Haloactinobacterium album gen. nov., sp. nov., a halophilic actinobacterium, and proposal of *Ruaniaceae* fam. nov.

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A Gram-staining-positive, facultatively anaerobic, non-motile and moderately halophilic actinobacterium, designated YIM 93306^T, was isolated from a salt lake in Xinjiang province, north-west China, and subjected to a polyphasic taxonomic study. Strain YIM 93306^T grew in the presence of 2–16 % (w/v) NaCl and did not grow without NaCl. The peptidoglycan type was A4 α with an L-Lys–L-Glu interpeptide bridge. The whole-cell sugars were glucosamine, arabinose, mannose and two unknown sugars. The predominant menaquinone was MK-8(H₄). The major fatty acids were iso-C_{15:0}, anteiso-C_{15:0} and anteiso-C_{17:0}. The polar lipids comprised diphosphatidylglycerol, phosphatidylglycerol, phosphatidylinositol, one unknown phosphoglycolipid and one unknown phospholipid. The DNA G + C content was 68.3 mol%. Phylogenetic analysis based on 16S rRNA gene sequences revealed that strain YIM 93306^T fell within the radius of the suborder *Micrococcineae*. Its closest phylogenetic neighbour was the type strain of *Ruania albidiflava* (AS 4.3142^T; 96.2 % 16S rRNA gene sequence similarity), the sole recognized species of the genus *Ruania*. Sequence similarities between strain YIM 93306^T and members of other genera of the suborder *Micrococcineae* were <95.2 %. On the basis of phylogenetic analysis, phenotypic characteristics and chemotaxonomic differences, a novel genus and species, *Haloactinobacterium album* gen. nov., sp. nov., is proposed. The type strain of the species is YIM 93306^T (=DSM 21368^T =KCTC 19413^T =CCTCC AB 208069^T). Based on phylogenetic characteristics and 16S rRNA gene signature nucleotide patterns, the genera *Ruania* and *Haloactinobacterium* gen. nov. are proposed to belong to a novel family, *Ruaniaceae* fam. nov.

The suborder *Micrococcineae* was proposed by Stackebrandt *et al.* (1997) based on phylogenetic and signature nucleotide analysis of the 16S rRNA gene sequence. At the time of writing, the suborder *Micrococcineae* comprises 15 families: *Beutenbergiaceae* (Zhi *et al.*, 2009), *Bogoriellaceae* (Stackebrandt & Schumann, 2000; Zhi *et al.*, 2009), *Brevibacteriaceae* (Breed, 1953; Stackebrandt *et al.*, 1997; Stackebrandt & Schumann, 2000; Zhi *et al.*, 2009), *Cellulomonadaceae* (Stackebrandt & Prauser, 1991; Stackebrandt *et al.*, 1997; Stackebrandt & Schumann 2000; Zhi *et al.*, 2009),

Dermabacteraceae (Stackebrandt *et al.*, 1997; Zhi *et al.*, 2009), *Dermacoccaceae* (Stackebrandt & Schumann, 2000; Zhi *et al.*, 2009), *Dermatophilaceae* (Austwick, 1958; Stackebrandt *et al.*, 1997; Stackebrandt & Schumann 2000; Zhi *et al.*, 2009), *Intrasporangiaceae* (Stackebrandt *et al.*, 1997; Stackebrandt & Schumann 2000; Zhi *et al.*, 2009), *Jonesiaceae* (Stackebrandt *et al.*, 1997; Zhi *et al.*, 2009), *Microbacteriaceae* (Park *et al.*, 1993; Stackebrandt *et al.*, 1997; Zhi *et al.*, 2009), *Micrococcaceae* (Pribram, 1929; Stackebrandt *et al.*, 1997; Zhi *et al.*, 2009), *Promicromonosporaceae* (Stackebrandt *et al.*, 1997; Zhi *et al.*, 2009), *Rarobacteraceae* (Stackebrandt & Schumann, 2000; Zhi *et al.*, 2009), *Sanguibacteraceae* (Stackebrandt & Schumann, 2000; Zhi *et al.*, 2009) and *Yaniellaceae* (Li *et al.*,

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain YIM 93306^T is FJ969847.

2005, 2008). The genus *Ruania* (Gu *et al.*, 2007) has not been classified in a family. The pattern of 16S rRNA gene signature nucleotides of the suborder *Micrococcineae* consists of nucleotides at positions 127:234 (A–U), 598:640 (U–G), 657:749 (U–A), 953:1228 (G–C), 986:1219 (A–U), 987:1218 (A–U) and 1362 (A) (Zhi *et al.*, 2009). In this paper, we report the characterization of strain YIM 93306^T and propose *Haloactinobacterium album* gen. nov., sp. nov. A new family, *Ruaniaceae* fam. nov., is proposed to accommodate the genera *Ruania* and *Haloactinobacterium* gen. nov.

Strain YIM 93306^T was isolated from a soil sample collected from Qijiaoing Lake, which is a salt lake in Xinjiang province, north-west China (43° 27' N 91° 29' E), after 3 weeks incubation at 37 °C on glucose–tryptone–yeast (GTY) agar [containing (l⁻¹): 1.0 g glucose, 0.5 g tryptone, 2.0 g yeast extract, 1.0 g CaCl₂, 15.0 g agar; final pH not adjusted] supplemented with 10 % (w/v) NaCl. NaCl was sterilized separately before being added to the medium. Strain YIM 93306^T was maintained on GTY agar slants at 4 °C and in 20 % (v/v) glycerol suspensions at –20 °C. Biomass for chemical and molecular studies was obtained by cultivation in GTY broth supplemented with 10 % NaCl at 37 °C and 150 r.p.m. for about 1 week.

Cell morphology was determined with cultures grown for 6, 12, 24, 48 and 72 h on GTY agar supplemented with 10 % NaCl at 37 °C. The Gram reaction was determined by Gram staining and the KOH lysis test (Cerny, 1978). Cell motility was confirmed by the development of turbidity throughout a tube containing semisolid medium (Leifson, 1960). Morphological characteristics were observed by light microscopy (model BH2; Olympus) and by transmission electron microscopy (model H-800; Hitachi). Growth was tested at 5–55 °C on GTY agar supplemented with 10 % NaCl at intervals of 5 °C. Tolerance to 0–20 % (w/v) NaCl (in intervals of 1 %) was tested using GTY agar as the basal medium. Growth at pH 4.0–10.0 (in intervals of 1 pH unit) was tested on GTY agar supplemented with 10 % NaCl, with the pH adjusted using the following buffer systems: 0.1 M citric acid/0.1 M sodium citrate (pH 4.0–5.0); 0.1 M KH₂PO₄/0.1 M NaOH (pH 6.0–8.0); and 0.1 M NaHCO₃/0.1 M Na₂CO₃ (pH 9.0–10.0). 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. Methyl red and Voges–Proskauer tests and hydrolysis of aesculin, casein, cellulose, chitin, dextrin, DNA, gelatin, starch, urea and Tweens 20, 40, 60 and 80 were determined as described by Cowan & Steel (1965). Oxidation of 95 different substrates was tested using Biolog GP2 MicroPlates (Biolog). Enzyme activity and acid production from carbohydrates were determined using API 20E, API ZYM and API 50CH test panels (bioMérieux) according to the manufacturer's instructions. Anaerobic growth was determined using the GasPak anaerobic system (BBL) according to the manufacturer's instructions. The morphological, cultural and physiological properties of strain

YIM 93306^T are given in the species description and in Table 1.

The peptidoglycan structure of the cell wall of strain YIM 93306^T was determined by using established procedures (Schleifer & Kandler, 1972; Schleifer, 1985; MacKenzie, 1987). Whole-cell sugars were detected by HPLC after pre-column derivatization with 1-phenyl-3-methyl-5-pyrazolone (Tang *et al.*, 2009). Polar lipids were extracted, examined by two-dimensional TLC and identified using described procedures (Minnikin *et al.*, 1984). Menaquinones were isolated according to Minnikin *et al.* (1984). The purified menaquinones were dissolved in acetone and separated by atmospheric-pressure photoionization-LC-MS (Tang *et al.*, 2008). For fatty acid analysis, cells of strain YIM 93306^T were cultured on tryptic soy agar (TSA; Difco) supplemented with 10 % NaCl at 37 °C for 4 days. Cellular fatty acid analysis was performed as described by Sasser (1990) using the Microbial Identification System (MIDI). Genomic DNA of strain YIM 93306^T for the determination of G + C content was prepared according to the method of Marmur (1961). The G + C content of the DNA was determined by reversed-phase HPLC of nucleosides according to Mesbah *et al.* (1989).

The peptidoglycan of strain YIM 93306^T contained Ala, Glu and Lys in a molar ratio of 1.5 : 1.6 : 1. Enantiomeric analysis of cell-wall diamino acids resulted in the detection of D-Ala, L-Ala, D-Glu, L-Glu and L-Lys. The peptides L-Ala←D-Glu and L-Lys←D-Ala were detected in the partial hydrolysate (4 M HCl, 100 °C, 16 h) of the peptidoglycan. Glutamic acid was detected as the N-terminus of the interpeptide bridge. From these results, it was concluded that strain YIM 93306^T contained peptidoglycan type A4α with an L-Lys–L-Glu interpeptide bridge (DSMZ, 2001). The whole-cell sugars were glucosamine (48.7 %), arabinose (28.3 %) and mannose (12.0 %), and there were minor amounts of two unknown sugars (8.0 and 3.1 %, respectively). The polar lipids comprised diphosphatidylglycerol, phosphatidylglycerol, phosphatidylinositol, one unknown phosphoglycolipid and one unknown phospholipid. The predominant menaquinone was MK-8(H₄) (88.1 %); minor amounts of MK-8 (3.1 %), MK-8(H₂) (4.2 %), MK-8(H₆) (1.5 %) and MK-9(H₄) (2.8 %) were also detected. Strain YIM 93306^T had a cellular fatty acid profile that contained major amounts of branched fatty acids and minor amounts of straight fatty acids: anteiso-C_{15:0} (34.4 %), iso-C_{15:0} (33.1 %), anteiso-C_{17:0} (14.8 %), C_{17:0} (8.7 %), iso-C_{16:0} (2.3 %), C_{16:0} (2.1 %), iso-C_{15:0} 3-OH (0.9 %) and iso-C_{15:0} 2-OH (0.9 %); other fatty acids were present in amounts less than 0.5 %. The G + C content of the DNA was 68.3 mol%.

Extraction of genomic DNA and PCR amplification of the 16S rRNA gene were performed as described by Li *et al.* (2007). Multiple alignments with sequences from the most closely related members of the suborder *Micrococcineae* and calculations of sequence similarities were performed with the EzTaxon server 2.0 (Chun *et al.*, 2007). Phylogenetic analyses were performed by using three tree-making

Table 1. Differential morphological, phenotypic and chemotaxonomic characters of strain YIM 93306^T and the type strain of the only species of the genus *Ruania*

Strains: 1, *Haloactinobacterium album* YIM 93306^T; 2, *Ruania albidiflava* AS 4.3142^T. Data are from this study and Gu *et al.* (2007). DPG, Diphosphatidylglycerol; GL, glycolipid; PG, phosphatidylglycerol; PGL, phosphoglycolipid; PI, phosphatidylinositol; PL, phospholipid; +, positive; –, negative.

Characteristic	1	2
Cell morphology	Rod	Coccoid
Colony colour	Cream white	Pale yellow
Facultative anaerobe	+	–
Growth with:		
0 % NaCl	–	+
15 % NaCl	+	–
Range for growth		
pH	6–10	5.5–12.5
Temperature (°C)	10–40	20–37
Methyl red test	–	+
Nitrate reduction	–	+
Enzymes (API ZYM)		
Esterase (C4)	+	–
Alkaline phosphatase	–	+
Leucine arylamidase	–	+
Valine arylamidase	–	+
Naphthol-AS-BI-phosphohydrolase	–	+
α -Glucosidase	–	+
α -Galactosidase	–	+
α -Fucosidase	–	+
Acid production (API 50CH) from:		
Arbutin	–	+
D-Adonitol	+	–
Cellobiose	+	–
D-Galactose	+	–
D-Glucose	+	–
D-Lyxose	–	+
D-Mannose	+	–
Turanose	+	–
D-Tagatose	+	–
Erythritol	+	–
Glycerol	+	–
N-Acetylglucosamine	+	–
Interpeptide bridge (A4z)	L-Lys–L-Glu	L-Lys–Gly–L-Glu–L-Glu
Whole-cell sugars	Glucosamine, arabinose, mannose, two unknown sugars	Galactose, glucose
Polar lipids	DPG, PG, PGL, PI, PL	DPG, PG, GL
Major fatty acids (>10 %)		
anteiso-C _{15:0}	34.4	37.3
iso-C _{15:0}	33.1	–
iso-C _{16:0}	–	14.3
anteiso-C _{17:0}	14.8	14.7
DNA G + C content (mol%)	68.3	70.0

algorithms: neighbour joining (Saitou & Nei, 1987), maximum likelihood (Felsenstein, 1981) and maximum parsimony (Fitch, 1971). A phylogenetic tree was constructed using the neighbour-joining method from K_{nuc}

values (Kimura, 1980) using MEGA version 4.0 (Tamura *et al.*, 2007). The topology of the phylogenetic tree was evaluated by the bootstrap resampling method of Felsenstein (1985) with 1000 replicates.

An almost-complete 16S rRNA gene sequence (1524 bp) was determined for strain YIM 93306^T. Phylogenetic analysis based on 16S rRNA gene sequences revealed that strain YIM 93306^T fell within the radius of the suborder *Micrococcineae* and that its closest phylogenetic neighbour was *Ruania albidiflava* AS 4.3142^T (96.2 % sequence similarity), the type strain of the sole recognized species of the genus *Ruania*.

Sequence similarities between strain YIM 93306^T and members of other genera of the suborder *Micrococcineae* were <95.2 %. In the phylogenetic tree based on the neighbour-joining algorithm, strain YIM 93306^T and *R. albidiflava* AS 4.3142^T formed two branches with a high bootstrap value (99 %) in a distinct clade. This relationship was supported by the other tree-making methods used in this study (Fig. 1).

Fig. 1. Phylogenetic dendrogram obtained by distance-matrix analysis of 16S rRNA gene sequences, showing the positions of strain YIM 93306^T and type strains of type species of genera in the suborder *Micrococcineae*. An asterisk indicates that the corresponding node was also recovered in the trees constructed with the maximum-likelihood and maximum-parsimony algorithms. Bootstrap values (>50 %) based on 1000 resampled datasets are shown at branch nodes. *Bifidobacterium gallicum* JCM 8224^T was used as an out-group. Bar, 0.02 substitutions per nucleotide position.

All of the above data confirmed that the new isolate should be assigned to the suborder *Micrococccineae*. Strain YIM 93306^T formed a monophyletic branch at the periphery of the evolutionary radiation occupied by the genus *Ruania*. Although strain YIM 93306^T was similar to *R. albidiflava* AS 4.3142^T by having MK-8(H₄) as the predominant menaquinone and A4α as the peptidoglycan type, it was different in some morphological and physiological properties (Table 1). Strain YIM 93306^T was a halophilic bacterium and it grew with 16 % NaCl but not without NaCl, whereas *R. albidiflava* AS 4.3142^T, as a non-halophilic actinobacterium, grew well without NaCl but not with 15 % NaCl. Also, strain YIM 93306^T exhibited some chemotaxonomic differences from *R. albidiflava* AS 4.3142^T (Table 1). For instance, strain YIM 93306^T contained glucosamine, arabinose, mannose and two unknown sugars as whole-cell sugars and L-Lys–L-Glu as the interpeptide bridge of the peptidoglycan, whereas *R. albidiflava* AS 4.3142^T contained galactose and glucose as the whole-cell sugars and L-Lys–Gly–L-Glu–L-Glu as the interpeptide bridge. Also, as well as anteiso-C_{15:0} and anteiso-C_{17:0} as major fatty acids, strain YIM 93306^T contained iso-C_{15:0} and *R. albidiflava* AS 4.3142^T contained iso-C_{16:0} as the additional major fatty acid. Therefore, on the basis of phenotypic, chemotaxonomic and phylogenetic differentiation of strain YIM 93306^T from its closest neighbour, *R. albidiflava* AS 4.3142^T, we propose

that strain YIM 93306^T represents a novel species in a new genus, *Haloactinobacterium album* gen. nov., sp. nov.

Representatives of the 15 described families in the suborder *Micrococccineae* showed 16S rRNA gene sequence similarities to *R. albidiflava* AS 4.3142^T and strain YIM 93306^T of between 92.0 and 95.2 %, and *R. albidiflava* AS 4.3142^T and strain YIM 93306^T formed a deep branch that was clearly distinguished from the families of the suborder *Micrococccineae*. Thus, although *R. albidiflava* AS 4.3142^T and strain YIM 93306^T clearly belong to the suborder *Micrococccineae*, they do not belong to any of the described families within the suborder. The 16S rRNA gene sequences of representatives of the 15 families of the suborder *Micrococccineae* (Zhi *et al.*, 2009), *R. albidiflava* AS 4.3142^T and strain YIM 93306^T were scanned for the signature nucleotides of the suborder *Micrococccineae*. We only found one difference between *R. albidiflava* AS 4.3142^T and strain YIM 93306^T, at position 602:636, where C–G was found in strain YIM 93306^T and G–U was found in *R. albidiflava* AS 4.3142^T (Table 2). There was only one position for *R. albidiflava* AS 4.3142^T and strain YIM 93306^T that was unique among the family of the suborder *Micrococccineae*: position 444:490, where C–U was found in *R. albidiflava* AS 4.3142^T and strain YIM 93306^T; all of the other signatures studied were found in at least one other family. However, strain YIM 93306^T and *R. albidiflava* AS 4.3142^T

Table 2. Patterns of 16S rRNA gene signature nucleotides detected in the family *Ruaniaceae* and the defined families of the suborder *Micrococccineae*

Families: 1, *Ruaniaceae*; 2, *Beutenbergiaceae*; 3, *Bogoriellaceae*; 4, *Brevibacteriaceae*; 5, *Cellulomonadaceae*; 6, *Dermabacteraceae*; 7, *Dermacoccaceae*; 8, *Dermatophilaceae*; 9, *Intrasporangiaceae*; 10, *Jonesiaceae*; 11, *Microbacteriaceae*; 12, *Micrococcaceae*; 13, *Promicromonosporaceae*; 14, *Rarobacteraceae*; 15, *Sanguibacteraceae*; 16, *Yaniellaceae*. Data for columns 2–16 were taken from Zhi *et al.* (2009).

Position	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
120	A	A	A	A	A	A	A	A	A	A	A	W	A	A	A	U
131:231	A–G	C–G	A–G	C–G	C–G	C–G	A–G	Y–K	A–G	A–G	G–R	C–G	A–G	C–G	C–G	A–G
196	C	G	U	A	U	U	C	A	G	C	U	C	U	A	U	C
342:347	C–G	C–G	U–G	C–G	C–G	C–G	C–G	C–G	C–G	C–G	C–G	C–G	C–G	C–G	C–G	C–G
444:490	C–U	A–U	A–U	A–U	A–U	A–U	A–U	A–U	A–U	A–U	A–U	A–U	A–U	A–U	A–U	U–U
580:761	C–G	C–G	C–A	C–G	C–G	U–A	U–A	U–A	U–A	C–G	C–G	C–G	C–G	C–G	C–G	C–G
602:636	S–K	C–G	C–G	C–G	C–G	C–G	C–G	C–G	C–G	C–G	C–G	C–G	G–U	G–U	G–U	C–G
670:736	A–U	A–U	A–U	U–A	A–U	A–U	A–U	A–U	A–U	A–U	A–U	A–U	A–U	A–U	A–U	A–U
822:878	G–C	G–C	G–C	G–C	G–C	G–C	G–C	G–C	G–C	U–C	G–C	G–C	G–C	G–C	G–C	G–C
823:877	G–C	G–C	G–C	G–C	G–C	G–C	G–C	G–C	G–C	A–G	G–C	G–C	G–C	G–C	G–C	G–C
826:874	C–G	C–G	C–G	C–G	C–G	C–G	C–G	C–G	C–G	U–G	C–G	C–G	C–G	C–G	C–G	C–G
827	U	U	U	U	U	U	U	U	U	G	U	U	U	U	U	U
843	U	U	C	C	U	C	C	U	U	C	C	C	U	U	C	U
950:1231	U–A	U–A	U–A	U–A	U–A	U–G	U–A	U–A	U–A	U–A	U–A	U–A	U–A	U–A	U–A	U–A
1047:1210	G–C	G–C	G–C	G–U	G–C	G–C	G–C	G–C	G–C	G–C	G–C	G–C	G–C	G–C	G–C	G–C
1109	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C
1145	G	G	G	A	G	G	G	G	G	G	R	G	G	G	G	G
1309:1328	G–C	G–C	A–U	G–C	G–C	G–U	G–C	G–C	G–C	G–C	G–C	G–C	G–C	G–C	G–C	G–C
1361	G	G	G	G	G	G	G	G	C	G	G	G	G	G	G	G
1383	U	U	U	C	Y	C	C	C	C	C	C	C	C	C	C	C

had a unique combination of 16S rRNA gene signature nucleotides compared with those for the 15 known families of the suborder *Micrococcineae* (Table 2). Higher hierarchical taxa in the class *Actinobacteria* should be based mainly on 16S rRNA gene signature nucleotide patterns and phylogenetic criteria (Stackebrandt *et al.*, 1997; Zhi *et al.*, 2009). Accordingly, it has been shown that the genus *Ruania* and strain YIM 93306^T are closely related phylogenetically and distinct from other families in the suborder *Micrococcineae*. Thus, *Ruaniaceae* fam. nov. is proposed to accommodate the genera *Ruania* and *Haloactinobacterium* gen. nov.

Description of *Ruaniaceae* fam. nov.

Ruaniaceae (Ru.a.ni.a'ce.ae. N.L. fem. n. *Ruania* type genus of the family; -aceae ending to denote a family; N.L. fem. pl. n. *Ruaniaceae* the *Ruania* family).

The family contains the type genus, *Ruania* Gu *et al.* 2007, as well as the genus *Haloactinobacterium* gen. nov. The pattern of 16S rRNA gene signature nucleotides is shown in Table 2.

Description of *Haloactinobacterium* gen. nov.

Haloactinobacterium (Ha.lo.ac.ti.no.bac.te'ri.um. Gr. n. *hals*, *halos* salt; Gr. n. *actis*, *actinos* a ray; L. neut. n. *bacterium* a rod; N.L. neut. n. *Haloactinobacterium* a halophilic actinobacterium).

Cells are aerobic, Gram-staining-positive, non-motile and moderately halophilic short rods (0.3–0.4 × 0.6–0.7 µm). No rod–coccus life cycle. Facultatively anaerobic in the presence of KNO₃. Does not form endospores. The peptidoglycan is type A4 α with L-Lys–L-Glu as the interpeptide bridge. The whole-cell sugars are glucosamine, arabinose, mannose and two unknown sugars. The predominant menaquinone is MK-8(H₄). The polar lipids are diphosphatidylglycerol, phosphatidylglycerol, phosphatidylinositol, one unknown phosphoglycerolipid and one unknown phospholipid. The major fatty acids are anteiso-C_{15:0}, iso-C_{15:0} and anteiso-C_{17:0}. The G+C content of DNA is 68–69 mol%. The type species is *Haloactinobacterium album*.

Description of *Haloactinobacterium album* sp. nov.

Haloactinobacterium album (al'bum. L. neut. adj. *album* white).

Exhibits the following properties in addition to those given in the genus description. Colonies are creamy white, circular, smooth, opaque and non-pigmented on GTY agar supplemented with 10% NaCl. Grows at 10–40 °C (optimum 37 °C), at pH 6.0–10.0 (optimum pH 7.0–8.0) and with 2–16% (w/v) NaCl (optimum 7–10% NaCl). Catalase-positive and oxidase-negative. Methyl red and Voges–Proskauer tests are negative. Cellulose and aesculin

are hydrolysed, but gelatin, casein, dextrin, starch, DNA, chitin, urea and Tweens 20, 40, 60 and 80 are not. Reduction of nitrate and production of H₂S, melanin and indole are negative. With API ZYM, positive for esterase (C4), esterase lipase (C8), cystine arylamidase, β -galactosidase, β -glucosidase, α -mannosidase and *N*-acetyl- β -glucosaminidase, but negative for lipase (C14), alkaline phosphatase, leucine arylamidase, valine arylamidase, trypsin, α -chymotrypsin, naphthol-AS-BI-phosphohydrolase, α -fucosidase, α -galactosidase, α -glucosidase and β -glucuronidase. With GP2 MicroPlates, oxidizes L-arabinose, D-fructose, L-fucose, D-galactose, α -D-glucose, maltose, D-mannose, D-psicose, D-ribose, sucrose, D-xylose, methyl β -D-galactoside, pyruvic acid, pyruvic acid methyl ester, DL- α -glycerol phosphate, DL-lactic acid, acetic acid, glycerol and amygdalin. Produces acid from cellobiose, DL-arabinose, D-fructose, L-fucose, D-galactose, D-glucose, maltose, D-mannose, L-rhamnose, D-ribose, D-tagatose, turanose, D-xylose, D-adonitol, erythritol, glycerol, methyl β -D-xylopyranoside, *N*-acetylglucosamine, aesculin and salicin, but not from D-fucose, gentiobiose, lactose, D-lyxose, melezitose, melibiose, raffinose, L-sorbose, starch, sucrose, trehalose, L-xylose, DL-arabitol, dulcitol, inositol, D-mannitol, D-sorbitol, xylitol, amygdalin, arbutin, glycogen, inulin, methyl α -D-mannopyranoside, methyl α -D-glucopyranoside, potassium 5-ketogluconate, potassium 2-ketogluconate or potassium gluconate. The DNA G+C content of the type strain is 68.3 mol%.

The type strain is YIM 93306^T (=DSM 21368^T =KCTC 19413^T =CCTCC AB 208069^T), isolated from a salt lake in Xinjiang province, north-west China.

Acknowledgements

This research was supported by the National Basic Research Program of China (2010CB833800), National Natural Science Foundation of China (30860002, 30870005 and U0932601), Key Project of International Cooperation (2007DFB31620), the 973 Pre-research Program of China (2008CB417214), Yunnan Provincial International Cooperative Program (2009AC017) and the 21C Frontier Program of Microbial Genomics and Applications from the MEST, Korea.

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