Zhihengliuella alba sp. nov., and emended description of the genus *Zhihengliuella*

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A Gram-positive, non-motile, white-pigmented, short rod actinobacterium, designated YIM 90734^T, was isolated from a saline soil sample collected from Ganjiahu Suosuo Forest National Nature Reserve in Xinjiang province, north-west China, and its taxonomic position was investigated by using a polyphasic approach. Strain YIM 90734^T grew optimally at 28–37 °C and pH 6.0–8.0 and in 5 % (w/v) NaCl. The peptidoglycan type was A4 α , L-Lys–L-Ala–L-Glu and tyvelose and mannose were the major cell-wall sugars. The predominant menaquinones were MK-10 and MK-9. Major cellular fatty acids (>10 % of total) were anteiso-C_{15:0} and anteiso-C_{17:0}. The polar lipids were diphosphatidylglycerol, phosphatidylglycerol, phosphatidylinositol, one unknown phospholipid and two unknown glycolipids. The DNA G + C content was 70.3 mol%. Phylogenetic analysis based on 16S rRNA gene sequences showed that strain YIM 90734^T belonged to the genus *Zhihengliuella*. The 16S rRNA gene sequence similarity between strain YIM 90734^T and the type strain of the only recognized *Zhihengliuella* species, *Zhihengliuella halotolerans*, was 97.7 %. However, the level of DNA–DNA relatedness of the two strains was 41.4 %. The DNA–DNA relatedness data and differential phenotypic properties, together with the phylogenetic distinctiveness, demonstrated that strain YIM 90734^T could be differentiated from *Z. halotolerans*. On the basis of the data presented, strain YIM 90734^T is considered to represent a novel species of the genus *Zhihengliuella*, for which the name *Zhihengliuella alba* sp. nov. is proposed. The type strain is YIM 90734^T (=KCTC 19375^T=DSM 21143^T). The description of the genus *Zhihengliuella* has also been emended.

The genus *Zhihengliuella* was first established by Zhang *et al.* (2007) and initially contained only one species, *Zhihengliuella halotolerans* (type strain YIM 70185^T), which was isolated from Qinghai province, north-west China. The genus *Zhihengliuella* is described as comprising a Gram-positive, non-motile, short-rod actinobacterium that was catalase-positive and oxidase-negative. The peptidoglycan type was A4 α , L-Lys–L-Ala–L-Glu. Cell-wall sugars contained tyvelose and glucose. The predominant menaquinones were MK-9 and MK-10 and the major fatty acids

were anteiso-C_{15:0} and iso-C_{15:0}. The major polar lipids were phosphatidylglycerol, diphosphatidylglycerol and phosphatidylinositol. The G + C content of the genomic DNA was about 66.5 mol% (Zhang *et al.*, 2007). In this paper, we describe the characterization and classification of a halotolerant actinobacterium, designated YIM 90734^T, which was isolated from a saline sample collected from Ganjiahu Suosuo Forest National Nature Reserve in Xinjiang province, north-west China and was considered to represent a novel species of the genus *Zhihengliuella*.

Strain YIM 90734^T was isolated from a saline soil sample after 3 weeks incubation at 37 °C on modified ISP 5 medium comprising (1⁻¹ distilled water, final pH 7.5): 1 g L-asparagine, 10 g glycerol, 5 g yeast extract, 1 g K₂HPO₄, 5 g KNO₃, 100 g NaCl and 15 g agar. NaCl was sterilized separately before being added to the medium. The resulting white colony was transferred twice on the same medium to purify the isolate. The strain was maintained on modified ISP 5 agar slants containing 5 % NaCl (w/v) at 4 °C and as

Abbreviations: OPA, *o*-phthalaldehyde; PMP, 1-phenyl-3-methyl-5-pyrazolone.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain YIM 90734^T is EU847536.

Chromatograms of OPA- and PMP-derivatization samples and a table showing the cell-wall sugar compositions of strain YIM 90734^T and *Zhihengliuella halotolerans* Yim 70185^T are available as supplementary material with the online version of this paper.

glycerol suspensions (20 %, v/v) at -20°C . Biomass for chemical and molecular studies was obtained by cultivation in shaken flasks (about 150 r.p.m.) using modified ISP 5 medium [5 % (w/v) NaCl, pH 7.5] at 37°C for 1 week.

Cell morphology was determined for cultures grown for 6, 12, 24 and 48 h on modified ISP 5 agar medium supplemented with 5 % (w/v) NaCl at 37°C . Cell morphology was examined by using transmission electron microscopy with a model H-800 transmission electron microscope (Hitachi). Gram staining was carried out by using the standard Gram reaction and was confirmed by using the KOH lysis test method (Cerny, 1978). Cell motility was confirmed by the presence of turbidity throughout the tube, including semisolid medium (Leifson, 1960). The temperature range for growth was determined by incubating cells for 7 days on modified ISP 5 medium at the following temperatures: 0, 4, 10, 15, 20, 28, 37, 45, 50 and 55°C . For NaCl tolerance experiments, modified ISP 5 medium was used as the basal medium and the following NaCl concentrations (w/v) were used: 0, 1, 3, 5, 10, 15, 20, 25 and 30 %. The pH range for growth was investigated between 4.0–10.0 at intervals of 1 pH unit, using the buffer system: pH 4.0–5.0: 0.1 M citric acid/0.1 M sodium citrate; pH 6.0–8.0: 0.1 M KH_2PO_4 /0.1 M NaOH; and pH 9.0–10.0: 0.1 M NaHCO_3 /0.1 M Na_2CO_3 . Catalase activity was determined by production of bubbles after the addition of a drop of 3 % H_2O_2 . Oxidase activity was determined by using oxidation of tetramethyl-*p*-phenylenediamine. Hydrolysis of casein, starch and Tweens 20, 40 and 80 was determined as described by Cowan & Steel (1965). Enzyme activities and acid production from carbohydrates were determined by using the API ZYM and API 50CHB system (bioMérieux), according to the manufacturer's instructions. Utilization of organic substrates was tested using Biolog GP2 microplates of the Microlog system (Biolog; 95 substrates). Strains were suspended in pre-warmed sterile saline medium (5 % NaCl), within the density range specified by the manufacturer. The API 50CHB, API ZYM and Biolog GP2 tests were performed in duplicate.

Cells of strain YIM 90734^T were Gram-positive, non-motile, short rods and formed white colonies. No spores were observed. Growth occurred at 4 – 45°C , with optimum growth at 28 – 37°C . The optimum NaCl concentration for growth was 5 %. Growth was very slow at pH 5.0 and pH 9.0. The detailed physiological and biochemical properties of strain YIM 90734^T are given in Table 1 and in the species description.

A purified cell-wall preparation was obtained and hydrolysed as described by Schleifer & Kandler (1972). *Z. halotolerans* YIM 70185^T was used as a reference strain for analysis of the cell-wall amino acids and sugars. Amino acids in cell-wall hydrolysates were analysed by using precolumn derivatization with *o*-phthalaldehyde (OPA) by using HPLC (Agilent 1100). Ten amino acid standards (10 μl , 0.2 mM; Sigma) and 10 μl hydrolysed purified cell

wall of strain YIM 90734^T were dissolved in 30 μl 0.1 M borax buffer and 10 μl OPA (Agilent Technologies) was added and allowed to react for 50 s at room temperature. Analysis of the precolumn derivatization of amino acids with OPA was carried out using the Agilent 1100 HPLC system, equipped with an Agilent four-unit pump, a 7125 injector, G1314A UV detector and a column oven (ABI). The analytical column used was a ZORBAX Eclipse-AAA (4.6×150 mm, 3.5 μm ; Agilent). The wavelength used for UV detection was 338 nm. Elution was carried out at a flow rate of 1.0 ml min^{-1} at 40°C . The mobile phase A contained CH_3COONa at 0.05 mol l^{-1} and 0.3 % tetrahydrofuran, and phase B was acetonitrile/methanol (1:1, by vol.), by using gradient elution of 0–50–50 % buffer B with a linear increase from 0 to 25 to 30 min. Cell-wall sugars were detected by using precolumn derivatization with 1-phenyl-3-methyl-5-pyrazolone (PMP) by HPLC (Agilent 1100). Seven monosaccharide standards (80 μl , 1.0 mM; Sigma) or 80 μl hydrolysed purified cell-wall of strain YIM 90734^T and 80 μl 0.25 M methanol solution of PMP and 80 μl 0.2 M NaOH were mixed. Each mixture was allowed to react for 30 min at 70°C , cooled to room temperature and neutralized with 80 μl 0.2 M HCl to pH 7.0, and extracted with isoamyl acetate. After vigorous shaking and centrifugation, the organic phase was carefully discarded to remove the excess reagents. The extraction process was repeated three times, using chloroform instead of isoamyl acetate for the third process; the aqueous layer was then collected and 10 μl was taken for HPLC analysis. The analytical column used was a ZORBAX Eclipse XDB-C18 (4×250 mm, 5 μm ; Agilent). The wavelength used for UV detection was 250 nm. Elution was carried out at a flow rate of 1.0 ml min^{-1} at 40°C for 30 min. Mobile phase A was acetonitrile, and phase B was 0.05 M sodium acetate (KH_2PO_4 -NaOH, pH 6.9), phase A:B=17:83 (v/v). Fatty acids were analysed as described by Sasser (1990) using the Microbial Identification System (MIDI). Menaquinones were extracted and purified as described by Komagata & Suzuki (1987). The purified menaquinones were dissolved in acetone and separated by using HPLC (Kroppenstedt, 1982). Polar lipids were extracted, examined by two-dimensional TLC and identified using published procedures (Minnikin *et al.*, 1984).

Strain YIM 90734^T contained Lys, Ala and Glu by HPLC (see Supplementary Fig. S1, available in IJSEM Online), which is characteristic of the genus *Zhihengliuella* (peptidoglycan type A4 α , L-Lys–L-Ala–L-Glu; Zhang *et al.*, 2007). Major cell wall sugars contained tyvelose and mannose; minor amounts of glucose, galactose and rhamnose were also detected (Supplementary Fig. S2, in IJSEM Online), similar to *Z. halotolerans* YIM 70185^T. Tyvelose was the characteristic sugar of the genus *Zhihengliuella*, but was not found in the genera *Kocuria*, *Nesterenkonia*, *Arthrobacter* and *Micrococcus* of the family *Micrococcaceae* (Zhang *et al.*, 2007). Detailed cell-wall sugars, phospholipids, menaquinones and the cellular fatty acid profile are given in Tables 1 and 2 and in the species description.

Table 1. Differential phenotypic characteristics of strain YIM 90734^T (*Z. alba* sp. nov.) and *Z. halotolerans* YIM 70185^T

Strains: 1, *Z. alba* YIM 90734^T; 2, *Z. halotolerans* YIM 70185^T.

Both strains are Gram-positive, short rods, non-motile, halotolerant, catalase-positive and oxidase-negative actinobacteria. Both strains are positive for esterase (C4), esterase lipase (C8), α -glucosidase, and hydrolysis of aesculin, gelatin and Tweens 40 and 80. Both strains produce acid from erythritol, D-ribose, D-lactose, D-xylose, maltose, D-fructose, amygdalin, starch, L-sorbose, L-rhamnose and D-mannitol, and can utilize the following substrates as sole carbon or nitrogen and energy sources: dextrin, mannan, Tween 40, Tween 80, D-fructose, α -D-glucose, *myo*-inositol, maltose, D-mannose, methyl α -D-glucoside, palatinose, D-arabitol, D-psicose, sucrose, D-tagatose, trehalose, α -ketovaleic acid and thymidine. Both strains are negative for nitrate reduction, H₂S production, methyl red and Voges-Proskauer test, α -galactosidase, β -glucuronidase, *N*-acetyl- β -glucosaminidase, α -mannosidase, α -fucosidase, and hydrolysis of urea, cellulose, casein and chitin. Both strains do not produce acid from D-arabinose, D-galactose, melezitose, D-mannose, dulcitol, cellobiose, methyl α -D-mannopyranoside, methyl α -D-glucopyranoside, *N*-acetylglucosamine, melibiose, trehalose, inulin, D-lyxose, D-tagatose, D-fucose, L-fucose, L-arabitol, potassium gluconate or potassium 2-ketogluconate, and do not utilize the following substrates as sole carbon or nitrogen and energy sources: α -cyclodextrin, glycogen, inulin, *N*-acetyl-D-glucosamine, amygdalin, arbutin, L-fucose, D-galacturonic acid, D-gluconic acid, lactulose, melezitose, methyl α -D-galactoside, 3-methyl-D-glucose, *p*-hydroxy-phenylacetic acid, lactamide, D-lactic acid methyl ester, L-lactic acid, succinic acid, *N*-acetyl-L-glutamic acid, L-alaninamide, L-alanine, glycyl L-glutamic acid, L-pyroglyutamic acid, putrescine and adenosine. +, Positive; –, negative.

Characteristic	1	2*
Pigmentation	White	Pale yellow*
NaCl range for growth (% w/v)	0–15	0–25*
Optimal NaCl concentration (% w/v)	5	10*
pH range for growth	5–9	6–10*
Optimum pH range	6–8	8–9*
Hydrolysis of:		
Starch	–	+
Tween 20	–	+
Utilization of (Biolog GP2):		
β -Cyclodextrin	–	+
<i>N</i> -Acetyl-D-galactosamine	+	–
L-Arabinose	–	+
Cellobiose	+	–
Gentiobiose	–	+
α -D-Lactose	+	–
Maltotriose	–	+
Melibiose	–	+
Methyl β -D-galactoside	–	+
Methyl β -D-glucoside	–	+
Methyl α -D-mannoside	–	+
Salicin	–	+
Sedoheptulosan	–	+
D-Sorbitol	–	+
Stachyose	–	+
Turanose	–	+
Acetic acid	–	+
α -Hydroxybutyric acid	–	+

Table 1. cont.

Characteristic	1	2*
β -Hydroxybutyric acid	–	+
γ -Hydroxybutyric acid	–	+
α -Ketoglutaric acid	–	+
D-Malic acid	–	+
L-Malic acid	–	+
Pyruvic acid methyl ester	–	+
Pyruvic acid	–	+
Succinamic acid	–	+
D-Alanine	–	+
L-Alanyl glycine	–	+
L-Asparagine	+	–
L-Glutamic acid	–	+
L-Serine	+	–
2,3-Butanediol	–	+
2'-Deoxyadenosine	+	–
Inosine	–	+
Uridine	–	+
Thymidine-5'-monophosphate	–	+
Uridine-5'-monophosphate	–	+
D-Fructose 6-phosphate	–	+
α -D-Glucose 1-phosphate	–	+
D-Glucose 6-phosphate	–	+
DL- α -Glycerol phosphate	–	+
Enzymic properties (API ZYM):		
Alkaline phosphatase	–	+
Lipase (C14)	–	+
Leucine arylamidase	+	–
Valine arylamidase	+	–
Cystine arylamidase	+	–
Trypsin	+	–
α -Chymotrypsin	+	–
Acid phosphatase	+	–
Naphthol-AS-BI-phosphohydrolase	+	–
β -Galactosidase	+	–
β -Glucosidase	+	–
Acid production from (API 50CHB):		
L-Arabinose	–	+
Glycerol	–	+
L-Xylose	+	–
D-Adonitol	–	+
D-Sorbitol	–	+
Methyl β -D-xylopyranoside	–	+
D-Glucose	+	–
Inositol	–	+
Arbutin	–	+
Aesculin	–	+
Salicin	–	+
Sucrose	+	–
Raffinose	–	+
Turanose	–	+
Glycogen	–	+
Xylitol	–	+
Gentiobiose	–	+
D-Arabitol	–	+
Potassium 5-ketogluconate	–	+
DNA G + C content (mol%)	70.3	66.5*

*Data for strain *Z. halotolerans* YIM 70185^T were from Zhang *et al.* (2007). Other data were from this study.

Table 2. Cellular fatty acid compositions of strain YIM 90734^T (*Z. alba* sp. nov.) and *Z. halotolerans* YIM 70185^T

Values are percentages of total fatty acids. —, Not detected or <0.1 %. Data for strain *Z. halotolerans* YIM 70185^T were from Zhang *et al.* (2007).

Fatty acid	YIM 90734 ^T	YIM 70185 ^T
Straight-chain		
C _{14:0}	0.9	0.8
C _{15:0}	—	0.2
C _{16:0}	1.3	2.5
C _{18:0}	0.4	—
Branched		
iso-C _{14:0}	0.9	0.8
iso-C _{15:0}	5.4	15.0
anteiso-C _{15:0}	61.3	63.9
anteiso-C _{15:1}	0.5	0.2
iso-C _{16:0}	6.8	7.1
iso-C _{17:0}	0.9	1.0
anteiso-C _{17:0}	15.1	8.5

Extraction of genomic DNA and PCR amplification of the 16S rRNA gene were performed as described by Li *et al.* (2007). The sequence obtained was compared with available 16S rRNA gene sequences from GenBank using the program BLAST to determine an approximate phylogenetic affiliation, and the sequences were aligned with those of closely related species by using the CLUSTAL_X (Thompson *et al.*, 1997) program. Phylogenetic analyses were performed using three tree-making 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 of Saitou & Nei (1987) from K_{nuc} values (Kimura, 1980), using MEGA version 4.0 (Tamura *et al.*, 2007). The topology of the phylogenetic tree was evaluated by using the bootstrap resampling method with 1000 replicates (Felsenstein, 1985).

The almost-complete 16S rRNA gene sequence of strain YIM 90734^T determined in this study comprised 1454 nucleotides. Comparative 16S rRNA gene sequence analysis showed that, phylogenetically, strain YIM 90734^T was related most closely to members of the family *Micrococcineae* (Fig. 1). In the phylogenetic tree based on the neighbour-joining algorithm, strain YIM 90734^T

Fig. 1. Phylogenetic tree based on 16S rRNA gene sequence constructed by using the neighbour-joining method showing the inter-relationships of strain YIM 90734^T and closely related recognized species. Numbers at branch points are bootstrap percentages (1000 resamplings; only values above 50% are shown). The sequence of *Brevibacterium linens* DSM 20425^T (X77451) was used as an outgroup. Bar, 1% sequence divergence.

clustered with the type strain of *Z. halotolerans*. This relationship was supported by all tree-making methods used in this study (data not shown). The 16S rRNA gene sequence similarity between strain YIM 90734^T and *Z. halotolerans* was 97.7 %. Levels of 16S rRNA gene sequence similarity of 96.1–96.6 % were shown between strain YIM 90734^T and the type strains of six recognized *Arthrobacter* species; *Arthrobacter rhombi* (96.6 %), *Arthrobacter pascens* (96.5 %), *Arthrobacter ramosus* (96.5 %), *Arthrobacter oryzae* (96.4 %), *Arthrobacter chlorophenolicus* (96.2 %) and *Arthrobacter phenanthrenivorans* (96.1 %).

The genomic G + C content was determined by using the method of Mesbah *et al.* (1989) with DNA from *Escherichia coli* K-12 as a control. The DNA of strain YIM 90734^T was hydrolysed and the resultant nucleotides were analysed by using reversed-phase HPLC. DNA–DNA hybridization was performed fluorometrically by using the methods of Ezaki *et al.* (1989) and He *et al.* (2005) with photobiotin-labelled DNA probes in microdilution wells. Hybridization was performed with five replications for each sample and the highest and lowest values in each sample were excluded. The DNA–DNA relatedness values were expressed as the mean of the remaining three values. The level of DNA–DNA relatedness between strain YIM 90734^T and *Z. halotolerans* YIM 70185^T was 41.4 %, a value that was well below the 70 % cut-off point recommended for assignment of strains to the same genomic species (Wayne *et al.*, 1987). The genomic G + C content of the DNA of strain YIM 90734^T was 70.3 mol%.

The chemotaxonomic properties of strain YIM 90734^T [A4 α , L-Lys–L-Ala–L-Glu as the peptidoglycan type; tyvelose as the major cell-wall sugar; MK-10 (64.0 %) and MK-9 (32.7 %) as predominant menaquinones; diphosphatidylglycerol, phosphatidylglycerol, phosphatidylinositol, one unknown phospholipid and two unknown glycolipids as the polar lipids] were different from those of members of the genus *Arthrobacter* (A3 α as peptidoglycan type; MK-9(H₂) as predominant menaquinone; no tyvelose in the cell-wall sugar), indicating the affiliation of this new isolate to the genus *Zhihengliuella* (Zhang *et al.*, 2007). The results of the 16S rRNA gene sequence analysis also supported the close affiliation of strain YIM 90734^T with the genus *Zhihengliuella*, which was confirmed by the high bootstrap resampling value (98 %), and formed a monophyletic branch at the periphery of the evolutionary radiation occupied by the genus *Arthrobacter*. Therefore, the chemotaxonomic and phylogenetic results clearly indicate that strain YIM 90734^T belonged to the genus *Zhihengliuella*. However, strain YIM 90734^T could be differentiated from *Z. halotolerans* YIM 70185^T by some morphological, physiological and chemotaxonomic properties (Tables 1 and 2 and Supplementary Table S1), i.e. colonies of strain YIM 90734^T are white, and growth does not occur in 25 % NaCl, whereas colonies of *Z. halotolerans* YIM 70185^T were pale yellow and growth occurred with up to 25 % NaCl. In addition, strain YIM 90734^T and *Z. halotolerans* YIM 70185^T could be differentiated by means

of hydrolysis of starch and Tween 20, acid production from carbohydrates, enzyme properties and utilization of sole carbon or nitrogen energy sources, as shown in Table 1. Furthermore, strain YIM 90734^T exhibited some differences with *Z. halotolerans* YIM 70185^T in their fatty acid compositions. For instance, anteiso-C_{15:0} (61.3 %) and anteiso-C_{17:0} (15.1 %) were the major fatty acids of strain YIM 90734^T, whereas the major fatty acids of *Z. halotolerans* YIM 70185^T were anteiso-C_{15:0} (63.9 %) and iso-C_{15:0} (15.0 %). Therefore, on the basis of the phenotypic and genotypic distinctiveness and levels of DNA–DNA hybridization, strain YIM 90734^T should be placed in the genus *Zhihengliuella* as representing a novel species, for which the name *Zhihengliuella alba* sp. nov. is proposed. As a consequence of the newly reported characteristics, the description of the genus *Zhihengliuella* (Zhang *et al.*, 2007) has been emended.

Emended description of the genus *Zhihengliuella* Zhang *et al.* 2007

The description of the genus is as given previously (Zhang *et al.*, 2007), but with the following amendments. Diagnostic cell-wall sugars are tyvelose and mannose. Major fatty acids are anteiso-C_{15:0} and iso-C_{15:0} or anteiso-C_{15:0} and anteiso-C_{17:0}. The G + C content of the genomic DNA is 66–70.3 mol%.

Description of *Zhihengliuella alba* sp. nov.

Zhihengliuella alba (al'ba. L. fem. adj. *alba* white, referring to the white colour of colonies).

Cells are aerobic, Gram-positive, short rods, 0.5–0.9 × 1.3–1.8 μ m in size, non-motile and without flagella. Colonies are circular, smooth and white on modified ISP 5 medium. Growth occurs in 0–15 % (w/v) NaCl, with good growth at 5 % (w/v) NaCl. Growth occurs at 4–45 °C and pH 5.0–9.0, with optimum growth at 28–37 °C and pH 6.0–8.0. Catalase-positive and oxidase-negative. Negative for milk peptonization, methyl red and Voges–Proskauer tests, H₂S production, nitrate reduction, and hydrolysis of starch, urea, cellulose, casein, chitin and Tween 20. Positive for hydrolysis of aesculin, gelatin, Tween 40 and Tween 80. Enzyme activities (API ZYM) are observed for esterase (C4), esterase lipase (C8), leucine arylamidase, valine arylamidase, cystine arylamidase, trypsin, α -chymotrypsin, acid phosphatase, naphthol-AS-BI-phosphohydrolase, β -galactosidase, α -glucosidase and β -glucosidase. Negative for alkaline phosphatase, lipase (C14), α -galactosidase, β -glucuronidase, *N*-acetyl- β -glucosaminidase, α -mannosidase and α -fucosidase. Acid is produced (API 50CHB) from erythritol, D-ribose, DL-xylose, D-glucose, D-fructose, L-sorbose, L-rhamnose, D-mannitol, amygdalin, maltose, sucrose and starch, but not from glycerol, L-arabinose, D-arabinose, D-adonitol, methyl β -D-xylopyranoside, D-galactose, D-mannose, dulcitol, inositol, D-sorbitol, methyl α -D-mannopyranoside, methyl α -D-glucopyranoside, *N*-acetylglucosamine, turanose, arbutin, aesculin, cellobiose,

salicin, D-lactose, melibiose, trehalose, inulin, melezitose, raffinose, glycogen, xylitol, gentiobiose, D-lyxose, D-tagatose, DL-fucose, DL-arabitol, potassium gluconate, potassium 2-ketogluconate and potassium 5-ketogluconate. The following substrates are utilized as sole carbon or nitrogen and energy sources (Biolog GP2): dextrin, mannan, Tweens 40 and 80, N-acetyl-D-galactosamine, D-arabitol, cellobiose, D-fructose, D-galactose, α -D-glucose, myo-inositol, α -D-lactose, maltose, D-mannitol, D-mannose, methyl α -D-glucoside, palatinose, D-psicose, raffinose, L-rhamnose, D-ribose, sucrose, D-tagatose, trehalose, xylitol, D-xyllose, α -ketovaleric acid, succinic acid monomethyl ester, propionic acid, pyruvic acid, L-asparagine, L-serine, glycerol, 2'-deoxyadenosine and thymidine. The following substrates are not utilized: α -cyclodextrin, β -cyclodextrin, starch, inulin, N-acetyl-D-glucosamine, amygdalin, L-arabinose, arbutin, L-fucose, D-galacturonic acid, gentiobiose, D-gluconic acid, lactulose, melezitose, melibiose, methyl α -D-galactoside, methyl β -D-galactoside, 3-methyl-D-glucose, methyl β -D-glucoside, methyl α -D-mannoside, salicin, sedoheptulosan, D-sorbitol, stachyose, turanose, acetic acid, α -hydroxybutyric acid, β -hydroxybutyric acid, γ -hydroxybutyric acid, ρ -hydroxyphenylacetic acid, α -ketoglutaric acid, lactamide, D-lactic acid methyl ester, L-lactic acid, D-malic acid, L-malic acid, pyruvic acid methyl ester, pyruvic acid, succinamic acid, succinic acid, N-acetyl-L-glutamic acid, L-alaninamide, DL-alanine, L-alanyl glycine, L-glutamic acid, glycyl L-glutamic acid, L-pyrroglutamic acid, putrescine, 2,3-butanediol, adenosine, inosine, uridine, adenosine-5'-monophosphate, thymidine-5'-monophosphate, uridine-5'-monophosphate, D-fructose 6-phosphate, α -D-glucose 1-phosphate, D-glucose 6-phosphate and DL- α -glycerol phosphate. Peptidoglycan type is A4 α , L-Lys-L-Ala-L-Glu. Major cell sugars contain tyvelose and mannose; minor amounts of glucose, rhamnose and galactose are also detected. Predominant menaquinones are MK-10 (64.0%) and MK-9 (32.7%); a minor amount of MK-8 (3.3%) is also detected. Polar lipids are diphosphatidylglycerol, phosphatidylglycerol, phosphatidylinositol, an unknown phospholipid and two unknown glycolipids. Major cellular fatty acids are anteiso-C_{15:0} and anteiso-C_{17:0}; minor amounts of C_{14:0}, iso-C_{14:0}, iso-C_{15:0}, anteiso-C_{15:1}, C_{16:0}, iso-C_{16:0}, iso-C_{17:0} and C_{18:0} are also detected. The DNA G+C content of the type strain is 70.3 mol%.

The type strain, YIM 90734^T (=KCTC 19375^T=DSM 21143^T), was isolated from a saline soil sample collected from Ganjiahu Suosuo Forest National Nature Reserve in Xinjiang province, north-west China.

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