3.5 μm long and 0.65–0.75 μm in diameter. Motile by a single flagellum in a polar position. Biomass is dark orange or slightly pinkish and non-bioluminescent. Psychrophilic growth at temperatures of 4–25 °C (optimum growth at 10 °C); no growth at 30 °C. Na+ is required for growth; grows at 1–4 % (w/v) NaCl (growth at 4 % NaCl is 32 % of optimum). No growth at 6 % NaCl. TMAO, MnO2, nitrate, nitrite and hexahydro-1,3,5-trinitro-1,3,5-triazine (RDX) are reduced. Negative for reduction of Fe(III) and elemental sulfur. Weak production of H2S from thiosulfide. Positive for oxidase, nitroreductase (reduction of nitrate, nitrite and nitro group of RDX), caseinase, chitinase, gelatinase and DNase. Weakly positive for catalase. Negative for alginate, amylose, agarase and lipase (hydrolysis of Tweens 20, 40 and 80). In API ID32A and API 20E tests, positive for urease, ornithine decarboxylase, lysine decarboxylase, N-acetyl-β-D-glucosaminidase, β-galactosidase, β-galactosidase-6-phosphate, alkaline phosphatase, arginine arylamidase, proline arylamidase, leucine glycine arylamidase, tyrosine arylamidase, alani ne arylamidase, leucine arylamidase and glutamyl glutamic acid arylamidase. In Biolog GN2 microplate tests, positive for metabolism of Tween 80, N-acetyl-D-glucosamine, acetate, β-hydroxybutyrate, DL-lactate, propionate, succinate, L-alanine, L-serine, L-threonine, L-leucine, L-aspartate, L-proline, L-alanyl glycine, glycy l L-aspartate, glycy l L-glutaminate, inosine, uridine and thymidine; weakly positive for Tween 40 and methylpyruvate. N-Acetyl-D-glucosamine is only oxidized to acid under oxic conditions. Galactose, lactose, fructose, sucrose, mannose and glucose are not oxidized or fermented to acids. Tween 40, malate, succinate, valerate, peptone and yeast extract are used as sole carbon and energy sources. Fatty acids C12:0 3-OH (1 %), iso-C13:0 (5 %), C14:0 (12 %), C14:1 (1 %), C15:0 (1 %), iso-C15:0 (8 %), C16:0 (19 %), C16:1ω7t (39 %), C18:0 (1 %), C18:1ω7t (4 %), C20:1 (1 %), C20:5ω3 (4 %) and C21:0 (1 %) are produced. Quinone composition is Q-7 (39.1 %), Q-8 (15.9 %), MK-7 (44.9 %) and MMK-7 (trace). The molar DNA G+C content is 46.4 ± 0.3 mol%.

The type strain is HAW-EB2T (=NCIMB 14238T =CCUG 54553T).

**Description of Shewanella atlantica sp. nov.**

*Shewanella atlantica* (at.lan’ti.ca. L. fem. adj. atlantica of the Atlantic Ocean, where the type strain was isolated).

Cells are Gram-negative, non-spore-forming, straight or slightly curved rods, 2–5 μm long and 0.5–0.6 μm in diameter. Motile by a single flagellum in a polar or subpolar position. Biomass is slightly pinkish and non-bioluminescent. Psychrophilic growth at temperatures of 4–25 °C (optimum growth at 10 °C); no growth at 30 °C. Na+ is required for growth; grows at 1–4 % (w/v) NaCl (growth at 4 % NaCl is 32 % of optimum). No growth at 6 % NaCl. TMAO, MnO2, nitrate, nitrite, thiosulfate and RDX are reduced. H2S is produced from thiosulfate. Negative for reduction of Fe(III) and elemental sulfur. Positive for oxidase, nitroreductase, chitinase, lipase (hydrolysis of Tweens 20, 40 and 80) and DNase. Weakly positive for catalase and caseinase. Negative for gelatinase, alginate and amylose. In API ID32A and API 20E tests, positive for urease, ornithine decarboxylase, lysine decarboxylase, N-acetyl-β-D-glucosaminidase, β-galactosidase, glutamate decarboxylase, β-galactosidase-6-phosphate, alkaline phosphatase, arginine arylamidase, proline arylamidase, leucine glycine arylamidase, alanine arylamidase, glycine arylamidase, leucine arylamidase, serine arylamidase and glutamyl glutamic acid arylamidase. In Biolog GN2 microplate tests, positive for metabolism of Tweens 40 and 80, N-acetyl-D-glucosamine, acetate, lactate,
Table 2. Characteristics that differentiate strains HAW-EB2^T and HAW-EB5^T and related species of Shewanella

Unless otherwise noted, properties of *S. woodyi*, *S. hanedai* and *S. benthica* were obtained in the present study using strains ATCC 51908^T, ATCC 33224^T and ATCC 43991^T, respectively, and under the same experimental conditions used for HAW-EB2^T and HAW-EB5^T. Other sources of data for reference species are indicated. +, Positive; −, negative; w, weak; ND, no data. In the present study, all strains were found to be positive for reduction of MnO_2_, activities of N-acetyl-D-glucosaminidase, alkaline phosphatase, arginine arylamidase, proline arylamidase, leucine glycine arylamidase, alanine arylamidase, glutamyl glutamic acid arylamidase and arabinosidase (the latter was weak for *S. benthica* ATCC 43991^T) and metabolism of Tweens 40 and 80, DL-lactate, L-alanine, L-serine, L-threonine, glycyl L-aspartate, glycyl L-glutamate, L-proline, L-leucine, L-alanyl glycine, inosine, uridine and thymidine. All strains were negative for metabolism of other substrates of GN2 microplates and activities of enzymes tested by API Rapid ID 32A.

<table>
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<th>Characteristic</th>
<th>HAW-EB2^T</th>
<th>HAW-EB5^T</th>
<th>S. sediminis</th>
<th>S. woodyi</th>
<th>S. hanedai</th>
<th>S. violacea</th>
<th>S. benthica</th>
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<tr>
<td>Methylypyruvate</td>
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<td>Propionate</td>
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<td>α-Hydroxybutyrate</td>
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<td>β-Hydroxybutyrate</td>
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<tr>
<td>Succinate</td>
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<tr>
<td>Bromosuccinate</td>
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<tr>
<td>Sampling depth (m)$</td>
<td>215</td>
<td>215</td>
<td>215</td>
<td>200–400</td>
<td>100–200</td>
<td>5110</td>
<td>5920</td>
</tr>
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</table>

*Data taken from the following studies: a, Zhao *et al.* (2005); b, Bowman (2005); c, Makemson *et al.* (1997); d, Jensen *et al.* (1980); e, Nogi *et al.* (1998).

†Relative amount of biomass obtained at 4 % NaCl shown in parentheses in comparison with that obtained at 2 % NaCl.
‡Gen, Gentiobiose; Glc, glucose; Glu, glutamate; Mal, maltose; Tre, trehalose.
§Sampling sites: strains HAW-EB2^T, HAW-EB5^T and *S. sediminis* HAW-EB3^T. Emerald Basin sediment, Atlantic Ocean off Halifax; *S. woodyi* strains, detritus, squid ink and seawater of Alboran Sea; *S. hanedai* strains, sediment and water of Antarctic, Arctic and Pacific Oceans; *S. violacea* strains, sediment of Ryuku Trench; *S. benthica* ATCC 43991^T, intestine of *Scopelarchus shellegi*, Puerto Rico Trench.

methylpyruvate, L-alanine, L-aspartate, L-serine, L-leucine, L-proline, L-threonine, L-alanyl glycin, glycyl L-aspartate, glycyl L-glutamate, inosine, uridine and thymidine; weakly positive for glycerogen, α-hydroxybutyrate, β-ketobutyrate, succinate and bromosuccinate. Acetate, malate, valerate, fructose, peptone and yeast extract are used as sole carbon and energy sources for growth. N-Acetyl-D-glucosamine is oxidized weakly and fermented to acid. Fructose and sucrose are fermented very slowly to acids. Galactose, lactose, mannose and glucose are not oxidized or fermented to acids. Fatty acids C_{12:0} 3-OH (3 %), iso-C_{13:0} (3 %), C_{13:0} 3-OH (5 %), C_{14:0} (4 %), C_{14:1} (1 %), anteiso-C_{15:0} (1 %), C_{15:0} (1 %), iso-C_{15:0} (11 %), C_{16:0} (19 %), C_{16,1ω7} (34 %), iso-C_{17:0} (1 %), C_{18:0} (2 %), C_{18:1ω7} (7 %), C_{20:1} (1 %), C_{20:5ω3} (6 %) and C_{22:1} (1 %) are produced. Quinone composition is Q-7 (13.5 %), Q-8
(10.3%), MK-7 (67.9%) and MMK-7 (8.3%). The molar DNA G+C content is 46.4 ± 1 mol%.

The type strain is HAW-EB5T (=NCIMB 14239T =CCUG 54554T).

Acknowledgements

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References


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