Two bacterial strains (JC130T and JA747T) were isolated from dry soils of a solar saltern. Phylogenetic analysis showed that strain JA747T clustered with species of the genus *Erythrobacter* belonging to the family *Erythrobacteraceae* of the class *Alphaproteobacteria* in the phylum *Proteobacteria*, while strain JC130T clustered with species of the genus *Pontibacter* belonging to the family *Cytophagaceae* of the phylum *Bacteroidetes*. Based on 16S rRNA gene sequence analysis, strain JA747T had highest similarity with *Erythrobacter gangjinensis* K7-2T (96.7 %) and other members of the genus *Erythrobacter* (<96 %). Strain JC130T had highest sequence similarity with *Pontibacter korlensis* X14-1T (98.1 %), *Pontibacter actiniarum* KMM 6156T (96.9 %) and other members of the genus *Pontibacter* (<96 %). However, strain JC130T showed less than 32 % DNA reassociation value (based on DNA–DNA hybridization) with *Pontibacter korlensis* NRRL B-51097T (=X14-1T) and *Pontibacter actiniarum* LMG 23027T (=KMM 6156T). Strain JA747T was positive for catalase and oxidase activity and negative for nitrate reduction, and hydrolysis of starch and casein. Phosphatidylglycerol, diphosphatidylglycerol, phosphatidylethanolamine and phosphatidylcholine were the major polar lipids for strain JA747T. C₁₈:₁ω7c, C₁₆:₁ω6c/C₁₆:₁ω7c, C₁₇:₁ω6c and C₁₆:₀ were the major fatty acids of strain JA747T. Strain JC130T was positive for catalase and oxidase, and negative for gelatinase and nitrate reduction. Phosphatidylethanolamine was the major polar lipid of strain JC130T. Major fatty acids of strain JC130T were iso-C₁₅:₀ and summed feature 4 (anteiso-C₁₇:₁ω/B/iso I). Based on the phenotypic, chemotaxonomic and molecular evidence presented, strains JA747T and JC130T are considered to represent two novel species of the genera *Erythrobacter* and *Pontibacter*, for which the names *Erythrobacter odishensis* sp. nov. (type strain JA747T=KCTC 23981T=NBRC 108930T) and *Pontibacter odishensis* sp. nov. (type strain JC130T=KCTC 23982T=LMG 26962T), respectively, are proposed. Emended descriptions of the genera *Erythrobacter* and *Pontibacter* are provided.

**Erythrobacter odishensis** sp. nov. and *Pontibacter odishensis* sp. nov. isolated from dry soil of a solar saltern

Y. Subhash,¹ L. Tushar,¹ Ch. Sasikala² and Ch. V. Ramana¹

¹Department of Plant Sciences, School of Life Sciences, University of Hyderabad, P.O. Central University, Hyderabad 500046, India
²Bacterial Discovery Laboratory, Centre for Environment, Institute of Science and Technology, J.N.T. University Hyderabad, Kukatpally, Hyderabad 500085, India

India is one of the major producers of natural salt, having a large number of solar salterns. Solar salterns are major niches for many salt-loving bacteria, although only a few novel species have been recorded so far from Indian solar salterns (Kumar et al., 2007; Kalyan Chakravarthy et al., 2010). Here we report the description of two novel strains recovered from a solar saltern in Odisha, eastern India. Based on 16S rRNA gene sequence analysis, the two novel strains (designated JA747T and JC130T) are shown to represent novel species of the genera *Erythrobacter* and *Pontibacter*, respectively.

Ten soil samples were collected randomly from an unused (at the time of sample collection) solar saltern at Humma, Odisha, India (GPS positioning of the sample collection site 19° 25′ N 85° 04′ E) during December 2011. These different samples collected from the same site were pooled together. One gram of air-dried soil was serially diluted to 10⁻⁴ dilution and 100 μl was spread on three different...
nutrient media. Nutrient medium 1 (pH 7.0) contained (per litre): 0.2 g KH₂PO₄, 0.25 g NH₄Cl, 0.5 g KCl, 0.15 g CaCl₂.2H₂O, 1.0 g NaCl, 0.62 g MgCl₂.6H₂O, 2.84 g Na₂SO₄, 2.83 g HEPES, 3.0 g yeast extract, 3.0 g peptone, 0.5 g Casamino acid, 0.5 g glucose and 3.0 g sodium pyruvate. Nutrient medium 2 was made by adding soil extract [10 g of air-dried soil was added in 1 litre of sterile distilled water and mixed by shaking (180 r.p.m. for 30 min, and filtered through a mesh)] to growth medium 1. Nutrient medium 3 was used for the enrichment and isolation for halophilic bacteria (Tapilatu et al., 2010). Strains JC127 and JC135 were obtained from nutrient medium 1. Strains JC136, JC138, JC139, JC130T and JA747T were isolated from nutrient medium 2, and strains JC125, JC126 and JC137 were obtained from nutrient medium 3. All strains were preserved by lyophilization and as glycerol (50%, v/v) stocks.

Well-grown colonies of the ten new isolates were used for PCR analysis. Primers 5'-GGTTGATCCTGCGTACGAG-3' and 5'-TACCTGTTACGACTTCA-3' (Escherichia coli positions 11–27 and 1489–1506, respectively) were used for sequencing of the 16S rRNA gene as described previously (Raj et al., 2013). Identification of phylotechinical neighbours and calculation of pairwise 16S rRNA gene sequence similarity were achieved using the NCBI-BLAST search (Altschul et al., 1997) and EzTaxon-e (Kim et al., 2012). The BLAST search analysis of 16S rRNA gene sequences (1396 and 1353 bp, respectively for strains JC130T and JA747T) revealed highest similarity for strain JC130T with Pontibacter korensis X14-1T (98.1%; <96.9% with other members of the genus Pontibacter) and for strain JA747T with Erythrobacter ganginensis K7-2T (96.6%; <96.5% with other members of the genus Erythrobacter).

The SINA alignment service (http://www.arb-silva.de/) and CLUSTAL W algorithm of MEGAS (Tamura et al., 2011) were used for sequence alignments, and phylogenetic analysis of the individual sequences was performed using MEGAS software. Distances were calculated by using the Kimura correction in a pairwise deletion manner (Kimura, 1980). Neighbour-joining (NJ), maximum-parsimony (MP) and maximum-likelihood (ML) methods in the MEGAS software (Tamura et al., 2011) were used to reconstruct phylogenetic trees. Percentage support values were obtained using a bootstrap procedure. The results of phylogenetic analysis based on 16S rRNA gene sequences suggested that strains JA747T and JC130T belong to the genera Erythrobacter and Pontibacter (combined trees based on the NJ, ML and MP methods are shown in Figs 1 and 2) of the families Erythrobacteraceae and Cytophagaceae, respectively. Genomic DNA was extracted and purified according to the method of Marmur (1961) and the G + C content of the DNA as determined by reversed-phase HPLC (Mesbah et al., 1989) was 59.5 and 47.5 mol% for strains JA747T and JC130T, respectively.

The taxonomic relationship between strain JC130T, P. korensis NRRL B-51097T and Pontibacter actiniarum LMG 23027T was examined using DNA–DNA hybridization which was determined using a membrane filter technique (Tourova & Antonov, 1988), using a nick translation kit supplied by BRT. Hybridization was performed with three replications for each sample (control: reversal of strains was used for binding and labelling) as described by Bhadra et al. (2005) and Seldin & Dubnau (1985). When strain JC130T was radioactively labelled, mean (±SD) levels of DNA–DNA reassociation with P. korensis NRRL B-51097T and P. actiniarum LMG 23027T were 30 ± 1 and 30 ± 2%, respectively. However, when P. korensis NRRL B-51097T and P. actiniarum LMG 23027T were labelled and used for DNA–DNA hybridization with JC130T in the reciprocal reaction, levels of relatedness were 29 ± 2 and 31 ± 1%, respectively.

Comparative taxonomic analysis of strain JA747T was done along with E. ganginensis KCTC 22330T (=K7-2T; phylogenetically closest to strain JA747T) and Erythrobacter longus DSM 6997T (=Och101T; representing the type species of the genus Erythrobacter, used in this study for genus confirmation). Similarly, strain JC130T was compared with P. korensis NRRL B-51097T (=X14-1T; phylogenetically closest to strain JC130T) and P. actiniarum LMG 23027T (=KMM 6156T; representing the type species of the genus Pontibacter).

Colonies of strains JA747T and JC130T were yellow brown and brown, respectively, when grown on nutrient medium 1. Morphological properties (cell shape, cell division, cell size, flagella) were observed under an Olympus model BH-2 phase-contrast light microscope. Cells of both strains were rod-shaped, non-motile and multiplied by binary fission. Cells of strain JA747T were 1–2 μm long and 0.5–0.6 μm wide (Fig. S1a, c, available in IJSEM Online), while cells of strain JC130T were 2–5 μm long and 1.0–1.2 μm wide (Fig. S1b, d). Utilization of organic substrates (d-glucose, d-fructose, fucose, lactose, d-galactose, d-mannitol, L-rhamnose, d-sorbitol, d-mannose, sucrose, Tween 80 and cellobiose) were tested using basal medium which contained (per litre) 0.55 g KCl, 2.38 g CaCl₂.2H₂O, 2.34 g Na₂SO₄, 0.16 g NaHCO₃, 8.8 g MgCl₂.6H₂O, 0.1 g ferric citrate, 20.0 g NaCl and 1.0 g yeast extract. The various organic substrates were added at a concentration of 0.1% (w/v) (Xu et al., 2010), and the pH was adjusted to 7.5 with 1 M NaOH. Organic substrate utilization by strains JA747T and JC130T is given in Tables 1 and 2, respectively. Organic substrate utilization was also tested using Biolog GN2 as per the instructions given by the manufacturer and the results are given in the species descriptions below.

Various biochemical tests such as hydrolysis of starch, gelatin, casein, Tween 80, chitinase, oxidase, catalase and nitrate reduction were carried out in the prescribed medium as mentioned by Cappuccino & Sherman (1998), and the results are given in Tables 1 and 2 for strains JA747T and JC130T, respectively. Sensitivity of strains JA747T and JC130T along with the reference strains...
to different antibiotics was tested after spreading cells on agar plates. The antibiotic discs (HiMedia Laboratories) contained (µg): chloramphenicol (30), gentamicin (120), kanamycin (30), nalidixic acid (30), penicillin-G (10), streptomycin (10) or tetracycline (30). The effects of the antibiotics on cell growth were assessed after 4 days and the comparative results are shown in Tables 1 and 2, respectively, for strains JA747T and JC130T. Buffered medium (K2HPO4–KH2PO4 buffer for pH 5–8 and NaHCO3–NaOH buffer for pH 9–11) was used for growth at different pH. Salt tolerance was tested at different concentration of NaCl in medium 1 at optimum temperature and pH. The temperature range (4–45°C) was tested at optimum pH and salt concentration in medium 1. Vitamin (biotin, niacin, p-aminobenzoic acid and vitamin B12) requirement was tested by replacing yeast extract with single and also combinations of vitamins as growth factors. Strains JA747T and JC130T showed no growth factor requirements.

The colour of aerobically grown cell suspension of strain JA747T was yellow brown, while that of strain JC130T was brown. In vivo absorption spectra as measured with a Spectronic Genesys 2 spectrophotometer in sucrose solution (Trüper & Pfennig, 1981) exhibited maxima at 400 and 520 nm for strain JA747T, and 390 and 490 nm for strain JC130T, which indicated the absence of bacteriochlorophyll-a (Bchl-a). Carotenoid composition as determined by C18-HPLC analysis (Venkata Ramana et al., 2010) indicated the presence of zeaxanthin (21 %), erythroxanthin (8.4 %), γ-carotene (2.3 %) and five unidentified carotenoids in strain JA747T (Fig. S2a). Strain JC130T had astaxanthin glucoside (1.9 %), astaxanthin (12 %) and six unidentified carotenoids (Fig. S2b).

The polar lipid profile was analysed by extracting polar lipids with methanol/chloroform/saline (2:1:0.8, by vol.) from 1 g freeze-dried cells as described by Kates (1972, 1986). Total polar lipid profiles were detected by spraying with 5 % (v/v) ethanolic molybdophosphoric acid and

Fig. 1. NJ phylogenetic tree showing the relationship of strain JA747T with close relatives of the family Erythrobacteraceae based on 16S rRNA gene sequences and rooted by using Rhodospirillum rubrum ATCC 11170T as the outgroup. Numbers at nodes represent bootstrap values (based on 1000 resamplings). Bootstrap percentages refer to NJ/ML/MP analysis. GenBank accession numbers for 16S rRNA gene sequences are shown in parentheses. Bar, 2 nt substitutions per 100 nt.

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further characterized by spraying with ninhydrin (for amino groups), molybdenum blue (for phosphates), Dragendorff’s reagent (for quaternary nitrogen) or α-naphthol (for sugars) (Kates, 1972; Oren et al., 1996; Tindall, 1990a, b). Phosphatidylglycerol (PG), diphasphatidylglycerol (DPG), phosphatidylethanolamine (PE), phosphatidylcholine (PC), an unidentified phospholipid (PL1) and an unidentified polar carotenoid (OrP1) were the major polar lipids of strain JA747T (Fig. S3a). Minor amounts of unidentified lipids (L1–4) were also detected in strain JA747T. Strain JA747T differs from *E. marinus* KCTC 23554T, *E. gangjinensis* KCTC 22330T and *E. longus* DSM 6997T as analysed by HPLC after extraction with a chloroform/methanol (2:1, v/v) mixture and purified by TLC (Hiraishi & Hoshino, 1984; Hiraishi et al., 1984; Imhoff, 1984). MK-7 was the major (>95 %) quinone of strain JC130T, *P. korlensis* NRRL B-51097T and *P. actiniarum* LMG 23027T. For cellular fatty acid analysis, strains JC130T and JA747T were grown at optimal conditions in nutrient medium 1 and bacterial cultures were harvested at the late exponential phase of growth. Forty milligrams of bacterial cells was then subjected to a series of four different reagents followed by saponification and methylation of fatty acids, thus enabling their cleavage from lipids. The fatty acid methyl esters thus obtained were analysed using a gas chromatograph equipped with Sherlock MIS software [Microbial ID; MIDI 6.0 version; Agilent: 6850 (peak identification was done based on the RTSBA6 database), www.midi-inc.com] (Sasser, 1990). Major fatty acids in strain JA747T were C18 : 1 ω7c, C16 : 1 ω6c and C16 : 0 (Table 2). C14 : 02-OH, C15 : 02-OH and C16 : 02-OH were the major fatty acid alcohols of strain JA747T. Q-10 was the major (>98 %) quinone of strain JA747T, *E. marinus* KCTC 23554T, *E. gangjinensis* KCTC 22330T and *E. longus* DSM 6997T as analysed by HPLC after extraction with a chloroform/methanol (2:1, v/v) mixture and purified by TLC (Hiraishi & Hoshino, 1984; Hiraishi et al., 1984; Imhoff, 1984). MK-7 was the major (>95 %) quinone of strain JC130T, *P. korlensis* NRRL B-51097T and *P. actiniarum* LMG 23027T.

**Fig. 2.** NJ phylogenetic tree showing the relationship of strain JC130T with close relatives of the family *Cytophagaceae* based on almost-complete 16S rRNA gene sequences and rooted by using *Reichenbachiella agariperforans* KMM 3525T as the outgroup. Numbers at nodes represent bootstrap values (based on 1000 resamplings). Bootstrap percentages refer to NJ/ML/MP analysis. GenBank accession numbers for 16S rRNA gene sequences are shown in parentheses. Bar, 2 nt substitutions per 100 nt.
Major fatty acids in strain JC130\textsuperscript{T} were iso-C\textsubscript{15}:0 and summed feature 4 (anteiso-C\textsubscript{17}:1B/iso I) with a large number of branched-chain fatty acids and fatty acid alcohols present in moderate to minor quantities (Table 2). Both strains JA747\textsuperscript{T} and JC130\textsuperscript{T} differ from their closest phylogenetic neighbours in their fatty acid composition (Tables 1 and 2).

Hopanoids were extracted according to Rohmer \textit{et al.} (1984) and were separated on a silica gel TLC plate (Kieselgel 60 F254; Merck) using double development with dichloromethane. The total hopanoid profile was detected by spraying with 0.1\% solution of barberine chlorohydrate in ethanol and visualizing the plates at 366 nm (Rohmer et al. 1984).

\begin{table}[h]
\centering
\begin{tabular}{|l|c|c|c|c|}
\hline
Characteristic & 1 & 2 & 3 & 4 \\
\hline
Colony colour & Yellow brown & Yellow orange & Yellow orange & Dark brown \\
\hline
Motility & \( \text{--} \) & \( \text{--} \) & \( \text{--} \) & \( + \) \\
\hline
Cell size (\( \mu \text{m} \)) & 0.5–0.6 \( \times \) 1–2 & 0.3–0.4 \( \times \) 0.6–0.8 & 0.3–0.5 \( \times \) 0.5–1.0 & 0.4–0.5 \( \times \) 1–5 \\
\hline
NaCl range (optimum; \%) & 0–9 (2) & 1–7 (2–3) & 0.5–6.0 (2–3) & 1–10 (2–3) \\
\hline
pH range (optimum) & 6.2–9.1 (6.5–7.5) & 6.5–9.3 (7–8) & 5.9–9.0 (7–8) & 6.0–9.0 (7–8) \\
\hline
\hline
Bchl-\textalpha & \( \text{--} \) & \( \text{--} \) & \( \text{--} \) & \( + \) \\
\hline
Nitrile reduction & \( \text{--} \) & \( \text{--} \) & \( \text{--} \) & \( + \) \\
\hline
Hydrolysis of: & & & & \\
Starch & \( + \) & \( + \) & \( \text{--} \) & \( \text{--} \) \\
\hline
Gelatin & \( \text{--} \) & \( \text{--} \) & \( + \) & \( + \) \\
\hline
Casein & \( + \) & \( \text{--} \) & \( \text{--} \) & \( + \) \\
\hline
Carbon source utilization (0.1\% w/v or v/v) & & & & \\
\text{D-Galactose} & \( + \) & \( \text{--} \) & \( \text{--} \) & \( + \) \\
\text{D-Mannitol} & \( + \) & \( + \) & \( \text{--} \) & \( \text{--} \) \\
\text{L-Rhamnose} & \( \text{--} \) & \( + \) & \( + \) & \( \text{--} \) \\
\text{D-Sorbitol} & \( + \) & \( \text{--} \) & \( \text{--} \) & \( + \) \\
\text{D-Mannose} & \( \text{--} \) & \( + \) & \( \text{--} \) & \( + \) \\
\text{Sucrose} & \( + \) & \( + \) & \( \text{--} \) & \( \text{--} \) \\
\text{Cellobiose} & \( + \) & \( \text{--} \) & \( + \) & \( \text{--} \) \\
\text{Tween 80} & \( \text{--} \) & \( + \) & \( \text{--} \) & \( + \) \\
\hline
Susceptibility to: & & & & \\
\text{Chloramphenicol} & \( + \) & \( \text{--} \) & \( \text{--} \) & \( + \) \\
\text{Gentamicin} & \( + \) & \( \text{--} \) & \( \text{--} \) & \( + \) \\
\text{Kanamycin} & \( + \) & \( \text{--} \) & \( \text{--} \) & \( + \) \\
\text{Nalidixic acid} & \( + \) & \( \text{--} \) & \( \text{--} \) & \( + \) \\
\text{Penicillin} & \( + \) & \( \text{--} \) & \( \text{--} \) & \( + \) \\
\text{Streptomycin} & \( + \) & \( \text{--} \) & \( \text{--} \) & \( + \) \\
\text{Tetracycline} & \( + \) & \( \text{--} \) & \( \text{--} \) & \( + \) \\
\hline
Fatty acid composition (\%) & & & & \\
\text{C\textsubscript{14}:0} & 1.0 & \( \text{--} \) & \( \text{--} \) & \( \text{--} \) \\
\text{C\textsubscript{14}:0 2-OH} & 1.9 & 4.9 & 5.7 & 6.5 \\
\text{C\textsubscript{15}:0 2-OH} & 1.8 & 1.3 & 3.0 & 9.7 \\
\text{C\textsubscript{16}:0} & 8.8 & 6.9 & 5.8 & 11.9 \\
\text{C\textsubscript{16}:0 2-OH} & 3.3 & 4.7 & 7.1 & 1.4 \\
\text{C\textsubscript{18}:0} & 1.0 & 1.4 & \( \text{--} \) & 1.2 \\
\text{C\textsubscript{16}:1\text{\textsubscript{10}5c}} & 1.6 & \( \text{--} \) & \( \text{--} \) & \( \text{--} \) \\
\text{C\textsubscript{16}:1\text{\textsubscript{10}6c/C\textsubscript{16}:1\text{\textsubscript{10}7c}}} & 12.8 & 16.0 & 12.0 & \( \text{--} \) \\
\text{C\textsubscript{17}:1\text{\textsubscript{10}6c}} & 11.0 & 8.7 & 13.7 & 3.6 \\
\text{C\textsubscript{17}:1\text{\textsubscript{10}8c}} & 1.0 & \( \text{--} \) & 1.4 & 5.1 \\
\text{C\textsubscript{18}:1\text{\textsubscript{10}5c}} & 1.0 & \( \text{--} \) & \( \text{--} \) & \( \text{--} \) \\
\text{C\textsubscript{18}:1\text{\textsubscript{10}7c}} & 43.0 & 50.9 & 41.1 & 52.3 \\
\text{C\textsubscript{18}:1\text{\textsubscript{10}7c 11-methyl}} & 2.5 & 3.6 & 7.6 & \( \text{--} \) \\
\text{C\textsubscript{18}:1\text{\textsubscript{10}9c}} & 1.7 & \( \text{--} \) & \( \text{--} \) & \( \text{--} \) \\
\text{DNA G+C content (mol\%)} & 59.5 & 61.4 & 66.7 & 62.5 \\
\hline
\end{tabular}
\caption{Differential characteristics between strain JA747\textsuperscript{T} and species of the genus \textit{Erythrobacter}}
\end{table}

Strains: 1, JA747\textsuperscript{T}; 2, \textit{E. gangjinensis} KCTC 22330\textsuperscript{T}; 3, \textit{E. marinus} HWDM-33\textsuperscript{3}; 4, \textit{E. longus} DSM 6997\textsuperscript{T}. All data are from the present study and were determined under identical growth conditions. All strains were positive for catalase and oxidase; did not utilize D-fructose, fucose or lactose; and utilized D-glucose. +, Positive/utilized/susceptible; --, absent/not utilized/resistant.
Table 2. Differential characteristics between strain JC130\textsuperscript{T} and species of the genus Pontibacter

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
<th>2</th>
<th>3</th>
</tr>
</thead>
<tbody>
<tr>
<td>Colony colour</td>
<td>Brown</td>
<td>Pink</td>
<td>Pink</td>
</tr>
<tr>
<td>Cell size (μm)</td>
<td>1.0–1.2</td>
<td>2.0–5.0</td>
<td>0.6–0.7</td>
</tr>
<tr>
<td>NaCl range (optimum; %)</td>
<td>0–9 (2)</td>
<td>0–8 (1.5–2.0)</td>
<td>0–10 (2)</td>
</tr>
<tr>
<td>pH range (optimum)</td>
<td>6.0–9.1 (6.5–7.5)</td>
<td>5.5–9.5 (7–8)</td>
<td>5.8–9.3 (7.0–8.6)</td>
</tr>
<tr>
<td>Temperature range (optimum; °C)</td>
<td>10–40 (25–30)</td>
<td>7–45 (30–37)</td>
<td>6–43 (25–28)</td>
</tr>
<tr>
<td>Hydrolysis of:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Starch</td>
<td>+</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>Gelatin</td>
<td>–</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Casein</td>
<td>+</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Carbon source utilization (0.1 % w/v or v/v)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>D-Glucose</td>
<td>+</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>D-Galactose</td>
<td>+</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>D-Mannitol</td>
<td>+</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>L-Rhamnose</td>
<td>+</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>D-Sorbitol</td>
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<td>–</td>
<td>–</td>
</tr>
<tr>
<td>D-Mannose</td>
<td>–</td>
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<td>+</td>
</tr>
<tr>
<td>Sucrose</td>
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<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Cellobiose</td>
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<td>–</td>
<td>–</td>
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<tr>
<td>Tween 80</td>
<td>+</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>Susceptibility to:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Nalidixic acid</td>
<td>+</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Penicillin</td>
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<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Streptomycin</td>
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<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Gentamicin</td>
<td>+</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Fatty acid composition (%)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>iso-C\textsubscript{15}:0</td>
<td>22.5</td>
<td>14.8</td>
<td>21.8</td>
</tr>
<tr>
<td>anteiso-C\textsubscript{15}:0</td>
<td>1.6</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>iso-C\textsubscript{16}:0 3-OH</td>
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<td>2.8</td>
<td>3.6</td>
</tr>
<tr>
<td>iso-C\textsubscript{16}:1 H</td>
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<td>1.2</td>
<td>–</td>
</tr>
<tr>
<td>iso-C\textsubscript{16}:0</td>
<td>7.6</td>
<td>1.0</td>
<td>–</td>
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<tr>
<td>C\textsubscript{16}:1 iso/5c</td>
<td>1.9</td>
<td>1.6</td>
<td>–</td>
</tr>
<tr>
<td>C\textsubscript{16}:0</td>
<td>2.4</td>
<td>–</td>
<td>–</td>
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<tr>
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<td>–</td>
<td>–</td>
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<tr>
<td>iso-C\textsubscript{17}:1 \textsubscript{0/9c}</td>
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<td>–</td>
<td>–</td>
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<tr>
<td>c\textsubscript{17}:0 9c</td>
<td>3.0</td>
<td>1.2</td>
<td>1.4</td>
</tr>
<tr>
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<td>–</td>
<td>–</td>
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<tr>
<td>C\textsubscript{17}:1 \textsubscript{0/9c}</td>
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<td>7.2</td>
<td>2.6</td>
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<tr>
<td>iso-C\textsubscript{17}:0 3-OH</td>
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<td>9.5</td>
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<tr>
<td>iso-C\textsubscript{18}:1 H</td>
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<td>–</td>
<td>–</td>
</tr>
<tr>
<td>C\textsubscript{18}:1 \textsubscript{10/9c}</td>
<td>1.3</td>
<td>2.8</td>
<td>2.0</td>
</tr>
<tr>
<td>C\textsubscript{18}:1 \textsubscript{10/7c}</td>
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<td>1.2</td>
<td>1.3</td>
</tr>
<tr>
<td>C\textsubscript{18}:0</td>
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<td>1.2</td>
<td>1.4</td>
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<tr>
<td>Summed feature 2*</td>
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<td>Summed feature 3*</td>
<td>5.3</td>
<td>11.3</td>
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<td>Summed feature 4*</td>
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<tr>
<td>Summed feature 5*</td>
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<td>1.1</td>
<td>2.2</td>
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<tr>
<td>DNA G + C content (mol%)</td>
<td>47.5</td>
<td>47.9</td>
<td>48.4</td>
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*Summed feature 2 contains C\textsubscript{13}:0 3-OH/iso-C\textsubscript{15}:1 H; summed feature 3 contains C\textsubscript{16}:1 \textsubscript{0/6d}\textsubscript{16}:1 \textsubscript{0/7c}; summed feature 4 contains anteiso-C\textsubscript{17}:1 \textsubscript{B/iso I}; summed feature 5 contains anteiso-C\textsubscript{18}:0 and/or C\textsubscript{18}:2 \textsubscript{0/6,9c}. Two novel species of Erythrobacteraceae

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Based on the differences in the colour of the colonies, NaCl tolerance, presence/absence of Bchl- a and bacteriohopanone derivatives (BHD1, 2), diploptero, an unidentified hopane and diploptene as major hopanoids (Fig. S5d), which is similar to P. actiniarum KMM 6156T (Fig. S5f) but differs from P. korlens NRRL B-51097T by the absence of unidentified hopanes (UH1, 2; Fig. S5e).

**Emeded description of the genus Erythrobacter Shiba & Simidu, 1982**

The description is as given by Shiba & Simidu (1982) with the following modifications. Motility is absent in some species. Some species hydrolyse casein and starch. C18:1ω7c, C16:1ω6c/C16:1ω7c, C17:1ω6c and C16:0 are the major fatty acids. Minor amounts of C14:0, C14:0 2-OH, C15:0 2-OH, C16:0 2-OH, C16:1ω9c 11-methyl, C18:1ω9c, C18:1ω9c and C18:0 are also present. Major quinone is Q-10. Major polar lipids of those species tested are PG, DPG, PE and PC. Major hopanoids are bacterial hopane derivatives (BHD1, 2), diploptero, an unidentified hopane (AH1) and unidentified hopanoids (UH1, 2). The G+C content of the genomic DNA is 58.9–67.0 mol%.

**Description of Erythrobacter odishensis sp. nov.**

*Erythrobacter odishensis* (o.dishe.‘en’is. N.L. masc. adj. *odishensis* of or belonging to Odisha, a coastal state in India rich in bacterial diversity).

Colonies are yellow brown. Cells are rod-shaped, 1.0–2.0 μm long and 0.5–0.6 μm wide, non-motile and multiply by binary fission. Zeaxanthin, erythroxythine, β-carotene and five unidentified carotenoids are present. Bchl-a is absent. Optimum growth occurs with 2% NaCl (range 0–9%), at pH 6.5–7.5 (range 6.2–9.1) and at 25–30°C (range 12–40°C). Good growth occurs on D-glucose, D-galactose, D-mannitol, D-sorbitol, sucrose and cellobiose. Growth does not occur on D-fructose, fucose, lactose, L-rhamnose, D-mannose or Tween 80. Starch and casein are hydrolysed but gelatin is not. Nitrate is not reduced. The following compounds are oxidized in the Biolog GN2 test system: α-cyclodextrin, dextrin, glycogen, N-acetyl-D-glucosamine, adonitol, D-arabitol, gentio- biose, x-D-glucose, myo-inositol, x-lactose, lactulose, maltose, L-rhamnose, D-sorbitol, 2-aminoethanol, 2,3-butanediol, succrose, acetic acid, cis-aconitic acid, β-hydroxybutyric acid, itaconic acid, x-ketobutyric acid, x-ketovaleric acid, DL-lactic acid, malonic acid, propionic acid, DL-β-glycolyl phosphate, L-alaminamide, D-alanine, L-alanine, L-α-linyl glycine, L-asparagine, L-glutamic acid, glycy l-L-aspartic acid, glycy l-L-glutamic acid, L-histidine, hydroxy-L-proline, L-ornithine, L-phenylalanine, L-proline, DL-carnitine, γ-amino- butyric acid, inosine, uridine, putrescine, x-D-glucose 1-phosphate and D-glucose 6-phosphate. Compounds not be oxidized are: Tween 40, Tween 80, N-acetyl-D-galactosamine, L-arabinose, cellobiose, 1-erythritol, D-fructose, L-fucose, D-galactose, D-mannitol, D-mannose, melibiose, methyl β-D-glucoside, trehalose, turanose, xylitol, pyruvic acid methyl ester, succinic acid monomethyl ester, citric acid, formic acid, D-galactonic acid lactone, D-galacturonic acid, D-glucuronic acid, D-glucosaminic acid, D-glucuronic acid, β-hydroxybutyric acid, γ-hydroxybutyric acid, hydroxyphenylactic acid, x-ketogluconic acid, gamma-aminobutyric acid, glycy l-L-aspartic acid, L-lysine, L-proline, L-serine, L-threonine, L-tryptophane, L-phenylalanine. Catalase and oxidase are positive. Sensitive to chloramphenicol, gentamicin, kanamycin, nalidixic acid and tetracycline but resistant to penicillin and streptomycin. C18:1ω7c, C16:1ω6c/C16:1ω7c, C17:1ω6 and C16:0 are the major fatty acids. Significant amounts of C14:0, C14:0 2-OH, C15:0 2-OH, C16:0 2-OH, C16:1ω5c 11-methyl, C18:1ω6c, C18:1ω9c and C18:0 are also present. Major quinone is Q-10. Major polar lipids are PG, DPG, PE and PC, unidentified phospholipids and an unidentified polar carotenoid. Minor amounts of unidentified lipids are also present. Bacteriohopane derivatives, diploptero, aminohopanes and diploptene are the major hopanoids. An unidentified aminohopane is present in minor amounts.

The type strain, JA747T (=KCTC 23981T =NRRL 108930T), was isolated from a soil sample of a solar salt pan in Humda, Odisha, India. The DNA G+C content of the type strain is 59.5 mol% (by HPLC).

**Emended description of the genus Pontibacter Nedashkovskaya et al. 2005**

The description is as given by Nedashkovskaya et al. (2005) with the following modifications. Motility is absent in some species. Some species hydrolyse casein and starch. Astaxanthin and astaxanthin glucoside are present. PE is the major polar lipid. Major hopanoids are bacterial hopane derivatives (BHD1, 2), diploptero and unidentified hopanoids, nitrate re-
Colonies are brown. Cells are rod-shaped, 2.0–5.0 μm long and 1.0–1.2 μm wide, non-motile and multiply by binary fission. Astaxanthin glucoside, astaxanthin and six unidentified carotenoids are present. Optimum growth occurs with 2% NaCl (range 0–9%), at pH 6.5–7.5 (range 6.0–9.1) and at 25–30 °C (range 10–40 °C). Catalase and oxidase are positive. Starch and casein are hydrolysed. Nitrate is not reduced. Growth occurs on D-galactose, D-mannitol, L-rhamnose, D-sorbitol, sucrose, cellobiose and Tween 80. Growth does not occur on D-glucose, D-fructose, fucose, lactose or D-mannose. The following compounds are oxidized in the Biolog GN2 test system: x-cyclodextrin, dextrin, glycogen, N-acetyl-D-glucosamine, adonitol, D-arabitol, gentiobiose, α-D-glucose, myo-inositol, α-lactose, lactulose, maltose, L-rhamnose, D-sorbitol, 2-aminoethanol, 2,3-butanediol, sucrose, acetic acid, cis-aconitic acid, β-hydroxybutyric acid, α-ketovaleric acid, DL-lactic acid, malonic acid, propionic acid, DL-α-glycerol phosphate, L-alaninamide, D-alanine, L-alanine, L-alanyl glycine, L-asparagine, L-glutamic acid, glycy1 L-aspartic acid, glycy1 L-glutamic acid, L-histidine, hydroxy-D-proline, L-ornithine, L-phenylalaneine, L-proline, DL-carotin, γ-amino-butyric acid, inosine, uridine, purines, x-D-glucose 1-phosphate, D-glucose 6-phosphate, Tween 40, N-acetyl-D-galactosamine, L-arabinose, cellobiose, α-erythritol, D-fructose, L-fucose, D-galactose, D-mannitol, D-mannose, melibiose, methyl β-D-glucoside, trehalose, turanose, xylitol, pyruvic acid methyl ester, succinic acid mono-methyl ester, citric acid, formic acid, D-galactonolactone, D-galacturonolactone, D-gluconic acid, D-glucosaminic acid, D-glucoronic acid, α-hydroxybutyric acid, γ-hydroxybutyric acid, α-ketoglutaric acid, succinamic acid, glucuronamide, L-aspartic acid, L-leucine, L-prolylglutamic acid, L-serine, L-threonine, urocanic acid, thymidine and phenylethylamine. Compounds not be oxidized are Tween 80, D-mannose, hydroxypynolactetic acid, itaconic acid, α-ketovaleric acid and D-serine. Sensitive to chloramphenicol, streptomycin, gentamicin, kanamycin, nalidixic acid and tetracycline but resistant to penicillin. Major fatty acids are iso-C15:0 and summed feature 4 (anteiso-C17:1B/iso I) with a large number of branched-chain fatty acids. Fatty acid alcohols are present in moderate to minor quantities. Major quinone is MK-7. PE and unidentified lipids are the major polar lipids with minor amounts of unidentified polar lipids and an unidentified aminolipid. Bacteriohopane derivatives, diploptene, diplopterol and an unidentified hopane are the major hopanoids.

The type strain, JC130T (=KCTC 23982T=LMG 26962T), was isolated from a soil sample from a solar saltern at Humma, Odisha, India. The DNA G+C content of the type strain is 47.5 mol% (by HPLC).

Acknowledgements

We thank Professor J. Euzéby for his expert suggestion concerning the correct species epithet and Latin etymology. S.Y. thanks CSIR for providing a fellowship. LMG, Belgium and NRRL, USDA, USA, provided P. actiniiarum LMG 23027T and P. korlensis NRRL B-51097T, respectively, on an exchange basis. KCTC, South Korea, provided E. gangjinensis KCTC 22330T and E. marinus KCTC 23554T on an exchange basis.

References


