Fodinibius salinus gen. nov., sp. nov., a moderately halophilic bacterium isolated from a salt mine

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A novel, moderately halophilic, rod-shaped bacterium, designated strain YIM D17^T, was isolated from a sample of sediment from a salt mine in Yunnan, south-western China. The taxonomy of strain YIM D17^T was investigated using a polyphasic approach. Strain YIM D17^T was Gram-stain-negative, strictly aerobic and non-motile and formed pink colonies on marine agar. Optimal growth occurred at 37 °C, pH 7.5–8.0 and in the presence of 10–15 % (w/v) NaCl. The major menaquinone was MK-7. The polar lipid profile was composed predominantly of diphosphatidylglycerol, phosphatidylcholine, phosphatidylethanolamine, one phospholipid, one glycolipid and one aminolipid. Minor amounts of other lipids were also detectable. The predominant cellular fatty acids were iso-C_{17:1}ω9c/10-methyl-C_{16:0} (24.0 %), iso-C_{15:0} (23.6 %) and C_{16:1}ω7c/C_{16:1}ω6c (13.8 %). The DNA G + C content was 43.0 mol%. Phylogenetic analysis based on 16S rRNA gene sequence comparisons showed that the isolate formed a distinct clade with the genera *Gracilimonas* and *Balneola* (both in the phylum *Bacteroidetes*) and was related to the species *Gracilimonas tropica*, *Balneola vulgaris* and *Balneola alkaliphila*, with sequence similarities of 85.6 %, 83.0 % and 82.8 % to the respective type strains. On the basis of its phenotypic, chemotaxonomic and phylogenetic features, strain YIM D17^T represents a novel species of a new genus, for which the name *Fodinibius salinus* gen. nov., sp. nov. is proposed. The type strain is YIM D17^T (=ACCC 10716^T=DSM 21935^T).

The taxonomy of the large group of bacteria formerly classified as the *Cytophaga*–*Flavobacterium*–*Bacteroides* group (Olsen *et al.*, 1994) is in need of clarification. Stoecker *et al.* (2006), for example, presented molecular evidence that indicated that the genus *Crenothrix* belonged to the order *Methylococcales* of the class *Gammaproteobacteria*. Consequently, other genera originally assigned to the family *Crenotrichaceae* within the order *Sphingobacteriales* are currently considered *Sphingobacteriales* genera *incertae sedis*. Such genera include *Rhodothermus* (Alfredsson *et al.*, 1988; Sako *et al.*, 1996) and *Salinibacter* (Antón *et al.*, 2002), both of which include species that

show extremophilic characteristics: *Rhodothermus* strains are thermophilic whereas strains of the genus *Salinibacter* are extreme halophiles. Recently, two new genera that were phylogenetically related to the genera *Rhodothermus* and *Salinibacter* were described and named *Balneola* (Urios *et al.*, 2006) and *Gracilimonas* (Choi *et al.*, 2009), respectively. These two genera, which were both isolated from seawater, do not exhibit any of the extreme features found in species of the genera *Rhodothermus* and *Salinibacter*. In this paper, the characterization and classification of a strain (from the phylum *Bacteroidetes*) that appears taxonomically novel at the genus level are reported.

During an investigation of the microbial diversity of the hypersaline environments in Yunnan, south-western China, strain YIM D17^T was isolated from a sediment sample (with 49.3 %, w/v, NaCl) collected from the Fenggang salt mine (23° 28' N 100° 43' E). The strain was isolated at 37 °C, by the standard dilution-plating technique, on marine agar 2216 (MA; Difco) supplemented with 10 % (w/v) NaCl (modified MA). It was subsequently maintained on modified MA slants, and preserved at

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Abbreviations: AL, aminolipid; DPG, diphosphatidylglycerol; GL, glycolipid; L, polar lipid; PC, phosphatidylcholine; PE, phosphatidylethanolamine; PL, phospholipid.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain YIM D17^T is HM153810.

Three supplementary figures are available with the online version of this paper.

–80 °C as a suspension in distilled water containing 20 % (v/v) glycerol.

Gram staining was carried out using the standard Gram reaction combined with KOH lysis (Gregersen, 1978). Cell morphology and flagella were examined by light microscopy (BH-2; Olympus) after Leifson staining (Murray *et al.*, 1994). Growth at various temperatures (4, 10, 15, 20, 25, 28, 37, 45, 50, 55 and 60 °C) and pH values (4.0–11.0, in increments of 0.5 pH unit, at 37 °C) was assessed on marine broth 2216 (MB; Difco) supplemented with 10 % (w/v) NaCl (modified MB). To test NaCl tolerance, growth on nutrient agar (Difco) and tryptone soy agar (TSA; BD), each containing no NaCl or 1, 3, 4, 5, 7, 8, 10, 12, 15, 20, 21, 22, 23, 24, 25 or 30 % (w/v) NaCl, was investigated at 37 °C. Growth under anaerobic conditions was explored by incubation on modified MA in an anaerobic jar (GasPak anaerobic systems; BBL). Accumulation of poly- β -hydroxybutyrate was observed by Sudan black staining (Smibert & Krieg, 1994) under a light microscope. Bacteriochlorophyll *a* was analysed spectrophotometrically by using the method of Cohen-Bazire *et al.* (1957) and following the recommendations of Allgaier *et al.* (2003). Catalase and oxidase activities were determined using 3 % (v/v) H₂O₂ and Kovacs' reagent (Kovacs, 1956), respectively. Glucose fermentation, arginine dihydrolase, indole production, β -galactosidase and urease activities, and hydrolysis of aesculin, casein, DNA, gelatin, starch, Tween 40 and Tween 80 were examined as described by Hansen & Sørheim (1991). Nitrate reduction was tested in modified MB medium containing 0.2 % KNO₃. Nitrite was monitored with the naphthylamine/sulphanilic acid reagent, and residual nitrate with zinc powder; gas production was detected in Durham tubes. H₂S production was tested in modified MB supplemented with 0.01 % (w/v) L-cysteine; the indicator (a strip of paper impregnated with lead acetate) was placed in the neck of the culture tube. Other enzyme activities were assayed by using the API ZYM kit (bioMérieux) according to the manufacturer's instructions, and cells suspended in autoclaved saline containing 10 % (w/v) NaCl. To explore carbon utilization, a potential carbon source, at a final concentration of 0.5 % (w/v or v/v), was added to a basal medium of artificial seawater (Cho & Giovannoni, 2006) (without NH₄Cl if an amino acid was being tested) supplemented with 10 % (w/v) NaCl. Antibiotic sensitivity was explored by placing commercial antibiotic discs (HiMedia) on modified MA plates that had been spread with the isolate and then incubating at 37 °C for 5 days.

Polar lipids of strain YIM D17^T, *Gracilimonas tropica* DSM 19535^T, *Balneola vulgaris* DSM 17893^T and *Balneola alkaliphila* DSM 19538^T (Urios *et al.*, 2008) were extracted (Minnikin *et al.*, 1979) and identified by two-dimensional TLC (Collins & Jones, 1980). Isoprenoid quinones of these four strains were also extracted (Collins *et al.*, 1977) and analysed by HPLC (Tamaoka *et al.*, 1983). Biomass for the quantitative analysis of fatty acids was obtained by scraping cells from cultures of strain YIM D17^T (grown on modified MA for 7 days at 37 °C), *Gracilimonas tropica* DSM 19535^T, *Balneola vulgaris* DSM 17893^T and *Balneola*

alkaliphila DSM 19538^T (all grown on MA for 3 days at 28 °C), *Salisaeta longa* DSM 21114^T (grown on DSMZ 1221 medium for 3 days at 37 °C), *Rhodothermus profundus* DSM 22212^T (grown on MA at 65 °C for 2 days) and *Rhodothermus marinus* DSM 4252^T (grown on DSMZ 630 medium at 65 °C for 2 days). Analysis of the cellular fatty acid pattern followed the method described by Sasser (1990) but used version 6.0 of the Sherlock Microbial Identification System (MIDI, 2005).

Genomic DNA extraction, PCR amplification of the 16S rRNA gene, and sequencing of the purified PCR product were carried out as described previously (Cui *et al.*, 2001). The sequenced length of the 16S rRNA gene of strain YIM D17^T was 1466 bp. The 16S rRNA gene sequences of the closely related taxa were retrieved from the GenBank database using BLAST (Altschul *et al.*, 1997) before all the sequences were aligned and the levels of similarity were calculated using CLUSTAL_X (Thompson *et al.*, 1997). Phylogenetic trees were constructed using the neighbour-joining (Saitou & Nei, 1987) and maximum-parsimony (Fitch, 1971) methods, in MEGA version 4 (Tamura *et al.*, 2007), while a maximum-likelihood (Felsenstein, 1981) tree was generated using the treeing algorithm contained in the PHYLIP package (Felsenstein, 1993). Evolutionary distances for the neighbour-joining tree were calculated by using the Kimura two-parameter model (Kimura, 1980). Bootstrap analysis with 1000 resamplings (Felsenstein, 1985) was used to evaluate tree topology.

The cells of strain YIM D17^T were Gram-stain-negative, catalase- and oxidase-positive, straight or slightly curved rods, 0.3 μ m wide and 1.0–3.0 μ m long (see Supplementary Fig. S1, available in IJSEM Online). Neither flagella nor endospores were observed. Growth occurred on nutrient agar supplemented with 4–23 % (w/v) NaCl (but not on TSA supplemented with various concentrations of NaCl). After growth on modified MA or on nutrient agar supplemented with 10 % (w/v) NaCl, at 37 °C for 7 days, colonies were pink, circular, convex and translucent, with regular margins. The temperature range for growth was 25–45 °C while the pH range for growth at 37 °C was 6.0–9.0. The isolate was sensitive to ampicillin (10 μ g), erythromycin (15 μ g) and chloramphenicol (30 μ g), and resistant to gentamicin (10 μ g), penicillin G (20 U), streptomycin (10 μ g), norfloxacin (10 μ g), carbenicillin (100 μ g) and ciprofloxacin (5 μ g). Phenotypically, the novel isolate differed from the recognized species to which it was most closely related (*G. tropica*, *B. vulgaris* and *B. alkaliphila*) in several features (Table 1). Other phenotypic characteristics of strain YIM D17^T are given in the species description.

The G+C content of the DNA of strain YIM D17^T, extracted according to the method of Cui *et al.* (2001), was determined to be 43.0 mol% by HPLC (Mesbah *et al.*, 1989), with the DNA of *Escherichia coli* DH5 α used as a standard.

Although strain YIM D17^T and *G. tropica* DSM 19535^T shared some major polar lipids, differences in their lipid

Table 1. Characteristics that distinguish strain YIM D17^T from closely related, recognized species

Strains: 1, YIM D17^T (data from this study); 2, *Gracilimonas tropica* DSM 19535^T (this study); 3, *Balneola vulgaris* DSM 17893^T (this study); 4, *Balneola alkaliphila* DSM 19538^T (this study); 5, *Salisaeta longa* S4-4^T (Vaisman & Oren, 2009); 6, *Salinibacter ruber* M31^T (Antón *et al.*, 2002); 7, *Rhodothermus marinus* DSM 4252^T (Alfredsson *et al.*, 1988; Sako *et al.*, 1996; Marteinsson *et al.*, 2010); 8, *Rhodothermus profundus* PRI 2902^T (Marteinsson *et al.*, 2010). +, Positive; w, weakly positive; –, negative; ND, no data available.

Characteristic	1	2	3	4	5	6	7	8
Colony colour	Pink	Pale pink	Orange	Pale yellow	Red	Red	Reddish	None
Cell shape	Rods, slightly curved	Long irregular rods	Rods	Rods	Rods, slightly curved	Rods, slightly curved	Rods	Rods
Motility	–	–	+	–	–	+	+	–
Salinity range for growth (% NaCl)	5–20	1–20	1–8	1–7	5–20	15–30	1–6	1–5
Temperature range for growth (°C)	25–45	20–37	10–45	15–37	25–50	27–52	50–85	55–80
pH range for growth	6.0–9.0	6.0–9.0	6.0–10.0	7.0–9.0	6.0–9.0	6.0–8.5	5.5–9.0	6.0–8.0
Nitrate reduced to nitrite	+	–	–	–	–	ND	ND	ND
Glucose fermentation	–	+	–	–	ND	ND	ND	ND
Hydrolysis of:								
Aesculin	+	+	–	–	ND	ND	ND	ND
Gelatin	+	+	–	–	w	+	ND	ND
Starch	–	+	–	+	w	+	ND	ND
Tween 40	+	+	–	+	ND	ND	ND	ND
Tween 80	+	+	–	–	ND	ND	ND	ND
Utilization of:								
Acetate	–	–	+	+	ND	–	+	–
Adenine	–	–	+	–	ND	ND	ND	ND
D-Glucose	–	+	+	–	+	–	+	–
Hypoxanthine	–	–	+	+	ND	ND	ND	ND
<i>myo</i> -Inositol	–	+	+	+	ND	ND	ND	–
Maltose	–	+	–	–	+	–	+	–
D-Mannitol	–	+	+	+	–	–	ND	–
D-Sorbitol	–	–	+	–	–	–	ND	–
Sucrose	–	–	+	+	+	–	+	–
Enzymic activities (API ZYM):								
Esterase (C4)	–	+	+	+	ND	ND	ND	ND
Trypsin	–	–	+	–	ND	ND	ND	ND
α -Chymotrypsin	–	+	+	+	ND	ND	ND	ND
Acid phosphatase	–	–	+	+	ND	ND	ND	ND
N-Acetyl- β -glucosaminidase	+	+	–	–	ND	ND	ND	ND
Major polar lipids	DPG, PE, PC, PG, GL, AL, PL, L	DPG, PE, PG, PC, GL, PL, L	DPG, PE, PG, GL, L	DPG, PE, PG, GL, AL, L	GL, phospholipids (no unambiguous phospholipids detected)	GL, phospholipids (no unambiguous phospholipids detected)	DPG, PE, PG, GL, PL	DPG, PE, PG, GL, PL
DNA G + C content (mol%)	43.0	42.3	41.7	39.5	62.9	66.5	64.4	60.9

profiles enabled these two strains to be distinguished (Table 1). Major polar lipid components of strain YIM D17^T (see Supplementary Fig. S2) were diphosphatidylglycerol (DPG), phosphatidylcholine (PC), phosphatidylethanolamine (PE), one unknown phospholipid (PL1), one unknown glycolipid (GL) and one unknown aminolipid (AL) detectable with molybdatophosphoric acid. Minor to trace amounts of two unknown phospholipids (PL2 and PL3) and three polar lipids (L1, L2 and L3) were also detected. *G. tropica* DSM 19535^T (Supplementary Fig. S2) had DPG, PE, PC, GL and an unknown phospholipid (PL1) as major lipids, and minor amounts of an unknown phospholipid (PL2) and three polar lipids (L4, L5 and L6). Unlike *G. tropica* DSM 19535^T, strain YIM D17^T contained the lipids AL, L1, L2 and L3, but had no detectable L4, L5 or L6.

In terms of polar lipid profiles, strain YIM D17^T appeared more similar to the two strains of the genus *Balneola* investigated (i.e. *B. vulgaris* DSM 17893^T and *B. alkaliphila*

DSM 19538^T) than to *G. tropica* DSM 19535^T but, unlike either *Balneola* strain, it had PC as its major polar lipid. The major polar lipids of *B. vulgaris* DSM 17893^T and *B. alkaliphila* DSM 19538^T (Supplementary Fig. S2) were DPG, PG, PE, GL and an unknown polar lipid (L). The fatty acid profiles also allowed the two *Balneola* strains to be distinguished from strain YIM D17^T (Table 2). The 16S rRNA gene sequence of the novel strain only showed a low level of similarity (<85.0%) with the corresponding sequences of *B. vulgaris* DSM 17893^T and *B. alkaliphila* DSM 19538^T. The polar lipids of *Salisaeta longa* and *Salinibacter ruber* have been investigated before, although those of *Salisaeta longa* have only previously been determined by one-dimensional TLC (Vaisman & Oren, 2009). The lipid patterns of the investigated strains of these two species differed significantly from those of strain YIM D17^T and *Gracilimonas tropica* DSM 19535^T, especially in terms of the glycolipid and phospholipid fractions (Table 1; Vaisman & Oren, 2009). The presence of PC in strain

Table 2. Cellular fatty acid compositions of strain YIM D17^T and the type strains of phylogenetically related species

Strains: 1, YIM D17^T; 2, *G. tropica* DSM 19535^T; 3, *B. vulgaris* DSM 17893^T; 4, *B. alkaliphila* DSM 19538^T; 5, *Salisaeta longa* DSM 21114^T; 6, *Salinibacter ruber* M31^T; 7, *R. marinus* DSM 4252^T; 8, *R. profundus* DSM 22212^T. All data are from this study except those for *Salinibacter ruber* M31^T, which are from Peña *et al.* (2005). Results are presented as percentages of the total fatty acids; the major fatty acids (10%) are highlighted in bold; fatty acids that represented <1% in all strains are omitted. —, Not detected.

Fatty acid	1	2	3	4	5	6	7	8
C _{14:0}	0.7	0.6	1.6	1.1	0.4	—	—	—
C _{15:0}	—	—	—	—	—	2.1	—	—
C _{16:0}	3.7	1.0	2.5	0.8	4.3	5.2	1.9	2.5
C _{18:0}	1.4	—	0.1	—	—	—	0.2	0.4
iso-C _{13:0}	0.4	1.1	10.2	16.0	0.1	—	—	—
iso-C _{14:0}	1.7	1.1	15.0	4.1	0.2	—	3.3	3.2
iso-C _{15:0}	23.6	42.4	25.6	36.3	16.4	34.6	7.3	5.9
anteiso-C _{15:0}	8.1	5.6	1.8	1.6	7.8	8.0	12.4	8.0
iso-C _{15:1} F	2.4	0.6	1.0	4.0	0.5	—	—	—
iso-C _{16:0}	3.8	2.6	6.8	1.8	6.6	3.9	—	—
iso-C _{17:0}	0.3	3.4	1.7	0.6	3.6	—	13.4	14.3
iso-C _{18:0}	—	—	—	—	—	—	6.8	7.6
anteiso-C _{17:0}	0.4	0.5	0.1	—	7.5	—	9.5	8.1
C _{15:1} ω6c	0.6	6.4	3.9	4.6	1.8	—	—	—
C _{15:1} ω8c	—	0.9	0.7	1.6	0.2	—	—	—
C _{16:1} ω5c	1.5	1.5	1.0	2.3	1.1	—	—	—
C _{17:1} ω6c	0.6	4.3	0.7	0.4	2.6	—	—	—
C _{17:1} ω8c	0.5	5.4	2.8	1.2	0.8	—	—	—
C _{18:1} ω7c	—	—	—	—	0.8	12.1	—	—
C _{18:1} ω9c	4.5	—	—	—	—	—	—	—
anteiso-C _{17:1} ω9c	1.4	0.8	—	—	1.0	—	—	—
10-methyl-C _{18:0}	3.1	—	—	—	—	—	—	—
C _{17:0} 2-OH	—	—	—	—	0.1	1.6	—	—
iso-C _{15:0} 2-OH	—	—	—	—	—	27.5*	—	—
iso-C _{17:0} 3-OH	0.3	—	—	—	0.9	4.1	0.2	—
C _{16:1} ω7c / C _{16:1} ω6c	13.8	8.5	17.2	14.7	27.2	—	—	—
iso-C _{17:1} ω9c / 10-methyl-C _{16:0}	24.0	12.0	5.1	6.2	—	—	—	0.4
iso-C _{15:1} H/C _{13:0} 3-OH	0.3	—	0.1	0.5	8.5	—	—	—

*Reported as iso-C_{15:0} 2-OH and/or C_{16:1}ω7c by Peña *et al.* (2005).

YIM D17^T distinguished it from the type strains of *R. profundus* and *R. marinus* (Marteinsson *et al.*, 2010; Tindall, 1991). The major respiratory quinone of strain YIM D17^T was menaquinone-7 (MK-7). The dominant fatty acids of this strain were iso-C_{17:1}ω9c/10-methyl-C_{16:0} (24.0 %), iso-C_{15:0} (23.6 %) and C_{16:1}ω7c/C_{16:1}ω6c (13.8 %). The cellular fatty acid profile of strain YIM D17^T was similar to those of the type strains of *G. tropica*, *B. vulgaris*, *B. alkaliphila* and *Salinibacter ruber*, but clear differences could also be observed (Table 2). In terms of their fatty acid profiles, the type strains of both *Rhodothermus* species investigated were substantially different from strain YIM D17^T (Table 2).

Phylogenetic analysis of its almost-complete 16S rRNA gene sequence revealed that strain YIM D17^T occupied a distinct lineage with species of the genera *Gracilimonas* and *Balneola*, within the phylum *Bacteroidetes* (Fig. 1 and Supplementary Fig. S3). The topologies of the phylogenetic tree constructed using the neighbour-joining algorithm (Fig. 1) were similar to those of the trees constructed using the maximum-likelihood and maximum-parsimony algorithms. Sequence analysis revealed that strain YIM D17^T was closely related to *G. tropica* CL-CB462^T (85.6 % 16S rRNA gene sequence similarity), *B. vulgaris* 131X/A01/164^T (83.0 %), *B. alkaliphila* CM41_14b^T (82.8 %), *Salisaeta longa* S4-4^T (77.6 %), *Salinibacter ruber* M31^T (77.2 %), *R. profundus* PRI 2902^T (76.8 %) and *R. marinus* DSM 4252^T (76.5 %). The novel strain exhibited less than 75.0 % 16S rRNA gene sequence similarity to other established members of the phylum *Bacteroidetes*. No DNA–DNA hybridization experiments were performed because all the levels of 16S rRNA gene sequence similarity that were observed were relatively low.

From the results of the phenotypic, chemotaxonomic, genotypic and phylogenetic analyses, strain YIM D17^T could not be assigned to any known taxon. Some phenotypic features (Table 1), its fatty acid (Table 2) and polar lipid profiles (Supplementary Fig. S2) and 16S rRNA gene sequence clearly differentiated this novel isolate from phylogenetically related, recognized taxa and indicated that the isolate represents a novel genus and species, for which the name *Fodinibius salinus* gen. nov., sp. nov. is proposed.

Description of *Fodinibius* gen. nov.

Fodinibius [Fo.di.ni'bi.us. L. fem. n. *fodina* mine; N.L. masc. n. *bius* from Gr. N. *bios* life; N.L. masc. n. *Fodinibius* a living (one) from a mine].

Cells are Gram-stain-negative, non-motile, moderately halophilic, non-spore-forming rods. Aerobic, catalase- and oxidase-positive. The major respiratory quinone is MK-7. The major polar lipids are diphosphatidylglycerol, phosphatidylethanolamine, phosphatidylcholine, one phospholipid, one glycolipid and one aminolipid. The dominant fatty acids are iso-C_{17:1}ω9c/10-methyl-C_{16:0}, iso-C_{15:0} and C_{16:1}ω7c/C_{16:1}ω6c. The genus *Fodinibius* is a member of the phylum *Bacteroidetes*. The type species is *Fodinibius salinus*.

Description of *Fodinibius salinus* sp. nov.

Fodinibius salinus (sa'li.nus. L. masc. adj. *salinus* of or belonging to salt).

Shows the following characteristics in addition to the description given above for the genus. Colonies are pink, circular, convex and translucent, with regular margins.

Fig. 1. Neighbour-joining tree based on 16S rRNA gene sequences showing the relationships between strain YIM D17^T and related genera. Bootstrap percentages (based on 1000 replications) >50 % are shown at branching points. *Bacteroides massiliensis* B84634^T was used as the outgroup. Bar, 0.02 substitution per nucleotide position.

Cells are 1.0–3.0 µm in length and 0.3 µm in width. Does not accumulate poly-β-hydroxybutyrate or produce bacteriochlorophyll *a*. Temperature range for growth is 25–45 °C (optimum 37 °C) and pH range for growth at 37 °C is 6.0–9.0 (optimum between 7.5 and 8.0). Growth at 37 °C occurs at NaCl concentrations of 4–23 % (w/v) (optimum between 10 and 15 %). Hydrolyses aesculin, gelatin, Tween 40 and Tween 80, but not DNA, casein or starch. Reduces nitrate to nitrite, but nitrite is not reduced. Arginine dihydrolase and urease are present. β-Galactosidase, glucose fermentation, indole production and H₂S production are absent. Assimilates citrate, aesculin and xanthine, but not acetate, aspartate, ethanol, D-galactose, glycerol, D-glucose, *myo*-inositol, α-lactose, maltose, D-mannose, D-mannitol, methanol, D-sorbitol, sucrose, D-xylose, adenine, glycine or hypoxanthine. Alkaline phosphatase, esterase lipase (C8), lipase (C14), leucine arylamidase, valine arylamidase, cystine arylamidase, naphthol-AS-BI-phosphohydrolase and *N*-acetyl-β-glucosaminidase are present but esterase (C4), trypsin, α-chymotrypsin, acid phosphatase, α-galactosidase, β-galactosidase, β-glucuronidase, α-glucosidase and β-glucosidase are absent. Sensitive to ampicillin (10 µg), erythromycin (15 µg) and chloramphenicol (30 µg), but resistant to gentamicin (10 µg), penicillin G (20 U), streptomycin (10 µg), norfloxacin (10 µg), carbenicillin (100 µg) and ciprofloxacin (5 µg).

The type strain YIM D17^T (=ACCC 10716^T=DSM 21935^T) was isolated from a salt sediment collected from Fenggang salt mine (23° 28' N 100° 43' E) in Yunnan, south-western China. The genomic DNA G + C content of the type strain is 43.0 mol%.

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