Amphibacillus cookii sp. nov., a facultatively aerobic, spore-forming, moderately halophilic, alkalithermotolerant bacterium

Benoit Pugin,1,2 Jenny M. Blamey,2 Bonnie K. Baxter3 and Juergen Wiegel1

1Department of Microbiology, University of Georgia, 1000 Cedar Street, Athens, GA 30602, USA
2Fundación Biociencia, José Domingo Cañas 2280, Ñuñoa, Santiago, Chile
3Great Salt Lake Institute, Westminster College, 1840 South, 1300 East, Salt Lake City, UT 84105, USA

Novel strains of facultatively aerobic, moderately alkaliphilic and facultatively halophilic bacteria were isolated from a sediment sample taken from the Southern Arm of Great Salt Lake, Utah. Cells of strain JW/BP-GSL-QD7 (and related strains JW/BP-GSL-RA and JW/BP-GSL-WB) were rod-shaped, spore-forming, motile bacteria with variable Gram-staining. Strain JW/BP-GSL-QD7 grew under aerobic conditions between 14.5 and 47 °C (optimum 39 °C), in the pH3.7–10.3 (optimum pH3.7–8.0), and between 0.1 and 4.5 M Na+ (optimum 0.9 M Na+). No growth was observed in the absence of supplemented Na+. Strain JW/BP-GSL-QD7 utilized L-arabinose, D-fructose, D-galactose, D-glucose, inulin, lactose, maltose, mannitol, D-mannose, pyruvate, D-ribose, D-sorbitol, starch, trehalose, xyitol and D-xylose under both aerobic and anaerobic conditions, and used ethanol and methanol only under aerobic conditions. Strains JW/BP-GSL-WB and JW/BP-GSL-RA had the same profiles except that methanol was not used aerobically. During growth on glucose, the major organic compounds formed under aerobic conditions were acetate and lactate, and under anaerobic conditions, the fermentation products were formate, acetate, lactate and ethanol. Oxidase and catalase activities were not detected and cytochrome was absent. No respiratory quinones were detected. The main cellular fatty acids were iso-C15:0 (39.1 %) and anteiso-C15:0 (36.3 %). Predominant polar lipids were diphosphatidylglycerol, phosphatidylglycerol and an unknown phospholipid. Additionally, a small amount of an unknown glycolipid was detected. The DNA G+C content of strain JW/BP-GSL-QD7 was 35.4 mol% (determined by HPLC). For strain JW/BP-GSL-QD7 the highest degree of 16S rRNA gene sequence similarity was found with Amphibacillus jilinensis (98.6 %), Amphibacillus sediminis (96.7 %) and Amphibacillus tropicus (95.6 %). The level of DNA–DNA relatedness between strain JW/BP-GSL-QD7 and A. jilinensis Y1T was 58 %. On the basis of physiological, chemotaxonomic and phylogenetic data, strain JW/BP-GSL-QD7 represents a novel species of the genus Amphibacillus, for which the name Amphibacillus cookii sp. nov. is proposed. The type strain is JW/BP-GSL-QD7 (=ATCC BAA-2118T=DSM 23721T).

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of strains JW/BP-GSL-QD7, JW/BP-GSL-WB and JW/BP-GSL-RA are HM057160, HM057164 and HM057162, respectively. Two supplementary figures are available with the online version of this paper.

The genus Amphibacillus currently comprises five recognized species, the type species Amphibacillus xylanus, Amphibacillus fermentum, A. tropicus, A. sediminis and A. jilinensis. Members of the genus Amphibacillus are rod-shaped, facultatively aerobic, have a lack of catalase activity and cytochromes are absent. A mixed water-sediment sample from an area with visible salt crusts was collected from the Southern Arm of Great Salt Lake, Utah (Antelope Island marina, 40°44′17′′ N, 111°52′28″ W). At that time, the sediment on the surface from which the sample was taken had a temperature of 40 °C and a pH of 7.4. The lake water at this relatively frequently sampled location usually has a pH around 7.3 and a total salt concentration of 12 % (w/v). The pore water of the sample had about 32 % (w/v) NaCl, as measured by refractive index. Enrichment cultures were prepared by inoculating 5 g soil
in 75 ml pre-reduced carbonate-buffered medium consisting of (l-1): 0.2 g KH2PO4, 0.1 g MgCl2·6H2O, 0.5 g NH4Cl, 0.2 g KCl, 100 g NaCl, 68 g Na2CO3, 38 g NaHCO3, 0.7 g cysteine/HCl, 5 g yeast extract, 5 g tryptone, 5 g sucrose, 1 ml trace element solution (Kevbrin & Zavarzin, 1992) and 10 ml vitamin solution (Wolín et al., 1963). The pH37°C was adjusted to 9.5 with KOH pellets. Enrichments were incubated under anaerobic conditions (O2-free N2 gas) at 37°C. After three successive transfers in liquid media, pure cultures were obtained in agar (2%, w/v) shake-roll tubes using the above medium (Ljungdahl & Wiegel, 1986). The independently obtained strains, JW/BP-GSL-QDT, JW/BP-GSL-WB and JW/BP-GSL-RA, were further characterized. The three strains obtained from separate enrichments inoculated from the same sediment sample had very similar growth behaviours and identical 16S rRNA sequences and thus, for further characterization, the type strain was chosen arbitrarily due to its slightly faster growth rate.

Colonies of the three strains appeared after 1 day in 2% (w/v) agar shake-roll tubes kept under a gas phase of O2-free N2 and incubated at 37°C. Colonies were 0.8–2 mm in diameter, circular and white. Cell morphology was observed via light microscopy (Olympus VANOX phase-contrast microscope). In the exponential growth phase, the rod-shaped cells were 0.5–0.6 μm in diameter and 2–7 μm in length (Fig. 1a). Cells generally occurred singly, in pairs and infrequently in short chains. Tumbling motility was observed. Gram staining was performed using the Burke method (Doetsch, 1981); it was positive at the early exponential growth phase and became negative during late exponential growth phase.

Formation of spores was induced on a solid agar plate incubated aerobically using a 10-fold reduction of yeast extract, tryptone and sucrose concentrations along with the addition of 6 mg MnCl2·4H2O l-1. Sporulation of strain JW/BP-GSL-QDT was observed after 1 day incubation at 37°C, though only rarely. Spores are circular, 1.2–1.3 μm in diameter, located terminally and caused the mother cell to swell (Fig. 1b). Viable cultures were obtained after cultures were heated at 100°C for 2 min.

When tested, the isolates were found to be facultatively aerobic and thus, unless otherwise indicated, the determination of properties were done under aerobic growth conditions in cotton-plugged tubes shaken at 160 r.p.m., using the carbonate-buffered medium supplemented with 0.5% (w/v) yeast extract, 0.5% (w/v) tryptone and 0.5% (w/v) sucrose. For all cultural and physiological analyses, the pH was set at 37°C using a pH electrode calibrated at 37°C to avoid the influence of temperature on pH (Wiegel, 1998). The salinity range for growth was assessed between 0 and 5 M Na+ using intervals of 0.1–0.2 M Na+. Due to the presence of the sodium carbonates used for pH control, salinity equivalents are given in M of Na+. The salinity range for growth of strains JW/BP-GSL-RA and JW/BP-GSL-QDT at 37°C and pH37°C 9.5 was 0.1–4.5 M Na+ [corresponding to 0.6–26.5% (w/v) NaCl equivalent] with an optimum of 0.9 M Na+ [corresponding to approximately 5% (w/v) NaCl equivalent]. Strain JW/BP-GSL-WB grew between 0.1 and 4.3 M Na+ with an optimum at 0.9 M Na+. No growth occurred in the absence of Na+ (substituting Na2CO3 and NaHCO3 with K2CO3 and KHCO3) or at 4.8 M Na+ and above. Maximum Na+ tolerance was neither increased nor decreased in the presence of supplemented 500 mM KCl.

The temperature range for growth was determined using a temperature gradient incubator (Scientific Industries) in a carbonate-buffered medium containing 0.9 M Na+ (0.32 M Na2CO3 and 0.23 M NaHCO3) and at pH37°C 9.5. The temperature range for growth was assessed between 4 and 59°C, with temperature intervals of 1.5–2°C. Strain JW/BP-GSL-QDT was mesophilic to slightly thermotolerant, growing in a temperature range of 14.5–47°C with a broad temperature optimum of 37–43°C (no growth observed at ≤12.5°C or at ≥49°C when incubated for up to 2 weeks). Strains JW/BP-GSL-RA and JW/BP-GSL-WB.
The pH range for growth was determined at an Na⁺ concentration of 0.9 M and at 37 °C using carbonates (0.32 M Na₂CO₃, 0.23 M NaHCO₃), imidazole (50 mM) and CAPS (50 mM) buffers. The pH range for growth was assessed between pH 37 °C 6 and 11.8, with intervals of 0.2–0.3 pH units. The pH 37 °C range for growth of the strain JW/BP-GSL-QD³ was 6.5–10.3, with an optimum at pH 37 °C 8.0, with no growth at pH 37 °C 6.3 and below, or at pH 37 °C 10.5 and above. Strains JW/BP-GSL-RA and JW/BP-GSL-WB both grew in a pH 37 °C range of 6.5–10.0 with an optimum pH 37 °C around 8.0. The doubling time for strain JW/BP-GSL-QD³ was 1.8 h under aerobic conditions at 37 °C, 160 r.p.m., pH 37 °C 8.0, 0.9 M Na⁺, with 0.5 % (w/v) yeast extract, 0.5 % (w/v) tryptone and 0.5 % (w/v) sucrose as substrates.

The strains were tested for utilization of various substrates (0.5 %, w/v) using carbonate-buffered medium containing 0.2 % (w/v) yeast extract, 0.9 M Na⁺, at 37 °C, pH 37 °C 9.5, and under both aerobic and anaerobic conditions. Cultures were incubated for up to 5 days and growth was judged positive if, in the third successive transfer, the OD₆₀₀ of the culture was twice that of a control culture incubated with only 0.2 % yeast extract. Strain JW/BP-GSL-QD³ used D-arabinose, D-fructose, D-galactose, D-glucose, inulin, lactose, maltose, mannitol, D-mannose, pyruvate, D-ribose, D-sorbitol, starch, trehalose, xylitol and D-xylene under both aerobic and anaerobic conditions. Ethanol and methanol were utilized under aerobic conditions. No growth was observed aerobically or anaerobically with citrate, formate, gluconic acid, L-glycine and trimethylamine. The substrate utilization profile for strains JW/BP-GSL-RA and JW/BP-GSL-WB was the same except for methanol, which was not used aerobically. The main organic products from glucose under aerobic conditions (shaking at 160 r.p.m.) were acetate and lactate. Under anaerobic conditions, formate, acetate, ethanol and lactate were the main organic fermentation products.

For the catalase test, the production of bubbles upon addition of 3 % H₂O₂ solution to cells was followed (Staphylococcus epidermidis ATCC 14990 was used as a positive control). Oxidase activity was determined by transferring cells to filter paper with freshly prepared 1 % (w/v) n,n-dimethyl-p-phenylenediamine hydrochloride. Strain JW/BP-GSL-QD³ was negative for both catalase and oxidase tests. Moreover, spectrophotometric analysis of the cell lysis lacked any evidence of cytochromes based upon a lack of an identifiable Soret peak. Methyl red and Voges–Proskauer tests (Lányi, 1987) were both negative. Biochemical characteristics were determined under both aerobic and anaerobic conditions using the API ZYM and API 20E system (bioMérieux) incubated at 37 °C for 4 and 18 h respectively. To perform these assays, cells were suspended in the optimum growth medium (0.9 M Na⁺, pH 37 °C 8.0) lacking sucrose, tryptone and yeast extract. The procedures were done according to the manufacturer's instructions. The same profiles were obtained aerobically and anaerobically for the three related strains, except for those under anaerobic conditions whose esterase lipase and β-galactosidase activities were negative. The following profiles were obtained: β-galactosidase, β-glucosidase, arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase, urease, tryptophan deaminase, esterase-C4 and esterase lipase activities were positive. Tryptophan deaminase, gelatinase, alkaline phosphatase, lipase-C14, leucine arylamidase, valine arylamidase, cysteine arylamidase, trypsin, x-chymotrypsin, acid phosphatase, napthol-AS-Bl-phosphohydrolase, α-galactosidase, β-glucuronidase, α-glucosidase, N-acetyl-β-glucosaminidase, α-mannosidase and α-fucosidase activities, nitrate reduction, H₂S production, indole production and acetoin production were negative. Citrate utilization was positive.

Polar lipid analyses, quinone analyses and cellular fatty acid composition were carried out by the Identification Service of the DSMZ and Dr B. J. Tindall, DSMZ, Braunschweig, Germany. For these three analyses, cells were grown at the DSMZ, in medium DSM 545 (http://www.dsmz.de/microorganisms/medium/pdf/DSMZ_Medium54a.pdf), under aerobic conditions at pH 8 and 37 °C. Cells in exponential phase were collected for analysis. Quinones and polar lipids were extracted using the two stage method described by Tindall (1990a, b). Polar lipids were analysed by 2D silica gel TLC (Tindall et al., 2007), and the predominant polar lipids of strain JW/BP-GSL-QD³ were diphosphatidylglycerol, phosphatidyglycerol and an unknown phospholipid (PL1). Additionally, a small amount of an unknown glycolipid was detected (the TLC plate is available as Fig. S1, available in IJSEM Online). One spot has not been labelled because it may not be a lipid, but rather a large hydrophobic peptide. Indeed, this ninhydrin-positive spot appears to be much smaller and weaker when stained with dodecamethylbodophosphoric acid. No quinones were detected from JW/BP-GSL-QD³, as is also the case for the other species of the genus Amphibacillus. Fatty acid methyl esters were obtained by saponification, methylation and extraction using the methods of Miller (1982) and Kuykendall et al. (1988). The fatty acid methyl ester mixtures were separated using the Sherlock Microbial Identification System (MIS; MIDI), which consisted of an Agilent model 6890N gas chromatograph fitted with a 5 % phenyl-methyl silicone capillary column (0.2 mm × 25 m), and a flame-ionization detector. Peaks were automatically integrated, and fatty acid names and percentages were calculated by using the MIS Standard Software and database (MIDI). The fatty acid profile was largely composed of iso-C₁₅:₀ (39.8 %) and anteiso-C₁₅:₀ (36.3 %). In addition, C₁₄:₀ (3.0 %), C₁₅:₀ (1.0 %), C₁₆:₀ (6.9 %), iso-C₁₄:₀ (1.0 %), iso-C₁₆:₀ (2.3 %), iso-C₁₇:₀ (2.0 %) and anteiso-C₁₇:₀ (6.7 %) were detected.

The resistance of strains JW/BP-GSL-QD³, JW/BP-GSL-RA and JW/BP-GSL-WB was tested using antibiotic discs on freshly inoculated agar plates. All strains were sensitive to erythromycin (15 µg), penicillin (10 IU), ampicillin (10 µg) and vancomycin (30 µg), but were not sensitive to...
tetracycline (30 μg), kanamycin (30 μg), streptomycin (10 μg), neomycin (30 μg) or bacitracin (10 IU).

The DNA of strains JW/BP-GSL-QDT, JW/BP-GSL-RA and JW/BP-GSL-WB were extracted using an UltraClean DNA isolation kit (Mo Bio). The DNA G+C content was 35.4 (±0.69; n=4) mol%, determined by HPLC according to the method described by Mesbah et al. (1989). The 16S rRNA genes were amplified via PCR using primers 27F and 1492R, and PrimeStar HS polymerase (Takara), with the thermocycler conditions of 10 s at 98 °C, 5 s at 58 °C and 90 s at 72 °C, repeated for a total of 30 cycles. The 16S rRNA genes were sequenced by Macrogen (Seoul, Korea), and subsequently compared with all GenBank entries by BLAST search (http://blast.ncbi.nlm.nih.gov/Blast.cgi).

The nearly complete 16S rRNA gene sequences of strains JW/BP-GSL-QDT, JW/BP-GSL-RA and JW/BP-GSL-WB were aligned with highly similar species using MEGA v5.05. A phylogenetic tree was constructed (Fig. 2) using the neighbour-joining method (Rzhetsky & Nei, 1992) and distances were computed using the Jukes–Cantor correction method (Jukes & Cantor, 1969). Numbers at nodes represent bootstrap percentages (1000 replicates) with only values above 70% shown. Bar, 0.001 nt substitution per 100 nt.

Phylogenetically, strains JW/BP-GSL-QDT, JW/BP-GSL-RA and JW/BP-GSL-WB belong to the rRNA family group 1 of bacilli and cluster within the genus Amphibacillus. Beside differences in the 16S rRNA gene sequences, JW/BP-GSL-QDT can be distinguished from the genus Paralibiacillus by its lack of catalase, quinones and cytochromes (Ishikawa et al., 2002), from the genus Natronobacillus by its lack of catalase (Sorokin et al., 2008), and from the genus Halolactibacillus by its fatty acid composition (Ishikawa et al., 2005). Indeed, strain JW/BP-GSL-QDT showed a fatty acid profile similar to Amphibacillus and Natronobacillus species, mainly composed of C16:0 iso-C15:0 and anteiso-C15:0, but not to Halolactibacillus species, which are mainly composed of anteiso-C13:0 and C16:0. The novel isolates can be distinguished from other Amphibacillus species and closely related genera by various physiological properties (Table 1). Compared with A. jilinensis and based on its low DNA–DNA relatedness...
Table 1. Differential characteristics of *Amphibacillus cookii* strain JW/BP-GSL-QD\(^T\) and related organisms

1, JW/BP-GSL-QD\(^T\); 2, *A. jilinensis* (data from Wu et al., 2010); 3, *A. sediminis* (An et al., 2007); 4, *A. fermentum* (Zhilina et al., 2001); 5, *A. tropicus* (Zhilina et al., 2001); 6, *A. xylanus* (Niimura et al., 1990); 7, *N. azotifigens* (Sorokin et al., 2008); 8, *Paralibacillus ryukyuensis* (Ishikawa et al., 2002); 9, *Halolactibacillus halophilus* (Ishikawa et al., 2005). ND, Not determined.

<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>
<th>8</th>
<th>9</th>
</tr>
</thead>
<tbody>
<tr>
<td>Source of isolation</td>
<td>Great Salt Lake, USA</td>
<td>Lake Jilin, China</td>
<td>Lake Hamana, Japan</td>
<td>Lake Magadi, Kenya</td>
<td>Lake Magadi, Kenya</td>
<td>Manure compost</td>
<td>Soda lake, Russia</td>
<td>Decaying marine algae</td>
<td>Decaying marine algae</td>
</tr>
<tr>
<td>Motility</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Spore formation</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>-</td>
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<tr>
<td>Rod size (μm)</td>
<td>0.5–0.6×2–7</td>
<td>0.4–0.6×2–3.2</td>
<td>ND</td>
<td>0.5–0.7×1.5–4</td>
<td>0.4–0.5×2–6</td>
<td>0.3–0.5×0.9–1.9</td>
<td>0.4–0.5×2–6</td>
<td>0.4–0.5×2.3–4.5</td>
<td>0.6–0.9×3.6–4.5</td>
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<tr>
<td>Temp. range (optimum) (°C)</td>
<td>14.5–47 (39)</td>
<td>15–45 (32)</td>
<td>17–55 (27)</td>
<td>18–56 (36–38)</td>
<td>18–56 (38)</td>
<td>25–45 (ND)</td>
<td>ND (36–38)</td>
<td>10–47.5 (37–40)</td>
<td>5–40 (30–37)</td>
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<td>Na(^+) range (optimum) (M)</td>
<td>0.1–4.5 (0.9)</td>
<td>0–2.8 (0.5)</td>
<td>0–1.0 (ND)</td>
<td>0.17–3.3 (1.87)</td>
<td>0.17–3.6 (1–1.87)</td>
<td>&lt;1 (ND)</td>
<td>0.2–4 (1.0–1.5)</td>
<td>0–3.8 (0.1–0.5)</td>
<td>0–4.1 (0.3–0.5)</td>
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<td>pH range (optimum)</td>
<td>6.5–10.3 (8)</td>
<td>7.5–10.5 (9.0)</td>
<td>7.0–9.0 (8.5)</td>
<td>7.0–10.5 (8.0–9.5)</td>
<td>8.5–11.5 (9.5–9.7)</td>
<td>8.0–10.0 (ND)</td>
<td>7.5–10.6 (9.5–10)</td>
<td>5.5–9.5 (7.0–8.5)</td>
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<td>Catalase activity</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>-</td>
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<tr>
<td>Major isoprenoid quinone</td>
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<td>None</td>
<td>None</td>
<td>None</td>
<td>None</td>
<td>None</td>
<td>None</td>
<td>None</td>
<td>MK-7</td>
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<tr>
<td>DNA G+C content (mol%)</td>
<td>35.4*</td>
<td>37.7†</td>
<td>42.3*</td>
<td>41.5†</td>
<td>39.2†</td>
<td>36†</td>
<td>36.1†</td>
<td>35.6*</td>
<td>39.6–40.7*</td>
</tr>
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</table>

*Determined by HPLC method.
†Determined by DNA melting (T\(_{\text{m}}\)).
(58 %), its dependence on Na\(^+\), its higher tolerance to salt (up to 4.5 M Na\(^+\)), and its higher optimal temperature for growth (39 °C), JW/BP-GSL-QD\(^T\) represents a novel species. The other two strains, JW/BP-GSL-RA and JW/BP-GSL-WB, share the same physiological differences to A. jilinensis as does the type strain.

However, from the topology of the 16S rRNA gene sequence-based trees, it is evident that the species content of the genus Amphibacillus in its actual state needs a revision. The type species Amphibacillus xylanus forms a group with Amphibacillus fermentum and all species from the genera Paraliobacillus and Halolactibacillus, while A. jilinensis, A. sediminis, A. tropicus and Natronobacillus azotifigens and the currently described novel species form a separate lineage. An extensive and detailed analysis of phylogenetic data combined with physiological and chemotaxonomic data of all the closely related genera is required to achieve an accurate reclassification of the genus Amphibacillus. This work is outside of the scope of this manuscript.

Until this work is done, the strains JW/BP-GSL-QD\(^T\), JW/BP-GSL-RA, and JW/BP-GSL-WB are placed in the presently described genus Amphibacillus, as Amphibacillus cookii sp. nov., which is based on the 16S rRNA gene sequence analysis, DNA–DNA hybridization results and differences in physiological and chemotaxonomic properties. Strain JW/BP-GSL-QD\(^T\) (=ATCC BAA-2118\(^T\)=DSM 23721\(^T\)) is designated the type strain.

**Description of Amphibacillus cookii sp. nov.**

*Amphibacillus cookii* (cook’i.i. N.L. gen. masc. n. *cookii*, named in honour of Gregory Cook, to recognize his contribution to the microbiology and bioenergetics of extremophiles).

The white circular colonies grown inside anaerobic 2 % agar shake roll-tubes contain tumbling motile cells of 0.5–0.6 \(\mu\)m in diameter and 2–7 \(\mu\)m in length and appear singly, in pairs and infrequently in short chains. Gram staining is positive during early exponential growth phase and becomes negative during late exponential growth phase. Cells are facultatively aerobic. The temperature range for growth of the type strain (values in parentheses indicate the other strains) is 14.5–47 (12–45) °C with an optimum at 39 (35) °C; no growth at \(\leq 12.5\) °C or at \(\geq 49\) °C. The pH\(^-\) range for growth is 6.5–10.3 (6.5–10.0) with an optimum at pH\(^+\) 8.0. No growth at \(\leq \text{pH} 6.3\) or at \(\geq \text{pH}\ 11.5\). The salinity range for growth is 6.5–10.3 (6.5–10.3) M Na\(^+\). No growth occurs in the absence of Na\(^+\) or at \(\geq 4.8\) M Na\(^+\). Oxidase and catalase activities are negative. Cytochrome is absent. Methyl red and Voges–Proskauer tests are negative. Yeast extract or tryptone is required for growth. In the presence of 0.2 % (w/v) yeast extract, L-arabinose, D-fructose, D-galactose, D-glucose, inulin, lactose, maltose, mannitol, D-mannose, pyruvate, D-ribose, D-sorbitol, starch, trehalose, xylitol and D-xylose are used as carbon and energy sources under both aerobic and anaerobic conditions. Ethanol and methanol are only used under aerobic conditions except strains JW/BP-GSL-RA and JW/BP-GSL-WB, which do not use methanol. The major organic products from glucose under aerobic conditions were acetate and lactate. Under anaerobic conditions, formate, acetate, ethanol and lactate were the major organic fermentation products. The main cellular fatty acids were iso-C\(_{15:0}\) (39.1 %) and anteiso-C\(_{15:0}\) (36.3 %). Predominant polar lipids are diphostidyglycerol, phosphatidyglycerol and an unknown phospholipid (PL1). No quinones were detected.

The type strain, JW/BP-GSL-QD\(^T\) (=ATCC BAA-2118\(^T\)=DSM 23721\(^T\)), was isolated from a mixed water and sediment sample containing a salt crust obtained from the South Arm of Great Salt Lake, Utah (Antelope Island marina, 40 44’172’’ N, 111 52’288’’ W). The G+C content of the genomic DNA is 35.4 % (HPLC).

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**References**


