Altererythrobacter halimoniae sp. nov. and Altererythrobacter endophyticus sp. nov., two endophytes from the salt marsh plant Halimione portulacoides

Cátia Fidalgo, Jaqueline Rocha, Ricardo Martins, Diogo Neves Proença, Paula V. Morais, Isabel Henriques and Artur Alves

Abstract

Two Gram-negative, rod-shaped, motile bacteria strains, named CPA5 and BR75, were isolated from the halophyte Halimione portulacoides. Both presented optimum growth at 30 °C, pH 7.0–7.5 and 1–2 % NaCl (w/v) for strain CPA5, and pH 7.5–8.0 and 2 % NaCl (w/v) for strain BR75. Phylogenetic analyses based on 16S rRNA gene sequences affiliated both strains to the genus Altererythrobacter. CPA5 presented highest 16S rRNA gene sequence similarity with Altererythrobacter aestuarii KYW147 (96.5%), followed by Altererythrobacter namhicola KYW48 (95.9%), Novosphingobium indicum H25 (95.6%) and Altererythrobacter oceanensis Y2 (95.5%). BR75 displayed highest similarity with Altererythrobacter marenensis MSW-14 (96.5%), followed by Altererythrobacter xinjiangensis S3-63 and Altererythrobacter luteolus SW-109 and Altererythrobacter indicus MSSRF26 (96.1%). Neither strain contained Bacteriochlorophyll a. The main fatty acids observed for CPA5 were C17:0ω6c and summed features 3 (C16:1ω7c and/or iso-C15:0 2-OH) and 8 (C18:1ω7c and/or C18:1ω6c). The latter summed feature was the dominant fatty acid observed for strain BR75 as well. The major polar lipids were phosphatidylethanolamine, unidentified phospholipids and unidentified glycolipids for both strains. The predominant ubiquinone was Q-10 for both strains, and the DNA G+C content were 63.4 mol% and 58.3 mol% for CPA5 and BR75, respectively. Based on phenotypic and genotypic results, both strains represent novel species belonging to the genus Altererythrobacter for which the names Altererythrobacter halimoniae sp. nov. (type strain CPA5=CECT 9130=LMG 29519) and Altererythrobacter endophyticus sp. nov (type strain BR75=CECT 9129=LMG 29518) are proposed.

The genus Altererythrobacter was described in 2007 [1], emended in 2012 [2] and 2016 [3], and belongs to the family Erythrobacteraceae [4]. At the time of writing, the genus contains 22 validly published species, several of which frequently isolated from marine and estuarine environments (e.g. [5–8]). Its occurrence in association with plants is rare and there is only one species that has been isolated from the rhizosphere of wild rice [9].

The genus Altererythrobacter comprises Gram-negative bacteria that do not produce H2S. Cells cannot grow in anaerobic conditions and nitrate is not reduced. Cell suspensions and colonies are yellow, and the methanol-soluble pigment indicates the absence of Bacteriochlorophyll a (BChl a). The main quinone is Q-10 [1] and the major polar lipids are phosphatidylethanolamine, phosphatidylglycerol, diposphatidylglycerol and sphingoglycolipid [2]. The DNA G+C content range is 54.5–67.5 mol%, and the catalase reaction can be positive or negative [3]. The major fatty acids include C18:1ω7c [1], C16:1ω7c and C17:1ω6c.

The diversity of the endophytic community of the halophyte Halimione portulacoides was assessed in a salt marsh in Aveiro, Portugal. Briefly, healthy specimens of the halophyte were collected, aboveground and belowground tissues from these specimens were separated, surface-sterilized, macerated in phosphate buffer solution and studied for their bacterial diversity [10]. This study focuses on two strains obtained in those isolation efforts: strain CPA5 and BR75, isolated from the aboveground and belowground tissues; and BR75, isolated from the belowground tissues of the halophyte. Strains CPA5 and BR75 were C17:0ω6c and summed features 3 (C16:1ω7c and/or iso-C15:0 2-OH) and 8 (C18:1ω7c and/or C18:1ω6c). The latter summed feature was the dominant fatty acid observed for strain BR75 as well. The major polar lipids were phosphatidylethanolamine, unidentified phospholipids and unidentified glycolipids for both strains. The predominant ubiquinone was Q-10 for both strains, and the DNA G+C content were 63.4 mol% and 58.3 mol% for CPA5 and BR75, respectively. Based on phenotypic and genotypic results, both strains represent novel species belonging to the genus Altererythrobacter for which the names Altererythrobacter halimoniae sp. nov. (type strain CPA5=CECT 9130=LMG 29519) and Altererythrobacter endophyticus sp. nov (type strain BR75=CECT 9129=LMG 29518) are proposed.

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Keywords: Erythrobacteraceae; endophytic; halophytes; taxonomy.

Abbreviations: BChl a, Bacteriochlorophyll a; GL, unidentified glycolipid; IAA, indole-3-acetic acid; Knuc, substitution rate; MA, marine agar; ML, maximum-likelihood; NJ, neighbour joining; PE, phosphatidylethanolamine; PL, unidentified phospholipid.

The GenBank/EMBL/DDBJ accession numbers for the 16SrRNA gene sequences of strains CPA5 and BR75 are KY310593 and KY310591, respectively.

Two supplementary figures are available with the online Supplementary Material.
BR75<sup>T</sup> were originally isolated from and routinely cultured on marine agar (MA, Difco Laboratories, France) culture medium, at 28 °C, under aerobic conditions.

Genomic DNA was extracted, subjected to PCR amplification for the 16S rRNA gene, and sequenced as described elsewhere [10]. Primers 27F [11] and 704F [12] were used for sequencing the 16S rRNA gene. The nearly full-length sequences obtained for CPA5<sup>T</sup> (1412 nt) and BR75<sup>T</sup> (1406 nt) were used for similarity analyses using the Identify tool included in the EzTaxon platform [13]. For strain CPA5<sup>T</sup>, the closest matches were observed with type strains Altererythrobacter aestuarii KW147<sup>T</sup> (96.5 % similarity of the 16S rRNA gene sequence), followed by Altererythrobacter namhicola KYW48<sup>T</sup> (95.9 %), Novosphingobium indicum H25<sup>T</sup> (95.6 %), and Altererythrobacter oceanensis Y2<sup>T</sup> (95.5 %).

For strain BR75<sup>T</sup>, the most closely related type strains were Altererythrobacter marensis MSW-14<sup>T</sup> (96.5 %), followed by Altererythrobacter xinjiangensis S3-63<sup>T</sup> and Altererythrobacter luteolus SW-109<sup>T</sup> (96.1 %) and Altererythrobacter indicus MSSRF26<sup>T</sup> (96.1 %). 16S rRNA gene sequence similarity percentages to other type strains were below 95.5 and 96.0 % for CPA5<sup>T</sup> and BR75<sup>T</sup>, respectively.

The 16S rRNA gene sequences of strains CPA5<sup>T</sup> and BR75<sup>T</sup> were aligned with the sequences of related type strains retrieved from the EzTaxon database [13]. The sequences were then aligned using CLUSTAL Omega [14] and edited using BioEdit version 7.2.5 [15]. MEGA version 6.0 [16] was used to cluster the sequences by applying the neighbour-joining (NJ, [17]) and maximum-likelihood (ML, [18]) methods. The Kimura two-parameter model [19] was used.
Table 1. Differential characteristics of CPA5T, BR75T and related type strains

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
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<tr>
<td>Motility</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Catalase activity</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+†</td>
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<tr>
<td>Hydrolysis of casein</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−†</td>
</tr>
<tr>
<td>NaCl (w/v) range</td>
<td>0–5 %</td>
<td>0–5 %</td>
<td>0–6 %*</td>
<td>0–9 %†</td>
</tr>
<tr>
<td>pH range</td>
<td>5–11.5</td>
<td>5–11.5</td>
<td>5–11*</td>
<td>6.1–11.1†</td>
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<tr>
<td>Temperature range</td>
<td>18–37°C</td>
<td>18–37°C</td>
<td>10–44°C</td>
<td>40°C*</td>
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</table>

**API 20NE results:**
- Reduction of nitrates to nitrates
- β-galactosidase (para-nitrophenyl-β-D-galactopyranoside)
- Assimilation of maltose

**API ZYM results:**
- Esterase (C4), esterase lipase (C8), α-chymotrypsin
- Lipase (C14)
- Valine arylamidase
- Cystine arylamidase
- Trypsin
- Acid phosphatase
- Naphthol-AS-BI-phosphohydrolase (C14)
- β-Galactosidase
- β-Glucuronidase
- α-Glucosidase
- β-Glucosidase

**API 50CH results (acid production):**
- Aesculin ferric citrate
- Salicin

**DNA G+C content (mol%)**
- 63.4
- 58.3
- 67.2†
- 63.1†

*Data from [6].
†Result differed from that published in [6].
‡Result differed from that published in [6].

In clustering, and bootstrap values based on 1000 replications were obtained in these phylogenetic analyses. The obtained phylogenetic trees clearly placed both strains in independent clusters in the genus Altererythrobacter (Fig. 1). An extended overview of the placement of strains CPA5T and BR75T in the context of the family Erythrobacteraceae is represented in Fig. S1 (available in the online Supplementary Material).

The optimal conditions for growth were tested using a base of MA medium. The range and optimum conditions were first tested at varying temperatures, then pH and finally NaCl concentrations. Tests were performed by incubating strains at 4, 18, 26, 30, 37, 42.5 and 50°C, pH from 4 to 12 in 0.5 intervals, and NaCl tolerance was tested using concentrations of 0, 0.5, 1, 2, 3, 5, 10, 15 and 20 % NaCl (w/v) in a medium composed of 5 g l−1 yeast extract (Alfa Aesar, MA) and 10 g l−1 tryptone casein peptone (Amresco, Texas, USA). Optimum temperature for growth was observed at 30°C for both strains. Optimum growth for CPA5T was observed at pH 7–7.5 and 1–2 % NaCl (w/v), and for strain BR75T at pH 7.5–8 and 2 % NaCl (w/v).

Biochemical and phenotypic tests were performed with cells grown on MA medium for 48 h, at 30°C. The Gram-staining reaction was performed with a kit, and manufacturer’s instructions (Merck, Germany) were followed. Catalase and oxidase activities were assessed using H2O2-reagent and oxidase strips, respectively (both from BioMérieux, France). Light microscopy was used for determination of cell size, morphology and motility. Additionally, cells grown in half-strength MA for 72 h were placed on cavity slides and gliding motility was assessed by using the hang-drop method [20]. Oxygen metabolism was assessed by observing growth on thioglycollate medium (Merck, Germany) for 7 days. The ability to produce H2S was assessed using Kligler’s iron agar (Merck, Germany). Ability to hydrolyse starch, Tween 20, xylan, casein and cellulose, and to produce indole-3-ace
dic acid (IAA) were assessed as described in [10]. To assess presence of Bacteriochlorophyll a and absorbance peaks of the pigments, cells were grown on MB, washed once with distilled water, vigorously resuspended in 90 % (v/v) acetone and centrifuged. The supernatant was then removed and kept at 4°C in the dark overnight. Absorption peaks were assessed from 300 to 800 nm using the Thermo Spectroscopy Genesys 6. Additional biochemical tests were performed for strains CPA5T and BR75T as well as type strains A. marenis KCTC 22370T and A. aestuarii KCTC 22735T, using API 20NE, API ZYM and API 50CH strips (bio-
Mérieux, France) following the manufacturer’s instructions, except for using 0.9 % (w/v) NaCl to prepare inocula. The results for biochemical and phenotypic tests are detailed in the description of the new species, and differentiating characteris
tics are stated in Table 1.

The assessment of respiratory quinones, polar lipids and fatty acids was conducted as described in [21] and performed with strains CPA5T, A. aestuarii KCTC 22735T, BR75T and A. marenis KCTC 22370T simultaneously. Cells were grown in MB at 30°C for 48 h to obtain biomass for quinone and polar lipids assays. The main quinone detected for all strains was Q-10, and Q-9 and Q-8 were detected in minor amounts. The main fatty acids were comprised in

\[
\begin{align*}
C_{17}:1ω6c \ (13.8 \%) & \text{ and summed features 3 (C}_{16}:1ω7\text{c and/or } iso-C_{15}\_0 \ 2\text{-OH; 21.4 \%) and 8 (C}_{18}:1ω7\text{c and/or } C_{18}:1ω6\text{c; 32.6 \%), comprising over } 67 \% \text{ of total fatty acids. For strain BR75T the main fatty acids were comprised in summed feature 8, representing 76.3 \% of total fatty acids. The results were in accordance to what is observed in other Altererythrobacter species; the characteristic fatty acid of the genus } C_{18}:1ω7\text{c} \text{ was present in the summed feature 8.}
\end{align*}
\]
Table 2. Fatty acid composition of strains CPA5\textsuperscript{T}, BR75\textsuperscript{T} and related type strains

<table>
<thead>
<tr>
<th>Saturated</th>
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<tr>
<td>C\textsubscript{15}:0</td>
<td>1.6</td>
<td></td>
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<tr>
<td>C\textsubscript{16}:0</td>
<td>7.1</td>
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<td>9.0</td>
<td>5.8</td>
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<tr>
<td>C\textsubscript{17}:0</td>
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<td></td>
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<td></td>
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<tr>
<td>C\textsubscript{18}:0</td>
<td>TR</td>
<td>1.1</td>
<td>TR</td>
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</table>

<table>
<thead>
<tr>
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<tbody>
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<td>C\textsubscript{16}:1\textsubscript{ω}6c</td>
<td>TR</td>
<td></td>
<td>1.5</td>
<td></td>
<td>1.4</td>
<td>1.9</td>
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<tr>
<td>C\textsubscript{17}:1\textsubscript{ω}6c</td>
<td>13.8</td>
<td>3.1</td>
<td>6.3</td>
<td>19.9</td>
<td>3.4</td>
<td>6.8</td>
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<tr>
<td>C\textsubscript{17}:1\textsubscript{ω}8c</td>
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<td>TR</td>
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<td>2.1</td>
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<tr>
<td>C\textsubscript{18}:1\textsubscript{ω}5c</td>
<td>1.3</td>
<td>TR</td>
<td>1.4</td>
<td></td>
<td>2.1</td>
<td>2.2</td>
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<tr>
<td>C\textsubscript{18}:1\textsubscript{ω}7c</td>
<td></td>
<td></td>
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<td></td>
<td>35.2</td>
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<tr>
<td>C\textsubscript{18}:1\textsubscript{ω}7\textsubscript{c} 11-methyl</td>
<td>9.4</td>
<td></td>
<td>13.3</td>
<td></td>
<td>24.0</td>
<td></td>
</tr>
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</table>

Hydroxyl

| C\textsubscript{14}:0 2-OH | 2.3| 8.1| 1.0| 7.5| 2.3| 1.3 |
| C\textsubscript{15}:0 2-OH | TR | TR | TR | 3.5|    |    |
| C\textsubscript{16}:0 2-OH | TR | TR |    | 3.1| 1.5| 1.4 |

Summed feature\*  

| 3 |     |     |     |     |
|---|-----|-----|-----|
| 21.4| 2.6| 19.4| 22.7| 8.7| 8.8 |
| 7 |     |     |     |     |
| 32.6| 76.3| 41.1| 50.4|    |

*Summed feature 3 contains C\textsubscript{16}:1\textsubscript{ω}7c and/or iso-C\textsubscript{15}:0 2-0H; summed feature 7 contains C\textsubscript{18}:1\textsubscript{ω}9c and/or C\textsubscript{18}:1\textsubscript{ω}12t and/or C\textsubscript{18}:1\textsubscript{ω}7c; summed feature 8 contains C\textsubscript{18}:1\textsubscript{ω}7c and/or C\textsubscript{18}:1\textsubscript{ω}6c.

in our analysis. The complete fatty acid composition for all tested strains is presented in Table 2. The polar lipid profiles obtained are depicted in Fig. S2, available in the online Supplementary Material. For strain CPA5\textsuperscript{T}, the polar lipids detected in major amounts included phosphatidylethanolamine (PE), an unidentified glycolipid (GL2) and three unidentified phospholipids (PL2, PL3 and PL5). The profile for the phylogenetically close relative \textit{A. aestuarii} KCTC 22735\textsuperscript{T} was similar to that obtained for strain CPA5\textsuperscript{T}, albeit presenting small differences in regards to the minor polar lipids. For strain BR75\textsuperscript{T}, the major polar lipids were PE, an unidentified glycolipid (GL2) and four unidentified phospholipids (PL2, PL3, PL4 and PL5). The profile was highly similar to that of \textit{A. marenis} KCTC 22370\textsuperscript{T} and only minor discrepancies in polar lipids amounts were observed. These results further indicate that strains CPA5\textsuperscript{T} and BR75\textsuperscript{T} belong to the genus \textit{Altererythrobacter} but present slight differences with the most closely related strains.

Determination of G+C content was performed by high-performance liquid chromatography [22]. The results obtained (63.4 mol\% for CPA5\textsuperscript{T} and 58.3 mol\% BR75\textsuperscript{T}) are in agreement with what has been previously observed in the genus (54.5–67.5 mol\%; [3]).

Detailed results for each strain are given in the respective species description section. Considering the phylogenetic and 16S rRNA gene sequencing data and the similarities in physiological and biochemical traits, it is clear that CPA5\textsuperscript{T} and BR75\textsuperscript{T} belong to the genus \textit{Altererythrobacter}. Given that the 16S rRNA sequence similarities did not surpass the threshold for genomic delimitation of a new species (97\% sequence similarity; [23, 24]), there was no need to perform DNA–DNA relatedness tests. Strains CPA5\textsuperscript{T} and BR75\textsuperscript{T} are, nevertheless, distinguishable from validly published species of the genus, as they present differences in certain traits (Table 1). Differences between the novel species BR75\textsuperscript{T} and the closely related reference strain of \textit{A. marenis} include the ability to hydrolyse casein, to assimilate malic acid, to produce acid from salicin, and activity of β-galactosidase, β-glucosidase and β-glucuronidase. Differences between CPA5\textsuperscript{T} and \textit{A. aestuarii} include motility and activity of lipase, acid phosphatase and β-glucosidase. Accordingly, strains CPA5\textsuperscript{T} and BR75\textsuperscript{T} represent novel species of the genus \textit{Altererythrobacter}, for which the names \textit{Altererythrobacter halimionae} sp. nov. and \textit{Altererythrobacter endophyticus} sp. nov. respectively, are proposed.

**DESCRIPTION OF ALTERERYTHROBACTER HALIMIONAE SP. NOV.**

\textit{Altererythrobacter halimionae} (ha.li.mi.o’nae. N.L. gen. n. halimionae of the marsh plant \textit{Halimione portulacoides}).

Cells are Gram-negative rods (1.59–3.56 µm in length, 0.5–0.96 µm in width), aerobic, motile but not by gliding. Colonies on MA after incubation at 30°C for 48 h is yellow, opaque, with smooth edges and a diameter of 0.5–1 mm. Growth is observed from 18 to 37°C (optimum 30°C), at pH 5.0 to 11.5 (optimum 7.0–7.5) and in the presence of 0.5 to 5.0% (w/v) NaCl (optimum 1–2% (w/v) NaCl), being slightly halophilic. Positive for catalase, oxidase, hydrolysis of Tween 20 and xylan and production of IAA (45.5 µg ml\textsuperscript{-1}). Does not hydrolyse casein, starch, cellulose, and does not produce H\textsubscript{2}S. Bacteriochlorophyll \textit{a} is absent and acetone-soluble peaks are observed at 454 and 482 nm.

In API 20NE strips, it is positive for hydrolysis of aesculin (β-glucosidase), and negative for reduction of nitrates, indole production, fermentation of D-glucose, arginine dihydrolase, urease, hydrolysis of gelatin (protease), para-Nitrophenyl-β-D-galactopyranoside (β-galactosidase), assimilation of D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, phenylacetic acid. In an API ZYM strip, it is negative for β-galactosidase, β-glucosidase, β-glucuronidase, α-glucosidase, β-glucosidase, N-acetyl-β-glucosaminidase, α-mannosidase and α-fucosidase. In API 50CH it is negative for acid production from glycerol,
erythritol, D-arabinose, L-arabinose, D-ribose, D-xylene, L-xylene, D-adenitol, methyl-β-D-xlyopyranoside, D-galactose, D-glucose, D-fructose, D-mannose, L-sorbose, L-rhamnose, dulcitol, inositol, D-mannitol, D-sorbitol, methyl-α-D-mannopyranoside, methyl-α-D-glucopyranoside, N-acetylgalcosamine, amygdalin, arbutin, aesculin ferric citrate, salicin, cellobiose, maltose, lactose (bovine), melibiose, D-sucrose, trehalose, inulin, melezitose, raffinose, starch, glycogen, xylitol, gentiobiose, turanose, D-lyxose, D-tagatose, D-fucose, L-fucose, D-arabitol, potassium gluconate, potassium 2-ketoglucurate, potassium 5-ketoglucurate. The main quinone is Q-10 and the main fatty acids are C_{17:1}ω6c and summed features 3 (C_{16:1}ω7c and/or iso-C_{15:0} 2-OH) and 8 (C_{18:1}ω7c and/or C_{18:1}ω6c). The major polar lipids comprise phosphatidylethanolamine and unidentified polar lipids.

The type strain CPA5^T (=CECT 9130^T=LMG 29519^T) was isolated from the surface-sterilized aboveground tissues of the halophyte Halimione portulacoides. The G+C content of the DNA of the type strain is 63.4 mol%.

**DESCRIPTION OF ALTERERYTHROBACTER ENDOPHYTICUS SP. NOV.**

*Altererythrobacter endophyticus* (en.do.phy’ti.cus. Gr. pref. endo within; Gr. n. phyton plant; L. neut. suff. -icus adjective suffix used with the sense of belonging to; N.L. masc. adj. *endophyticus* within plant, endophytic).

Cells are Gram-negative aerobic rods (1.46–3.95 μm in length, 0.59–1.41 μm in width), motile but not by gliding. After incubation at 30 °C for 48 h on MA, colony is yellow, opaque, with smooth edges and 0.5–1.2 mm in diameter. Growth occurs from 18 to 37 °C (optimum 30 °C), at pH 5.0–11.5 (optimum 7.5–8.0) and in the presence of 0.5 to 5.0% (w/v) NaCl [optimum 2% (w/v) NaCl], being slightly halophilic. Bacteriochlorophyll a is absent, and acetone-soluble peaks are observed at 454 and 482–483 nm. Cells are catalase and oxidase positive, and hydrolyse casein, Tween 20 and xylan, and produce IAA (90.8 μg ml⁻¹). H₂S is not produced, and starch and cellulose are not hydrolysed. In an API 20NE strip, it is positive for hydrolysis of asucin (β-glucosidase), para-Nitrophenyl-β-D-galactopyranoside (β-galactosidase) and assimilation of malic acid. It is negative for reduction of nitrates, indole production, fermentation of D-glucose, arginine dihydrolase, urease, hydrolysis of gelatin (protease), assimilation of D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, maltose, potassium gluconate, capric acid, adipic acid, trisodium citrate and phenylacetic acid. In the API ZYM strip, it is positive for alkaline phosphatase, esterase (C4), esterase lipase (C8), leucine arylamidase, valine arylamidase, α-chymotrypsin, acid phosphatase, Naphthol-AS-Bl-phosphohydrolase, β-glucuronidase, and β-glucosidase, and weakly positive for lipase (C14) and β-galactosidase. It is negative for cysteine arylamidase, trypsin, α-galactosidase, N-acetyl-β-glucosaminidase, α-mannosidase and α-fucosidase. In API 50CH it is positive for acid production from asucin.

ferric citrate, and negative for glycerol, erythritol, D-arabinose, L-arabinose, D-ribose, D-xylene, L-xylene, D-adenitol, methyl-β-D-xlyopyranoside, D-galactose, D-glucose, D-fructose, D-mannose, L-sorbose, L-rhamnose, dulcitol, inositol, D-mannitol, D-sorbitol, methyl-α-D-mannopyranoside, methyl-α-D-glucopyranoside, N-acetylgalcosamine, amygdalin, arbutin, aesculin ferric citrate, salicin, cellobiose, maltose, lactose (bovine), melibiose, D-sucrose, trehalose, inulin, melezitose, raffinose, starch, glycopen, xylitol, gentiobiose, turanose, D-lyxose, D-tagatose, D-fucose, L-fucose, D-arabitol, potassium gluconate, potassium 2-ketoglucurate, potassium 5-ketoglucurate. The predominant fatty acids are those contained in summed feature 8 (C_{18:1}ω7c and/or C_{18:1}ω6c), and the principal respiratory quinone is Q-10. The major polar lipids comprise phosphatidylethanolamine and unidentified polar lipids.

The type strain BR75^T (=CECT 9129^T=LMG 29518^T) was isolated from the surface-sterilized belowground tissues of the halophyte Halimione portulacoides. The G+C content of the DNA of the type strain is 58.3 mol%.

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**Conflicts of interest**

The authors declare that there are no conflicts of interest.

**References**


