Aidingimonas halophila gen. nov., sp. nov., a moderately halophilic bacterium isolated from a salt lake

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Two Gram-negative, facultatively anaerobic, catalase-positive, oxidase-negative, non-motile, rod-shaped and moderately halophilic bacterial strains, designated YIM 90637^T and BH 017, were isolated from a salt lake in Xinjiang province, north-west China, and subjected to a polyphasic taxonomic study. Phylogenetic analysis based on 16S rRNA gene sequences revealed that the two novel isolates were affiliated with the family *Halomonadaceae*; the two strains shared 100% sequence similarity, but showed similarities of 94.7% with the type strain of *Modicisalibacter tunisiensis*, 93.2–94.7% with members of the genus *Chromohalobacter*, 93.2–95.0% with members of the genus *Halomonas* and less than 92.0% with other members of the family *Halomonadaceae*. However, DNA–DNA relatedness data and phenotypic properties demonstrated that strains YIM 90637^T and BH 017 were representatives of the same species. The major fatty acids were C_{19:0} cyclo ω 8c and C_{16:0}. The relative amount of C_{19:0} cyclo ω 8c was notably higher than that found in most species of the family *Halomonadaceae* for which fatty acid composition has been determined. The genomic DNA G + C content was 57.2–57.5 mol% and the only respiratory quinone was ubiquinone 9. Based on evidence from the polyphasic taxonomic study, it was concluded that the two strains should be classified as representatives of a novel species in a new genus, for which name *Aidingimonas halophila* gen. nov., sp. nov. is proposed; the type strain of *Aidingimonas halophila* is YIM 90637^T (=KCTC 12885^T=CCTCC AB 207002^T).

The family *Halomonadaceae* was first proposed on the basis of results obtained with the 16S rRNA cataloguing technique (Franzmann *et al.*, 1988). The family *Halomonadaceae* belongs to the class *Gammaproteobacteria* and, at the time of writing, included four genera of halophilic bacteria (*Halomonas*, *Chromohalobacter*, *Modicisalibacter* and *Cobetia*) and three genera of non-halophilic bacteria

(*Zymobacter*, *Halotalea* and *Carnimonas*) (Okamoto *et al.*, 1993; Dobson & Franzmann, 1996; Mata *et al.*, 2002; Ventosa *et al.*, 1998; Ben Ali Gam *et al.*, 2007; Ntougias *et al.*, 2007). *Halomonas* is the largest genus in the family *Halomonadaceae* and currently comprises more than 50 species. More than half of the taxa in the family *Halomonadaceae* have been reclassified because of their heterogeneous features (Franzmann *et al.*, 1988; Mellado *et al.*, 1995; Dobson & Franzmann, 1996; Arahall *et al.*, 2002a, b) and the description of the family has been emended three times (Dobson & Franzmann, 1996; Ntougias *et al.*, 2007; Ben Ali Gam *et al.*, 2007). Nevertheless, the taxonomic status of some taxa, e.g. *Cobetia marina*, *Halomonas marisflavi*, *Halomonas indalini*, *Halomonas avicenniae* and *Halomonas salaria*, is still

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The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of strains YIM 90637^T and BH 017 are FJ418176 and EU191906, respectively.

The polar lipid composition of strain YIM 90637^T and the cellular fatty acid profiles of strains YIM 90637^T and BH 017 are available as supplementary material with the online version of this paper.

in doubt (Kim *et al.*, 2007). In this paper, two novel bacterial strains, designated YIM 90637^T and BH 017, are described and their morphological, physiological, chemotaxonomic and phylogenetic characteristics are identified. Due to their unique taxonomic position, it is concluded that the two isolates represent a novel species in a new bacterial genus in the family *Halomonadaceae*.

The two strains were isolated from sediment samples taken from Aiding Lake, which is situated in the southern part of the Turpan Basin in Xinjiang Uygur Autonomous Region, north-west China, about 40 km south of the city of Turpan. Aiding Lake is a salt lake with an area of 124 km² and, at 155 m below sea level, is the lowest place in China and the second lowest place in the world, next only to the Dead Sea. The mineral content of the water is as high as 200 g l⁻¹ due to many years of strong evaporation. The major ions are (mg l⁻¹) Na⁺ (127764.8), K⁺ (529.1), Ca²⁺ (151.9), Mg²⁺ (597.8), Cl⁻ (177529.5), SO₄²⁻ (29635.2) and HCO₃⁻ (200.1). Strain YIM 90637^T was isolated by the dilution plating method on cellulose-casein-multisalts medium described by Tang *et al.* (2008), whereas strain BH 017 was isolated on marine agar 2216 (MA; Difco) with the addition of 8% (w/v) NaCl (final NaCl concentration 9.94%, w/v). The two strains were maintained on modified ISP 2 agar (Shirling & Gottlieb, 1966) slants containing 10% NaCl (w/v) at 4 °C and as 20% (w/v) glycerol suspensions at -20 °C. The modified ISP 2 medium contained (per l distilled water) 4 g yeast extract, 10 g malt extract, 4 g glucose, 100 g NaCl and 15 g agar. The medium was adjusted to pH 7.0. Biomass for chemical and molecular studies was obtained by cultivation in shaken flasks (about 150 r.p.m.) using ISP 2 medium supplemented with 10% NaCl at 37 °C for about a week.

Gram staining was carried out by the standard Gram reaction and was confirmed by using the KOH lysis test method (Cerny, 1978). Morphology was examined by transmission electron microscopy with a model H-800 transmission electron microscope (Hitachi) using cells from exponentially growing cultures. Motility was observed both on modified ISP 2 medium with 0.3% agar under high-moisture conditions and in a hanging-drop preparation under an oil-immersion objective. Accumulation of poly- β -hydroxybutyrate was determined by the Sudan black staining method under a light microscope (Smibert & Krieg, 1994). Colony morphology was observed on modified ISP 2 medium containing 10% NaCl after incubation at 37 °C for 7 days. Growth at various temperatures (0, 4, 10, 15, 20, 28, 30, 37, 40, 45, 50 and 55 °C) was tested on modified ISP 2 medium containing 10% NaCl. The pH range for growth was investigated between pH 4.0 and 10.0 (at intervals of 1.0 pH unit) using the buffer system described by Xu *et al.* (2005). Liquid cultures were cultivated in tubes at 37 °C for 2–3 weeks using modified ISP 2 containing 10% NaCl as the basal medium. Growth at various salt concentrations [0–30% NaCl (w/v) at intervals of 1%] was tested by using ISP 2 without any added salts as the basal medium.

Catalase activity was determined by production of bubbles after the addition of a drop of 3% H₂O₂. Oxidase activity was observed by oxidation of tetramethyl-*p*-phenylenediamine. Reduction of nitrate, the methyl red and Voges–Proskauer tests and hydrolysis of aesculin, gelatin, casein, starch and Tweens 20, 40, 60 and 80 were determined as described by Cowan & Steel (1965). Metabolic properties and enzyme activities were determined by means of the API 20NE, API 20E, API 50CHB and API ZYM systems (bioMérieux) according to the manufacturer's instructions. Utilization of organic substrates was tested using Biolog GN2 microplates. Strains were prepared using pre-warmed sterile saline medium (10% NaCl), within the density range specified by the manufacturer. Antibiotic susceptibility was determined on agar using the disc diffusion method (Reva *et al.*, 1995). Anaerobic growth experiments were performed in ISP 2 medium supplemented with 0.15 mM nitrate and 0.035 mM nitrite using the GasPak Anaerobic system (BBL) according to the manufacturer's instructions. Phenotypic, chemotaxonomic and phylogenetic features of the two strains were compared with those of members of related genera of the family *Halomonadaceae*; data are shown in Table 1.

For fatty acid analysis, strains YIM 90637^T and BH 017 were cultured on tryptic soy agar (Difco) containing 10% NaCl at 37 °C for 48 h and GC was performed as described by Sasser (1990) using the Microbial Identification system (MIDI). Isoprenoid quinones were extracted and purified as described by Komagata & Suzuki (1987). The purified ubiquinone was dissolved in acetone and separated by reversed-phase HPLC. Polar lipids were extracted, examined by two-dimensional TLC and identified using published procedures (Minnikin *et al.*, 1984). Levels of DNA–DNA relatedness were determined according to the optical renaturation method (De Ley *et al.*, 1970; Huß *et al.*, 1983; Jahnke, 1992), DNA–DNA hybridization was performed in triplicate.

Extraction of genomic DNA and PCR amplification of the 16S rRNA gene were done as described by Li *et al.* (2007). The obtained sequences were compared with reference 16S rRNA gene sequences retrieved from GenBank and EMBL by BLAST searching and similarity searches were performed using the EzTaxon server (<http://147.47.212.35:8080>; Chun *et al.*, 2007). Multiple alignments and calculations of sequence evolutionary distances were carried out using CLUSTAL_X (Thompson *et al.*, 1997) software. Gaps at the 5' and 3' ends of the alignment were omitted from further analysis. Phylogenetic analyses were performed using three tree-making algorithms, the neighbour-joining (Saitou & Nei, 1987), maximum-likelihood (Felsenstein, 1981) and maximum-parsimony (Fitch, 1971) methods. A phylogenetic tree was constructed using the neighbour-joining method using MEGA version 4.0 (Tamura *et al.*, 2007). The topology of the phylogenetic tree was evaluated by the bootstrap resampling method with 1000 replicates (Felsenstein, 1985). Genomic DNA for determination of the G + C contents of strains YIM 90637^T and BH 017 was

Table 1. Selected characteristics that differentiate members of the genus *Aidingimonas* gen. nov. from those of related genera in the family *Halomonadaceae*

Genera: 1, *Aidingimonas* gen. nov. (strains YIM 90637^T and BH 017; data from this study); 2, *Halomonas* (Vreeland, 2005); 3, *Modicisalibacter* (Ben Ali Gam *et al.*, 2007); 4, *Chromohalobacter* (Ventosa, 2005; Sánchez-Porro *et al.*, 2007; Aguilera *et al.*, 2007); 5, *Cobetia* (Arahal *et al.*, 2002a); 6, *Zymobacter* (Okamoto *et al.*, 2005); 7, *Halotalea* (Ntougias *et al.*, 2007); 8, *Carnimonas* (Garriga *et al.*, 2005). +, Positive; –, negative; v, variable; ND, no data available.

Characteristic	1	2	3	4	5	6	7	8
Cell length (µm)	0.7–1.5	0.6–1.9	0.6–4.0	0.6–4.2	1.6–4.0	0.7–2.4	ND	0.5–1.7
Cell morphology	Straight rods	Straight or curved rods or coccoid	Straight rods	Straight or curved rods	Straight rods	Rods with rounded ends	Rods	Straight or curved rods
Colour	Colourless to yellow brown	White or yellow	Cream	White, yellow or brown	Cream	Milky white	Pale yellow	White
Motility	–	v	+	+	–	+	+	–
Oxygen relationship								
Aerobic	+	+	+	+	+	+	+	+
Facultatively anaerobic	+	v	–	v	–	+	–	–
Oxidase test	–	+	–	v	–	–	+	+
Ranges for growth								
NaCl (% w/v)	1–25	0–32.5	1–25	0–30	0.5–20	ND	0–15	0–8
Temperature (°C)	10–45	4–45	4–45	0–45	10–42	15–37	5–45	ND
pH	5–9	4.5–10	5–10	5–10	5–10	4.7–8.1	5–11	ND
Nitrate reduction	+	+	+	+	–	–	–	–
Gelatin liquefaction	–	v	–	–	ND	–	–	–
Enzyme activities								
Urease	+	v	–	–	+	ND	–	–
Arginine dihydrolase	+	–	ND	ND	ND	–	–	–
Ornithine decarboxylase	–	+	ND	v	ND	–	–	ND
Lysine decarboxylase	–	+	ND	v	ND	–	–	ND
Hydrolysis of:								
Starch	–	–	–	–	–	ND	–	+
Aesculin	–	v	–	–	–	ND	ND	+
Utilization as sole carbon source of:								
L-Arabinose	+	v	ND	+	–	–	ND	–
Citrate	+	+	–	+	–	–	+	+
Maltose	+	+	–	ND	–	+	+	+
D-Ribose	+	ND	–	ND	ND	ND	ND	ND
Xylitol	+	ND	–	ND	ND	ND	ND	ND
D-Mannose	+	+	–	ND	–	v	+	+
L-Lysine	–	+	ND	ND	ND	ND	–	ND
L-Phenylalanine	–	+	ND	ND	ND	ND	ND	ND
L-Leucine	–	+	ND	ND	ND	ND	ND	ND
Major respiratory quinone	Q-9	Q-9	Q-9	ND	ND	ND	Q-9	Q-9
Major fatty acids (>10%)	C _{19:0} cyclo ω8c, C _{16:0}	C _{16:1} ω7c, C _{16:0} , C _{17:0} cyclo, C _{18:1} , C _{19:0} cyclo 11–12	C _{16:0} , C _{16:1} ω7c, C _{18:1} ω7c, C _{19:0} cyclo ω8c	C _{16:0} , C _{18:1} ω7c, C _{19:0} cyclo ω8c	C _{16:0} , C _{17:0} , C _{16:1} ω7c, C _{18:1} ω7c	C _{16:0} , C _{18:1} ω9c, C _{19:0} cyclo	C _{18:1} ω7c, C _{16:0} , C _{19:0} cyclo ω8c, C _{12:0} 3-OH	C _{16:0} , C _{16:1} , C _{18:1} , C _{19:0} cyclo
Polar lipids*	DPG, PE, PI, PIM, 2PL, 2PGL, GL	DPG, PG, PE, 1PL	ND	ND	ND	ND	ND	DPG, PG, PE, 3PL
DNA G + C content (mol%)	57–58	52–68	53.7	56–66	62–64	55–56	64.4	56

*DPG, Diphosphatidylglycerol; GL, unknown glycolipid; PE, phosphatidylethanolamine; PG, phosphatidylglycerol; PGL, unknown phosphoglycolipid; PI, phosphatidylinositol; PIM, phosphatidylinositol mannoside; PL, unknown phospholipid.

prepared according to the method of Marmur (1961); DNA G+C contents were determined by reversed-phase HPLC (Mesbah *et al.*, 1989).

Morphological, cultural, physiological and biochemical characteristics of strains YIM 90637^T and BH 017 are given in the genus and species descriptions and shown in Table 1. Comparative 16S rRNA gene sequence analyses revealed that strains YIM 90637^T and BH 017 shared 100 % sequence similarity and were most closely related to members of the family *Halomonadaceae*. Strains YIM 90637^T and BH 017 exhibited a DNA–DNA relatedness value of 76.5 %, which is higher than the 70 % cut-off point recommended for assignment of strains to the same genomic species, indicating that the two strains represent one unique species (Wayne *et al.*, 1987). In view of their phenotypic, phylogenetic and genetic similarities, strains YIM 90637^T and BH 017 are representatives of the same species.

In addition, as shown in Table 1, several phenotypic and physiological characteristics can be used to differentiate strains YIM 90637^T and BH 017 from related genera in the family *Halomonadaceae*. Strains YIM 90637^T and BH 017 can be distinguished clearly from their closest phylogenetic relative, members of the genus *Modicisalibacter*, by their lack of motility, citrate utilization, urease activity, and utilization of citrate, lactose, maltose, D-ribose, xylitol and D-mannose. Strains YIM 90637^T and BH 017 differ from the members of the genus *Chromohalobacter* in terms of motility and urease activity. The oxidase reaction distinguished strains YIM 90637^T and BH 017 clearly from members of the genus *Halomonas*. Strains YIM 90637^T and BH 017 could also be distinguished from *Cobetia* strains by their ability to reduce nitrate and utilize citrate, lactose, maltose and mannose and their inability to hydrolyse casein. In summary, strains YIM 90637^T and BH 017 showed distinctive phenotypic and physiological features when compared with their closest relatives, i.e. members of the genus *Modicisalibacter* and other genera in the family *Halomonadaceae* (Table 1).

Strains YIM 90637^T and BH 017 had cellular fatty acid profiles that contained large amounts of straight-chain, unsaturated fatty acids. The major components (>10 % of total fatty acids) were C_{19:0} cyclo ω 8c and C_{16:0} (see Supplementary Table S1 in IJSEM Online). The profiles were similar to those of the type strains of previously described species belonging to the genera *Modicisalibacter*, *Chromohalobacter*, *Halomonas* and *Cobetia*, confirming the position of these strains in the family *Halomonadaceae* (Yoon *et al.*, 2002; Peçonek *et al.*, 2006). However, the relative amount of C_{19:0} cyclo ω 8c was notably higher than that observed in most species of the family *Halomonadaceae*. Moreover, some species of the genera *Halomonas*, *Carnimonas* and *Zymobacter* do not possess C_{19:0} cyclo ω 8c. C_{16:1} ω 7c is the major fatty acid in members of the genera *Modicisalibacter* and *Cobetia*, but was not found in strains YIM 90637^T and BH 017. In

summary, the fatty acid profiles of strains YIM 90637^T and BH 017 differed from those of other members of the family *Halomonadaceae*, which supports the assignment of these strains to a new genus. The polar lipids of strains YIM 90637^T and BH 017 comprised diphosphatidylglycerol, phosphatidylethanolamine, phosphatidylinositol, phosphatidylinositol mannosides, two unknown phospholipids, two unknown phosphoglycerolipids and one unknown glycolipid. The DNA G+C contents of strains YIM 90637^T and BH 017 were 57.5 and 57.2 mol%, respectively, which fall within the range given for species of the family *Halomonadaceae* (52.0–74.6 mol%).

Almost-complete 16S rRNA gene sequences were determined for strains YIM 90637^T and BH 017 and the result of alignments showed that they had highest 16S rRNA gene sequence similarity to members of the family *Halomonadaceae*. In a phylogenetic tree based on the neighbour-joining algorithm, strains YIM 90637^T and BH 017 formed a distinct phylogenetic lineage within the family *Halomonadaceae* and clustered with the type strain of *Modicisalibacter tunisiensis* (Fig. 1). 16S rRNA gene sequence similarity between strains YIM 90637^T and BH 017 and members of genera within the family *Halomonadaceae* was as follows: 94.7 % to *Modicisalibacter tunisiensis* LIT2^T, 93.2–94.7 % to members of the genus *Chromohalobacter*, 93.2–95.0 % to members of the genus *Halomonas*, 91.3 % to *Cobetia marina* DSM 4741^T, 89.8 % to *Zymobacter palmae* T109^T, 90.8 % to *Halotalea alkalilenta* AW-7^T, and 90.0 % to *Carnimonas nigrificans* CTCBS1^T. This low level of sequence similarity indicated that strains YIM 90637^T and BH 017 could be assigned to a new genus that was, phylogenetically, as distant from the genus *Halomonas* as from the genera *Chromohalobacter* and *Modicisalibacter*. Topologies of phylogenetic trees constructed using the maximum-likelihood and maximum-parsimony algorithms were similar to that of the tree constructed by neighbour-joining analysis (data not shown).

According to the 16S rRNA signature nucleotides that are characteristic of the family *Halomonadaceae* given in the emended description of Ben Ali Gam *et al.* (2007), strains YIM 90637^T and BH 017 possessed all 18 characteristic bases at positions 484 (A), 486 (C), 640 (A), 660 (A), 668 (A), 669 (A), 737 (U), 738 (U), 745 (U), 776 (U), 1124 (U or G), 1297 (U), 1298 (C), 1423 (A), 1424 (C), 1439 (U), 1462 (A) and 1464 (C). These 16S rRNA signature nucleotides were all present in the sequence of *Modicisalibacter tunisiensis* LIT2^T. However, there was at least one base position that differed from those of other genera in the family *Halomonadaceae*. When the sequences of positions 61–106 (including positions 76–93) were folded using the standard conditions of the RNA structure program (version 4.2), members of the genera *Carnimonas*, *Chromohalobacter*, *Cobetia* and *Modicisalibacter* formed a 6 bp stem, whereas members of the genera *Zymobacter* and *Halotalea* and strains YIM 90637^T and BH 017 formed a 7 bp stem (data not shown).

Fig. 1. Phylogenetic position of YIM 90637^T, BH 017 and representatives of some related taxa. The topology was inferred using the neighbour-joining method (Saitou & Nei, 1987) based on bootstrap analysis of 1000 trees; bootstrap values are shown at nodes. Asterisks indicate branches that were recovered with all three tree-making methods [maximum-likelihood (Felsenstein, 1981), maximum-parsimony (Fitch, 1971) and neighbour-joining]. The sequence of *Oceanospirillum linum* ATCC 11336^T was chosen arbitrarily as an outgroup. Bar, 0.01 substitutions per site.

On the basis of chemotaxonomic, phylogenetic and phenotypic differences between the two isolates and their closest neighbours in the family *Halomonadaceae*, it is proposed that strains YIM 90637^T and BH 017 represent a novel species in a new genus in the family *Halomonadaceae* for which the name *Aidingimonas halophila* gen. nov., sp. nov. is proposed.

Description of *Aidingimonas* gen. nov.

Aidingimonas (Ai.ding.i.mo'nas. N.L. n. *Aiding* a lake located in Xinjiang province of north-west China; L. fem. n. *monas*, *monad* a unit, a monad; N.L. fem. n. *Aidingimonas* a monad from Aiding Lake).

Cells are Gram-negative, facultatively anaerobic, non-endospore-forming, short rods. Non-motile without flagella. Moderately halophilic. Positive for catalase activity. Negative for oxidase activity and nitrate reduction. Ubiquinone 9 is present. Major fatty acids are C_{19:0} cyclo ω 8c and C_{16:0}. The DNA G+C content is about 57–58 mol% (HPLC). The polar lipid pattern consists of diphosphatidylglycerol, phosphatidylethanolamine, phosphatidylinositol, phosphatidylinositol mannosides, two

unknown phospholipids, two unknown phosphoglycolipids and one unknown glycolipid. The genus belongs to the family *Halomonadaceae*. The type species is *Aidingimonas halophila*.

Description of *Aidingimonas halophila* sp. nov.

Aidingimonas halophila (ha.lo'phi.la. Gr. n. *hals*, *halos* salt; Gr. adj. *philos* loving; N.L. fem. adj. *halophila* salt loving).

Exhibits the following properties in addition to those given for the genus. Colonies are colourless to yellow brown, flat and opaque with slightly irregular edges on modified ISP 2 medium. Cells are straight rods (0.1–0.3 × 0.7–1.5 μ m). Growth occurs at 10–45 °C, at pH 5.0–10.0 and in 1–25 % (w/v) NaCl, with optimal growth at 37 °C, pH 7.0–8.0 and 5–10 % NaCl. Non-endospore-forming. Does not contain poly- β -hydroxybutyrate granules or produce exopolysaccharide. Growth occurs under anoxic conditions in the presence of nitrate ion as electron acceptor. The Voges-Proskauer test is variable. Indole and H₂S are not produced. Milk peptonization and coagulation and the methyl red test are negative. Gelatin, aesculin, casein, starch, and Tweens 40, 60 and 80 are not hydrolysed, but

positive for hydrolysis of Tween 20 and urea. *o*-Nitrophenyl β -D-galactopyranosidase, phenylalanine deaminase and lysine and ornithine decarboxylase tests are negative, but positive for arginine dihydrolase. Citrate can be utilized. In the API ZYM system, positive for alkaline phosphatase, esterase (C4), esterase lipase (C8), acid phosphatase, naphthol-AS-BI-phosphohydrolase and α -glucosidase, but negative for lipase (C14), leucine arylamidase, valine arylamidase, cystine arylamidase, trypsin, α -chymotrypsin, α -galactosidase, β -glucosidase, β -galactosidase, β -glucuronidase, *N*-acetyl- β -glucosaminidase, α -mannosidase and α -fucosidase. Acid is produced from L-arabinose, D-ribose, D-xylose, D-galactose, D-glucose, cellobiose, maltose, lactose, melibiose, gentiobiose, D-fucose and potassium 5-ketogluconate (API 50CHB). The following substrates are utilized as sole carbon or nitrogen and energy sources in the Biolog GN2 system: α -cyclodextrin, dextrin, glycogen, Tweens 40 and 80, *N*-acetyl-D-glucosamine, adonitol, L-arabinose, D-arabitol, cellobiose, erythritol, D-fructose, L-fucose, D-galactose, gentiobiose, α -D-glucose, *myo*-inositol, α -lactose, maltose, D-mannitol, D-mannose, melibiose, methyl β -D-glucoside, D-psicose, raffinose, L-rhamnose, D-sorbitol, sucrose, trehalose, turanose, xylitol, methyl pyruvate, monomethyl succinate, acetic acid, *cis*-aconitic acid, citric acid, formic acid, D-galactonic acid lactone, D-galacturonic acid, D-gluconic acid, D-glucosaminic acid, D-glucuronic acid, β -hydroxybutyric acid, α -ketoglutaric acid, DL-lactic acid, malonic acid, propionic acid, D-saccharic acid, succinic acid, bromosuccinic acid, succinamic acid, glucuronamide, L-alaninamide, D- and L-alanine, L-alanyl glycine, L-asparagine, L-aspartic acid, L-glutamic acid, glycyl L-aspartic acid, glycyl L-glutamic acid, L-histidine, hydroxy-L-proline, L-ornithine, L-proline, D- and L-serine, L-threonine, γ -aminobutyric acid, urocanic acid, uridine, putrescine, 2-aminoethanol, 2,3-butanediol, glycerol, glucose 1-phosphate and glucose 6-phosphate. The following substrates in the Biolog GN2 system are negative: *N*-acetyl-D-galactosamine, lactulose, α -hydroxybutyric acid, γ -hydroxybutyric acid, *p*-hydroxyphenylacetic acid, itaconic acid, α -ketobutyric acid, α -ketovaleric acid, quinic acid, sebamic acid, L-leucine, L-phenylalanine acid, L-pyroglytamic acid, DL-carnitine, inosine, thymidine, phenylethylamine and DL- α -glycerol phosphate. Sensitive to the following antibiotics (per disc): amoxicillin (10 μ g), chloramphenicol (30 μ g), ciprofloxacin (5 μ g), erythromycin (15 μ g), netilmicin (10 μ g), norfloxacin (10 μ g), penicillin (10 U), sulfamethoxazole/trimethoprim (23.75/1.25 μ g), tetracycline (30 μ g) and vancomycin (30 μ g). Resistant to clindamycin (2 μ g), gentamicin (10 μ g), novobiocin (5 μ g), streptomycin (10 μ g) and tobramycin (10 μ g). The fatty acids (>1 %) are C_{19:0} cyclo ω 8c, C_{16:0}, C_{18:1} ω 7c, C_{12:0} 3-OH, C_{10:0}, C_{17:0} cyclo and C_{12:0}.

The type strain is YIM 90637^T (=KCTC 12885^T=CCTCC AB 207002^T), isolated from a salt lake in Xinjiang province, north-west China. The DNA G+C content of the type strain is 57.5 mol%.

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