

# *Aquibacillus salifodinae* sp. nov., a novel bacterium isolated from a salt mine in Xinjiang province, China

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**Abstract** A Gram-positive, rod-shaped, strictly aerobic bacterium, strain WSY08-1<sup>T</sup>, was isolated from a salt mine in Wensu county, Xinjiang province, China. Spherical to ellipsoidal endospores were observed to be formed in terminal swollen sporangia. Strain WSY08-1<sup>T</sup> was found to be able to grow at 20–45 °C (optimum 37 °C), 0–10 % (w/v) NaCl (optimum 4 %, w/v) and pH 6.0–9.0 (optimum 7.0). Catalase and oxidase activities were observed to be positive. The cell-wall peptidoglycan of strain WSY08-1<sup>T</sup> was found to contain *meso*-diaminopimelic acid. Menaquinone-7 (MK-7) was identified as the predominant isoprenoid quinone. The polar lipids were found to consist of phosphatidylglycerol, diphosphatidylglycerol, an unknown glycolipid, two unknown phospholipids and an unknown lipid. The major cellular fatty acids were identified as anteiso-C<sub>15:0</sub> and anteiso-C<sub>17:0</sub>. The DNA G+C content was determined to be 36.9 mol%. Analysis of the 16S

rRNA gene sequence showed that strain WSY08-1<sup>T</sup> is closely related to *Aquibacillus halophilus* B6B<sup>T</sup>, *Aquibacillus koreensis* BH30097<sup>T</sup> and *Aquibacillus albus* YIM 93642<sup>T</sup> (97.6, 96.9 and 96.5 % similarity, respectively). The level of DNA–DNA relatedness between strains WSY08-1<sup>T</sup> and *A. halophilus* B6B<sup>T</sup> was 31.4 %. On the basis of its phenotypic, chemotaxonomic and genotypic characteristics, strain WSY08-1<sup>T</sup> is considered to represent a novel species in the genus *Aquibacillus*, for which the name *Aquibacillus salifodinae* sp. nov. is proposed. The type strain is WSY08-1<sup>T</sup> (=JCM 19761<sup>T</sup> = CGMCC 1.12849<sup>T</sup>).

**Keywords** *Aquibacillus salifodinae* sp. nov. · Polyphasic taxonomy · 16S rRNA gene · Salt mine

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## Introduction

The genus *Aquibacillus* was proposed by Amoozegar et al. (2014) with the description of *Aquibacillus halophilus* as well as the transfer of *Virgibacillus koreensis* to *Aquibacillus koreensis* and *Virgibacillus albus* to *Aquibacillus albus*. Therefore, at the time writing, this genus, belonging to the family *Bacillaceae*, comprises three species with validly published names and the type species is *A. halophilus*. The type strains of all three species were isolated from saline environments. Members of the genus *Aquibacillus* are

Gram-stain positive, rod-shaped, motile, produce endospores, moderately halophilic, catalase- and oxidase-positive. Chemotaxonomically they are characterized by having MK-7 as the predominant respiratory quinone, phosphatidylglycerol and diphosphatidylglycerol as the major polar lipids, anteiso-C<sub>15:0</sub> as the major fatty acid and *meso*-diaminopimelic acid (*meso*-DAP) as the diagnostic diamino acid in the peptidoglycan. The DNA G+C content of members of this genus ranges from 35.8–41.0 mol%.

During our surveys on bacterial diversity of a salt mine in Wensu county, Akesu area in Xinjiang province of China, a bacterial strain named WSY08-1<sup>T</sup> was obtained. By using a polyphasic taxonomic approach, we conclude that strain WSY08-1<sup>T</sup> represents a novel species of the genus *Aquibacillus*, for which the name *Aquibacillus salifodinae* sp. nov. is proposed.

## Materials and methods

### Bacterial strains and culture condition

Strain WSY08-1<sup>T</sup> was isolated from a salt mine sample (salt crystal, 41°34'52"N, 80°43'37"E) in Xinjiang province, China. Marine broth 2216 (MB, Difco) was used for isolation. The medium was solidified with 2.0 % agar (MA). To enrich bacteria about 3 g salt sample was suspended in 30 ml MB at 28 °C for 2 days. The enrichment culture was diluted and spread onto MA plates which were incubated at 28 °C. After 3 days of incubation, one of the aerobic isolates, strain WSY08-1<sup>T</sup>, was observed to produce cream-pigmented, circular and elevated colonies on MA plates. One of these colonies was picked up and purified by repeated restreaking. The isolate was routinely cultured on MA plates and maintained at –80 °C with 25 % (v/v) glycerol.

Biomass for chemotaxonomic and molecular studies was obtained by cultivation in shaking flasks with MB at 28 °C for 2 days. The recommended Minimal Standards for describing new taxa of aerobic, endospore-forming bacteria were followed (Logan et al. 2009). The reference type strain *A. halophilus* B6B<sup>T</sup> were obtained from Korean Collection for Type Cultures (KCTC; Korea); *A. koreensis* JCM 12387<sup>T</sup> and *A. albus* JCM 17364<sup>T</sup> were obtained from the Japan Collection of Microorganisms (JCM; Japan).

Reference type strains were cultured under the same conditions as strain WSY08-1<sup>T</sup> for comparative analyses.

### Morphological, physiological and biochemical characterization

Cell morphology was determined by optical microscopy (BX40; Olympus) and transmission electron microscopy (JEM-1230; JEOL) (Huo et al. 2010). Motility was detected by optical microscopy using the hanging drop technique (Skerman 1967). Gram staining was performed by following the method outlined by Dussault (1955). To determine the growth conditions of strain WSY08-1<sup>T</sup>, MB-1 medium with various NaCl concentrations (0–15 %, at intervals of 1 %, w/v) was used. MB-1 medium contained (per 1 distilled water): peptone (Becton–Dickinson) 5.0 g, yeast extract (Becton–Dickinson) 1.0 g, Ferric citrate 0.1 g, MgCl<sub>2</sub>·6H<sub>2</sub>O 12.6 g, MgSO<sub>4</sub>·7H<sub>2</sub>O 6.64 g, CaCl<sub>2</sub> 1.8 g, KCl 0.55 g, KBr 0.08 g, SrCl 34.0 mg, Boric acid 22.0 mg and NH<sub>4</sub>NO<sub>3</sub> 2.4 mg. The ranges of pH and temperature for growth were determined by using MB medium according to Zhang et al. (2013).

Catalase and oxidase activities and nitrate and nitrite reduction were tested according to (Dong and Cai 2001). Indole, methyl red and Voges-Proskauer tests, H<sub>2</sub>S production, as well as hydrolysis of aesculin, casein, gelatin and starch were performed as described by Zhu (2011). Esterase activity was detected as outlined by (Gutiérrez and González 1972). To analyze the use of accessory electron acceptors, sodium thiosulfate (20 mM), sodium sulfate (20 mM), sodium sulfite (5 mM), sodium nitrite (5 mM) and sodium nitrate (20 mM) were respectively added to sterile MB. Oxygen was removed as described by Grishchenkov et al. (2000). The same medium lacking L-cysteine and resazurin was used as aerobic control. Other enzyme activities and physiological properties were determined by using API ZYM, API 20E and API 20NE kits, using distilled water supplemented with 4 % (w/v) NaCl to suspend the cells. Acid production tests were carried out by using API 50CH kits, using modified MB from which yeast extract and peptone were omitted and 0.05 g/L yeast extract was added. Utilization of single carbon sources for growth was performed using Biolog GP2 96-well Microplates (Biolog) by using the modified MB. All API tests were performed according to the

**Table 1** Differential characteristics among strains WSY08-1<sup>T</sup>, *A. albus* YIM 93642<sup>T</sup>, *A. koreensis* BH30097<sup>T</sup> and *A. halophilus* B6B<sup>T</sup>

Characteristic	1	2	3	4
Spore shape	E or S	E or S <sup>a</sup>	E <sup>k</sup>	E
sporangia	Swollen	Swollen <sup>a</sup>	Swollen <sup>k</sup>	non-Swollen
Cell size (µm)	0.4–0.6 × 5.0–8.1	0.3–0.5 × 2.0–6.0 <sup>a</sup>	0.5–0.7 × 2.0–7.0 <sup>k</sup>	0.3–0.5 × 4.0–6.0
Anaerobic growth	–	–	+	–
Temperature range (optimum) (°C)	20–45 (37)	15–45 (25–30) <sup>a</sup>	10–45 (25) <sup>k</sup>	20–40 (35)
pH range (optimum)	6.0–9.0 (7.0)	4.0–9.0 (7.0) <sup>a</sup>	5.0–9.0 (7.0) <sup>k</sup>	6.5–9.0 (7.0)
NaCl range (optimum) (% w/v)	0–10 (4)	1–17 (5–10) <sup>a</sup>	1–20 (5–10) <sup>k</sup>	0.5–20 (10)
Nitrate reduction	+	+	–	–
Voges-Proskauer	–	+	–	–
Hydrolysis of				
Starch	–	+	–	–
Tween 80	+	+	–	–
Acid production from				
D-galactose	–	–	–	+
D-glucose	+	–	w	+
Glycerol	w	+	–	–
Lactose	–	+	–	+
D-mannitol	–	+	–	+
D-mannose	+	–	–	–
D-melibiose	–	+	–	–
Starch	–	+	–	–
D-trehalose	+	+	w	–
D-xylose	+	–	+	+
DNA G+C content (mol%)	36.9	37.5	41.0	35.8
Polar lipids	PG, DPG, GL, PLs, L	PG, DPG, GL	PG, DPG, PL, GL	PG, DPG, GL, PL

*Taxa 1* strain WSY08-1<sup>T</sup>, 2 *A. albus* YIM 93642<sup>T</sup>, 3 *A. koreensis* BH30097<sup>T</sup>, 4 *A. halophilus* B6B<sup>T</sup>. Data of strains WSY08-1<sup>T</sup>, *A. albus* YIM 93642<sup>T</sup> and *A. koreensis* BH30097<sup>T</sup> are from this study unless otherwise indicated. Data of strain *A. halophilus* B6B<sup>T</sup> were taken from Amoozegar et al. (2014)

<sup>a, k</sup> For strains *A. albus* YIM 93642<sup>T</sup> and *A. koreensis* BH30097<sup>T</sup> were taken from Zhang et al. (2012) and Lee et al. (2006), respectively

– Negative, + positive, w weakly positive, E ellipsoidal, S, spherical, R resistant, Su susceptible

manufacturer’s instructions (bioMérieux). Antibiotic sensitivity tests were determined on MA plates with antibiotic discs containing the following amount (µg per disc, unless indicated): amikacin (30), ampicillin (10), bacitracin (0.04 IU), chloramphenicol (30), ciprofloxacin (5), erythromycin (15), gentamicin (10), kanamycin (30), neomycin (30), norfloxacin (10), novobiocin (30), nystatin (100), penicillin G (10 IU), polymyxin (300 IU), rifampicin (5), streptomycin (10), sulfamethoxazole (300), tobramycin (10) and vancomycin (30).

### Chemotaxonomic characterization

For chemotaxonomic experiments, late exponential phase cells of strains WSY08-1<sup>T</sup>, *A. koreensis* JCM 12387<sup>T</sup> and *A. albus* JCM 17364<sup>T</sup> were harvested from MB. The isomer type of the diamino acid in the cell-wall peptidoglycan and isoprenoid quinones were determined as described by Komagata and Suzuki (1987). Polar lipids of strain WSY08-1<sup>T</sup> and reference strains were extracted and separated on silica gel 60 F<sub>254</sub> aluminium-backed thin-layer plates

**Table 2** Cellular fatty acids for strain WSY08-1<sup>T</sup> together with type strains of related species

Fatty acid	1	2	3	4
Saturated fatty acids				
C <sub>14:0</sub>	tr	tr	1.8	1.0
C <sub>15:0</sub>	tr	1.2	3.0	–
C <sub>16:0</sub>	1.1	6.0	3.6	2.8
Branched fatty acids				
iso-C <sub>14:0</sub>	3.1	5.1	12.5	3.4
iso-C <sub>15:0</sub>	4.1	4.8	3.1	5.3
anteiso-C <sub>15:0</sub>	72.7	56.2	46.9	75.1
iso-C <sub>16:0</sub>	3.3	13.5	17.5	4.2
anteiso-C <sub>17:0</sub>	10.0	9.3	5.8	4.4
Unsaturated fatty acids				
C <sub>16:1</sub> ω7c alcohol	1.9	tr	2.7	–
Summed feature 4 <sup>a</sup>	1.4	–	tr	–

<sup>a</sup> Summed feature 4 contained iso-C<sub>17:1</sub> I and/or anteiso-C<sub>17:1</sub> B (as defined by MIDI)

*Taxa* 1 strain WSY08-1<sup>T</sup>, 2 *A. albus* YIM 93642<sup>T</sup>, 3 *A. korensis* BH30097<sup>T</sup>, 4 *A. halophilus* B6B<sup>T</sup>. Values are percentages of the total fatty acid content. *tr*, trace component (<1 %); –, not detected. All data were obtained in this study under the same experimental conditions except data for strain *A. halophilus* B6B<sup>T</sup> which were taken from Amoozegar et al. (2014)

(10 × 10 cm, Merk 5554) and further analyzed as described by Minnikin et al. (1984). Fatty acid methyl esters were obtained from freeze-dried cells as described by Kuykendall et al. (1988) and their identification and quantification were performed using the Sherlock Microbial Identification System (MIDI) with the standard MIS Library Generation Software version 4.5 (Microbial ID).

### Molecular studies

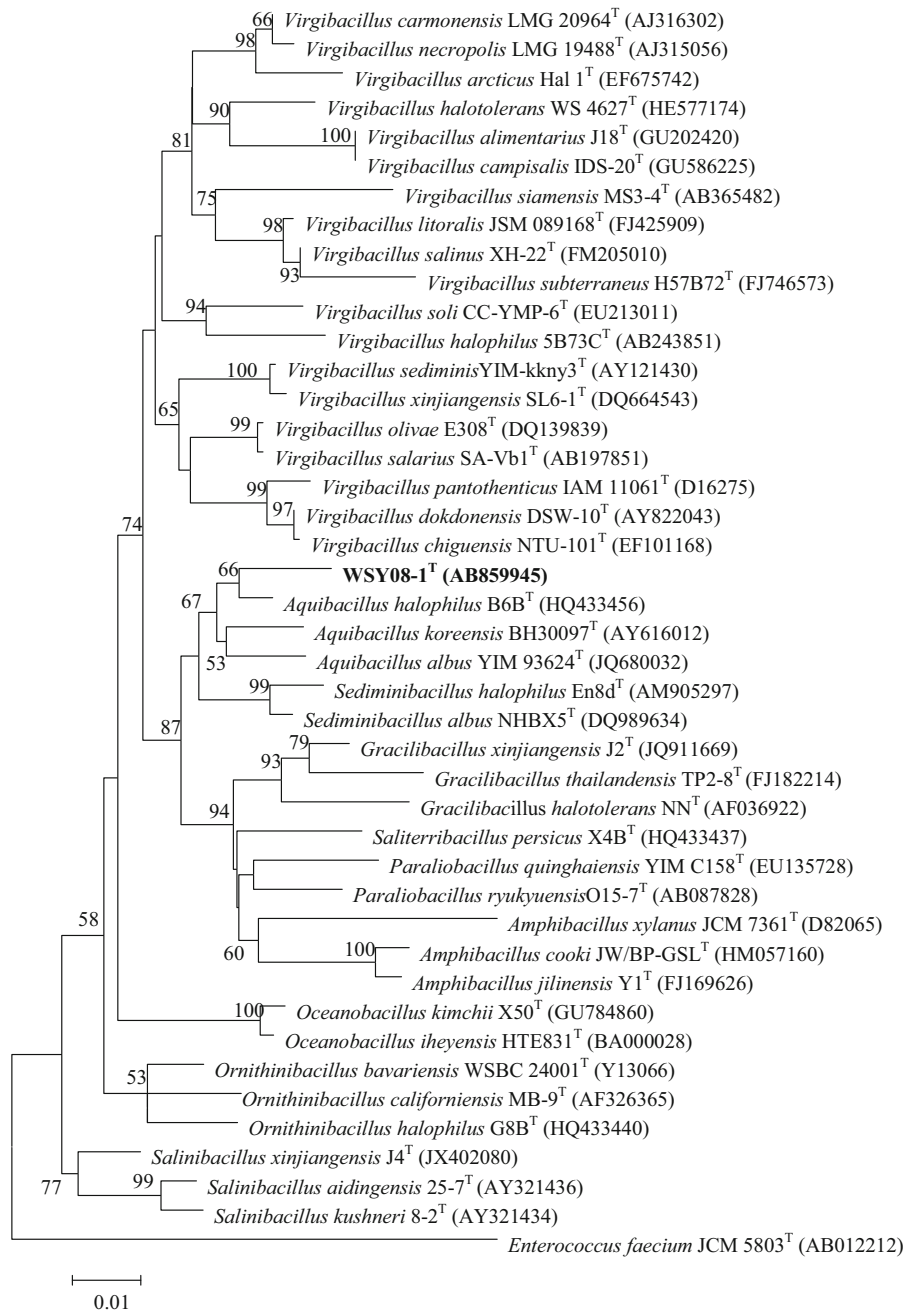
The 16S rRNA gene was amplified and analyzed as described previously (Xu et al. 2007). PCR products were cloned into vector pMD19-T (TaKaRa) and then sequenced. The sequence was compared with closely related sequences of reference species using the EzTaxon-e server (Kim et al. 2012) and BLAST (<http://www.ncbi.nlm.nih.gov/BLAST/>). Multiple sequences were aligned with CLUSTAL W1.8 (Thompson et al. 1994). Phylogenetic trees were constructed by the neighbour-joining (Saitou and Nei 1987), the maximum-parsimony (Fitch 1971) and the maximum-likelihood (Felsenstein 1981) methods within the MEGA 5 program package (Tamura et al. 2011). Evolutionary distances were calculated according to the algorithm of Kimura's two-parameter model (Kimura 1980) for the neighbour-joining method.

The DNA G+C content was determined by reversed-phase HPLC as described by Mesbah and Whitman (1989). DNA–DNA hybridizations were performed by using the thermal denaturation and renaturation method (De Ley et al. 1970) as modified by Huß et al. (1983), using a Beckman DU 800 Spectrophotometer. The experiments were carried out in quadruplicate.

### Results and conclusion

#### Morphological, physiological and biochemical characteristics

Colonies of strain WSY08-1<sup>T</sup> on MA plates after 2 days incubation were observed to be 0.1–0.3 mm in diameter, cream-pigmented, circular and elevated. Strain WSY08-1<sup>T</sup> was found to be strictly aerobic. Cells were observed to be Gram-stain positive, rod-shaped (0.4–0.6 × 5.0–8.1 μm), motile by means of peritrichous flagella and endospore-forming. Spherical to ellipsoidal endospores were observed to be formed terminal in swollen sporangia (Fig. S1). The physiological and biochemical characteristics of strain WSY08-1<sup>T</sup> that differentiate it from the reference strains are shown in Table 1. The detailed physiological and biochemical characteristics of the type strain WSY08-1<sup>T</sup> are given in the species description.



**Fig. 1** Maximum-likelihood phylogenetic tree based on 16S rRNA gene sequences showed the relationships of strain WSY08-1<sup>T</sup> and related species. Bootstrap values based on 1,000 replications are listed as percentages at branching points.

Bootstrap values higher than 50 % are indicated at branch-points. *Enterococcus faecium* JCM 5803<sup>T</sup> was used as outgroup. Bar 1 % sequence divergence

The type strain was found to be sensitive to ampicillin, bacitracin, chloramphenicol, ciprofloxacin, erythromycin, gentamicin, kanamycin neomycin,

norfloxacin, novobiocin, penicillin G, rifampicin, sulfamethoxazole, tobramycin and vancomycin; and resistant to amikacin, nystatin, polymyxin and streptomycin.

## Chemotaxonomy results

The cell wall peptidoglycan of strain WSY08-1<sup>T</sup> was found to contain *meso*-diaminopimelic acid as the diamino-acid. The isoprenoid quinones were identified as MK-7 (94 %) and MK-6 (6 %). The polar lipids were found to include phosphatidylglycerol, diphosphatidylglycerol, an unknown glycolipid, two unknown phospholipids and an unknown lipid (Fig. S2). The major fatty acids were identified as anteiso-C<sub>15:0</sub> (72.7 %) and anteiso-C<sub>17:0</sub> (10.0 %). The complete fatty acid profiles of strain WSY08-1<sup>T</sup> and the reference type strains are summarized in Table 2.

## Molecular characterization

The nearly complete 16S rRNA gene sequence (1,528 bp) of strain WSY08-1<sup>T</sup> was determined (GenBank accession number AB859945). Based on 16S rRNA gene sequence analysis, the validly named species that shared highest sequence similarities to strain WSY08-1<sup>T</sup> were identified as *A. halophilus* B6B<sup>T</sup> (97.6 %), followed by *A. koreensis* BH30097<sup>T</sup> (96.9 %), *A. albus* YIM 93624<sup>T</sup> (96.5 %), *Sediminibacillus halophilus* En8d<sup>T</sup> (96.4 %) and *Virgibacillus carmonensis* JCM 16508<sup>T</sup> (96.0 %). Type strains of other species shared lower sequence similarities (<96 %) to strain WSY08-1<sup>T</sup>. Phylogenetic trees revealed that strain WSY08-1<sup>T</sup> clustered with *A. halophilus* B6B<sup>T</sup>, *A. koreensis* BH30097<sup>T</sup> and *A. albus* YIM 93624<sup>T</sup> in a separate clade (Fig. 1; Fig. S3 and Fig. S4). DNA–DNA hybridization between strains WSY08-1<sup>T</sup> and *A. halophilus* B6B<sup>T</sup> showed a low relatedness value of 31.4 %.

The genomic G+C content of strain WSY08-1<sup>T</sup> was determined to be 36.9 mol%, which is in the range for the members of the genus *Aquibacillus*.

## Taxonomic conclusion

Based on its characterisation as Gram-positive, rod-shaped, endospore-forming, moderately halophilic cells; positive for catalase and oxidase activities; the major fatty acid (anteiso-C<sub>15:0</sub>); the major polar lipids (phosphatidylglycerol and diphosphatidylglycerol); the predominant menaquinone (MK-7); the cell-wall peptidoglycan diamino acid (*meso*-diaminopimelic acid); the G+C content (36.9 mol%); and the phylogenetic analyses, all these data suggest that strain

WSY08-1<sup>T</sup> should belong to the genus *Aquibacillus*. However, strain WSY08-1<sup>T</sup> showed notable differences in comparison to the type strains of the most closely related species *A. halophilus* B6B<sup>T</sup>, *A. koreensis* BH30097<sup>T</sup> and *A. albus* YIM 93642<sup>T</sup> with regard to morphological characteristics, growth ranges (temperature, pH and NaCl tolerance), nitrate reduction, Voges–Proskauer, hydrolysis of starch and Tween 80, and acid production from carbohydrates (Table 1). The cellular fatty acid profile of strain WSY08-1<sup>T</sup> was qualitatively similar to that of the reference strains but differences in the proportions of some fatty acids were noted (Table 2). Differences in the polar lipid profile also existed compared to the reference strains (Fig. S4). Strain WSY08-1<sup>T</sup> shared low 16S rRNA gene sequence similarities to the type strains *A. halophilus* B6B<sup>T</sup>, *A. koreensis* BH30097<sup>T</sup> and *A. albus* YIM 93624<sup>T</sup> (97.6, 96.9 and 96.5 %, respectively). DNA–DNA hybridization data (31.4 %) clearly differentiated strain WSY08-1<sup>T</sup> from strain *A. halophilus* B6B<sup>T</sup>.

Based on the phenotypic, chemotaxonomic and genotypic characteristics described above, strain WSY08-1<sup>T</sup> was identified as a novel species within the genus *Aquibacillus*, for which the name *Aquibacillus salifodinae* sp. nov. is proposed.

## Description of *Aquibacillus salifodinae* sp. nov.

*Aquibacillus salifodinae* (sa.li.fo.di'nae. L. n. *sal*, salt; L. n. *fodina*, a pit; N.L. gen. n. *salifodinae* of a saltpit, salt mine).

Cells are Gram-positive, strictly aerobic, motile by means of peritrichous flagella and rod-shaped (0.4–0.6 × 5.0–8.1 μm). Spherical to ellipsoidal endospores are formed in terminal swollen sporangia. Colonies are 0.1–0.3 mm in diameter, cream-pigmented, circular and elevated. Growth occurs at 20–45 °C (optimum 37 °C), 0–10 % (w/v) NaCl (optimum 4 %, w/v) and pH 6.0–9.0 (optimum 7.0). Catalase and oxidase activities are positive. Nitrate is reduced to nitrite but not to nitrogen. Indole, methyl red, Voges–Proskauer, H<sub>2</sub>S production, hydrolysis of starch, casein and gelatin, as well as the production of arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase and urease are negative. Clearly positive in the Biolog GP2 MicroPlate system for the oxidation of acetic acid, *N*-acetylglucosamine,

*N*-acetyl-L-glutamic acid, adenosine-5'-monophosphate, L-alaninamide, L-alanyl-glycine, amygdalin, L-asparagine, L-arabinose, arbutin, D-cellobiose,  $\alpha$ -cyclodextrin, 2'-deoxy adenosine, L-fructose, D-fructose, D-fructose-6-phosphate, D-galactose, gentiobiose, D-gluconic acid, D-glucose,  $\alpha$ -D-glucose-1-phosphate, D-glucose-6-phosphate, L-glutamic acid, D-L- $\alpha$ -glycerol phosphate, glycyl-L-glutamic acid, glycerol, glycogen,  $\gamma$ -hydroxybutyric acid, m-inositol, inosine, inulin,  $\alpha$ -ketoglutaric acid,  $\alpha$ -ketovaleric acid, lactamide,  $\alpha$ -D-lactose, lactulose, D-malic acid, L-malic acid, maltose, mannan, D-mannose, D-melezitose, D-melibiose,  $\alpha$ -methyl-D-galactoside,  $\beta$ -methyl-D-galactoside, 3-methyl-glucose,  $\alpha$ -methyl-D-glucoside,  $\alpha$ -methyl-D-mannoside, palatinose, propionic acid, D-psicose, pyruvic acid, L-pyroglutamic acid, D-raffinose, L-rhamnose, D-ribose, salicin, sedoheptulosan, D-sorbitol, succinamic acid, succinic acid, succinic acid mono-methyl ester, sucrose, D-tagatose, thymidine, thymidine-5'-monophosphate, trehalose, Tween 40 and 80, uridine-5'-monophosphate, xylitol and D-xylose. Other substrates in the GP2 MicroPlate are not utilized as sole carbon source. According to the API 50 CH system, positive for acid production from *N*-acetylglucosamine, D-adonitol, aesculin, amygdalin, L-arabinose, L-arabitol, arbutin, cellobiose, D-fructose, gentiobiose, D-glucose, 2-ketogluconate, 5-ketogluconate, D-lyxose, maltose, D-mannose,  $\beta$ -methyl-D-xylopyranoside, D-ribose, salicin, sucrose, trehalose and D-xylose; Weakly positive of glycerol, L-sorbose, D-tagatose and xylitol; other substrates of the API 50 CH system are not converted to acid. With API ZYM systems, alkaline phosphatase, esterase (C4), esterase lipase (C8),  $\beta$ -glucosidase,  $\beta$ -glucuronidase, naphthol-AS-BI-phosphohydrolase are positive; acid phosphohydrolase is weakly positive; lipase (C14), leucine arylamidase, valine arylamidase, cysteine arylamidase, trypsin,  $\alpha$ -chymotrypsin,  $\alpha$ -galactosidase,  $\beta$ -galactosidase,  $\alpha$ -glucosidase. *N*-acetyl- $\beta$ -glucosaminidase,  $\alpha$ -mannosidase and  $\alpha$ -fucosidase are negative. The cell-wall peptidoglycan contains *meso*-diaminopimelic acid as the diamino-acid. MK-7 is the predominant menaquinone and MK-6 is also present. The polar lipids are phosphatidylglycerol, diphosphatidylglycerol, an unknown glycolipid, two unknown phospholipids and an unknown lipid. The major fatty acids are anteiso-C<sub>15:0</sub> and anteiso-C<sub>17:0</sub>. The DNA G+C content of the type strain is 36.9 mol% (as determined by HPLC).

The type strain WSY08-1<sup>T</sup> (= JCM 19761<sup>T</sup> - = CGMCC 1.12849<sup>T</sup>) was isolated from a salt mine taken from Wensu county, Xinjiang province, China. The GenBank accession number of the 16S rRNA gene sequence of the type strain is AB859945.

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