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Halomonas qijiaojingensis sp. nov. and *Halomonas flava* sp. nov., two moderately halophilic bacteria isolated from a salt lake

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Abstract Two moderately halophilic, Gram-negative, rod-shaped bacteria, designated YIM 93003^T and YIM 94343^T, were isolated from a salt lake in Xinjiang province, north-west China. The two strains YIM 93003^T and YIM 94343^T grew at 20–40°C, pH 6–9, 0.5–24% (w/v) NaCl and at 20–40°C, pH 6–9, 0.5–23% (w/v) NaCl, respectively. No growth occurred in absence of NaCl. Phylogenetic analyses based on 16S rRNA gene sequences showed that strains YIM 93003^T and YIM 94343^T were phylogenetically affiliated to the genus *Halomonas* and exhibited sequence similarity of 97.5% and 97.4% to the type strain *Halomonas anticariensis* DSM 16096^T, respectively. The strains possessed chemotaxonomic markers that were consistent with their classification in the genus *Halomonas* (Q-9 as predominant respiratory quinine; C18:1ω7*c*, C16:0 and C16:1 ω7*c*/iso-C15:02-OH as the major fatty acids). The DNA–DNA hybridization values for strains YIM 93003^T and YIM 94343^T, YIM 93003^T and DSM 16096^T, YIM 94343^T and DSM 16096^T were 38.1 ± 3.0, 18.3 ± 4.7, and 20.8 ± 4.6%, respectively. The G+C contents of the strains YIM 93003^T and YIM 94343^T were 63.4 and 64.0 mol%, respectively. Based on comparative analysis of physiological, biochemical and chemotaxonomic data, including low DNA–DNA hybridization results, two novel species, *Halomonas qijiaojingensis* sp. nov., and *Halomonas flava* sp. nov.,

Chao Chen, Rong Shi, and Bing-Bing Liu contributed equally to this work.

The GenBank accession numbers of 16S rRNA gene sequences of strains YIM 93003^T and YIM 94343^T are HQ832735 and HQ832736, respectively.

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are proposed. The type strains are YIM 93003^T (=CCTCC AB 208133^T =KCTC 22228^T) and YIM 94343^T (=CCTCC AB 2010382^T =KCTC 23356^T), respectively.

Keywords *Halomonas qijiaojingensis* sp. nov · *Halomonas flava* sp. nov · Polyphasic taxonomy · 16S rRNA gene

Introduction

Micro-organisms requiring salt for growth, the halophiles, are found among all the domains of life, the Archaea, Eucarya, and Bacteria (Oren 2002). The different branches of the phylum Proteobacteria have various halophilic representatives with close relatives that are non-halophilic (Oren 2002). Among the bacterial families that form part of the class *Gammaproteobacteria*, the family *Halomonadaceae* is mainly represented by halophilic and halotolerant species belonging to different genera. The genus *Halomonas* was first established by Vreeland et al. (1980) and the members are mainly represented by halophilic and halotolerant species. The aim of this study was to determine the exact taxonomic position of the halophilic strains YIM 93003^T and YIM 94343^T using phenotypic, phylogenetic and genomic characteristics, from which they were finally determined as two new species belonging to the genus *Halomonas*.

Materials and methods

Strains and culture conditions

The samples used in this study were shore sediments obtained from Qijiaojing Lake, which is a salt lake in Xinjiang province, north-west China (43°23′01″ N 91°36′11″ E). Two strains, YIM 93003^T and YIM 94343^T were isolated by using the dilution-plating technique on Glucose–Tryptone–Yeast (GTY) medium (contained 10% NaCl) described by Tang et al. (2010) and incubated at 37°C for 1 week. Colonies were picked and repeatedly re-streaked onto tryptic soy agar (TSA, BD) medium containing 5% NaCl, until purity was confirmed. Strains YIM 93003^T and YIM 94343^T were maintained on TSA slants containing 5% NaCl at 4°C and in 10% (v/v) glycerol suspensions at −80°C. Strain YIM 93003^T was deposited in the Collection Center of Typical Cultures, China (CCTCC) as strain CCTCC AB 208133^T and in the Korean Collection for Type Cultures (KCTC) as strain KCTC 22228^T. Strain YIM 94343^T was deposited in the CCTCC as strain CCTCC AB 2010382^T and in the KCTC as strain KCTC 23356^T. Biomass for chemical and molecular studies was obtained by cultivation in shake flasks (about 200 r.p.m) using tryptic soy broth (TSB, BD) containing 5% NaCl at 37°C for about 3 days.

Phenotypic characterization

Gram staining was carried out using the standard Gram reaction combined with the KOH lysis test (Cerny 1978). Colony morphology was observed on TSA medium containing 5% NaCl (pH 7.5) after incubation at 37°C for 6, 12, 24, 48, and 72 h and cellular morphology was examined using scanning electron microscopy (QUANTA200; FEI). Cell motility was confirmed by the presence of turbidity throughout a tube containing semisolid medium (Leifson 1960). Accumulation of Poly-β-hydroxyalkanoates (PHB) was determined by the Sudan Black staining method (Smibert and Krieg 1994) under a light microscope. Extracellular polysaccharide production was observed using the phenol/sulfuric acid method with glucose as a standard (Zhou et al. 2007). Growth was tested at various temperatures (4, 10, 15, 20, 28, 37, 40, 45, 50, and 55°C) on TSA medium containing 5% NaCl, pH 7.5 for 3–10 days. The pH range for growth was investigated between pH 4.0 and 10.0 (in increments of 1 pH unit) with the buffer system described by Xu et al. (2005). Liquid cultures were grown in tubes at 37°C for 3–14 days, using TSB medium containing 5% NaCl, pH 7.5 as the basal medium. The salt concentrations ranged from 0 to 30% (w/v) at intervals of 1% were tested by using TSA medium without NaCl as the basal medium. Catalase activity was determined by assessing bubble production after the addition of a drop of 3% H_2O_2. Oxidase activity was determined by assessing the oxidation of tetramethyl-*p*-phenylenediamine. Hydrolysis of casein, gelatin, starch, Tweens (20, 40, 60, 80) and urease activity were determined as described by Cowan and Steel (1965). Methyl red and Voges–Proskauer tests, hydrolysis of aesculin and ONPG,

indole and H_2S production from L-cysteine, nitrate and nitrite reduction, oxidation/fermentation of D-glucose, respiration in fumarate, nitrate and nitrite, DNAse activity were tested as recommended by Smibert and Krieg (1994). The utilization of different compounds as sole carbon or nitrogen and energy sources was tested as described by Carrasco et al. (2006). Antibiotic susceptibility was determined by the method of Williams (1967). Other enzymatic activities were assayed by using API ZYM strips (bioMérieux) according to the manufacturer's instructions. Acid production from carbohydrates was determined by using the API 50 CHB system (bioMérieux). *Halomonas anticariensis* DSM 16096^T, obtained from the German Collection of Microorganisms and Cell Cultures (DSMZ), was used as a reference strain for physiological and biochemical characteristics tests. All the tests in this study were repeated three times.

Chemotaxonomy and determination of G+C content of DNA

Chemotaxonomic properties, including quinones and fatty acids were analyzed. For fatty acids analysis, cells of strains YIM 93003^T and YIM 94343^T were cultured on tryptic soy broth (TSB; BD) containing 5% NaCl, pH 7.5 at 37°C shaking for 48 h (about 200 r.p.m), cellular fatty acids were extracted, methylated and analysed by using the Sherlock Microbial Identification System (MIDI) according to the manufacturer's instructions. The fatty acid methyl esters were analyzed by using the Microbial Identification software package (Sherlock Version 4.0; MIDI database: TSBA40). Isoprenoid quinones were extracted and purified as described by Komagata & Suzuki (1987). The purified ubiquinones were dissolved in acetone and separated by reversed-phase HPLC. To determine the G+C contents of strains YIM 93003^T and YIM 94343^T, genomic DNAs were prepared according to the method of Marmur (1961). The G+C contents of the DNAs were determined by reversed-phase HPLC (Mesbah et al. 1989) with DNA from *H. anticariensis* DSM 16096^T as a control.

16S rRNA gene sequencing, phylogenetic analysis and DNA–DNA hybridizations

Extraction of genomic DNA and PCR amplification of 16S rRNA gene was done as described by Li et al. (2007). The two sequences obtained were compared with reference 16S rRNA gene sequences retrieved from GenBank/EMBL by means of a BLAST search and the EzTaxon server 2.0 (Chun et al. 2007). Multiple alignments with sequences of the most closely related bacteria and calculations of levels of sequence similarity were carried out using CLUSTAL_X (Thompson et al. 1997). Phylogenetic analyses were performed using three tree-making algorithms: neighbor-joining (Saitou and Nei 1987), maximum likelihood (Felsenstein 1981), and maximum parsimony (Fitch 1971). A neighbor-joining phylogenetic tree was constructed from Knuc values (Kimura 1980) using MEGA, version 4.0 (Tamura et al. 2007), a maximum-parsimony phylogenetic tree was constructed by using MEGA, version 4.0 (Tamura et al. 2007), and a maximum likelihood phylogenetic tree was constructed by using PHYML (Guindon and Gascuel 2003). The topology of the phylogenetic tree was evaluated using the bootstrap resampling method, with 1000 replicates (Felsenstein 1985). The sequence of *Marinospirillum alkaliphilum* Z4^T (AF275713) was used as an outgroup. DNA–DNA relatedness were studied by using the optical renaturation method (De Ley et al. 1970; Huß et al. 1983; Jahnke 1992) on a UV–Vis spectrophotometer (model UV1601; Shimadzu) under optimal hybridization conditions. Every hybridization experiment was performed with three replicates and the DNA–DNA relatedness values expressed as the means of the three values.

Results and discussion

Phenotypic characteristics

Two novel strains were isolated from samples of shore sediments obtained from Qijiaojing Lake, a salt lake in Xinjiang province, north-west China. Strains YIM 93003^T and YIM 94343^T had typical morphological characteristics consistent with members of the genus *Halomonas*. The cells of the novel strains YIM 93003^T and YIM 94343^T were both aerobic, Gram-negative rods of sizes 0.4–0.7 × 1.8–2.8 and 0.4–0.5 × 1.7–2.4 μm, respectively. Neither strain was motile. After incubation at 37°C for 48 h, the colonies on TSA medium were circular with entire margins, convex, smooth and yellow; and

Table 1 Different characteristics between the novel species and its closest phylogenetic neighbor, *H. anticariensis* DSM 16096^T

Characteristics	YIM 93003^T	YIM 94343^T	DSM 16096^T
Cell size (μm)	0.4–0.7 × 1.8–2.8	0.4–0.5 × 1.7–2.4	(0.8–1.0 × 3.0–3.5)*
Exopolysaccharide production	−	−	(+)*
Poly-β-hydroxyalkanoates	−	−	(+)*
NaCl range (%, w/v)	0.5–24	0.5–23	0.5–23 (0.5–15)*
Voges–Proskauer	−	+	− (−)*
Hydrolysis of:			
Aesculin	−	+	− (−)*
Urea	+	−	+ (+)*
Utilization of:			
L-Arabinose	+	+	−
Dulcitol	+	+	−
Xylitol	+	+	−
D-Galactose	+	−	+
D-Mannitol	+	+	−
D-Xylose	+	−	+
Glycerol	+	+	−
DL-α-Alanine	+	−	+
Susceptible to:			
Tobramycin	+	−	+(+)*
Erythromycin	−	+	+
Penicillin G	−	+	−
DNA G+C content (mol%)	63.4	64.0	61.4*

All strains were able to utilize D-glucose, maltose, sodium lcitrate, D-sorbitol, sucrose and trehalose as sole carbon sources, but inositol, lactose, L-rhamnose and raffinose are not utilized. Utilize alanine, glutamic acid, histidine, hypoxanthine, L-arginine, L-asparagine, L-threonine, lysine, ornithine, phenylalanine, proline, tyrosine, valine and xanthine as sole nitrogen sources, but DL-methionine and glycine are not utilized

Note: For comparative purposes *H. anticariensis* DSM 16096^T was used as reference. Data in the brackets marked * for strain *H. anticariensis* DSM 16096^T were taken from Martínez-Cánovas et al. (2004). Other data were obtained in this study. +, positive; −, negative

approximately 1–2 and 1–1.5 mm in diameter, respectively. The two strains grew well on TSA medium, with growth observed for the temperature range 20–40°C (optimal growth for each at 37°C) an the pH range 6–9 (optimal growth for each at pH 7.5). The NaCl range for growth of strains YIM 93003^T and YIM 94343^T was 0.5–24% (w/v) NaCl and 0.5–23% (w/v) NaCl, respectively, with optimal growth for both at 5–7% (w/v) NaCl. The phenotypic characteristic of strains YIM 93003^T and YIM 94343^T were distinctly different from *H. anticariensis* DSM 16096^T, which is shown in detail in Table 1. The detailed physiological and biochemical characteristics of the strain are given in the species description.

Chemotaxonomic characteristics

The predominant respiratory quinone found in strain YIM 93003^T and YIM 94343^T were Q-9, and the major cellular fatty acids of strain YIM 93003^T were C18:1ω7*c* (43.5%), C16:0 (22.1%) and Summed feature 3 (C16:1 ω7*c*/iso-C15:02-OH) (12.3%); in strain YIM 94343^T are C18:1ω7*c* (48.5%), C16:0 (23.3%) and Summed feature 3 (C16:1 ω7*c*/iso-C15:02-OH) (12.6%). The fatty acids that account for more than 0.1% total fatty acids in both strains YIM 93003^T, YIM 94343^T and DSM 16096^T are detailed in Table 2. The chemotaxonomic properties of strains YIM 93003^T and YIM 94343^T, such as the predominant respiratory quinine and the major fatty acids

Table 2 Fatty acid profiles of strains YIM 93003^T, YIM 94343^T and *H.anticariensis* DSM 16096^T

Fatty acid (%)	YIM 93003^T	YIM 94343^T	DSM 16096^T
Saturated fatty acids			
C10:0	4.9	3.0	3.4
C11:0	Tr	–	Tr
C12:0	5.3	4.2	4.7
C13:0	0.1	0.1	0.1
C14:0	0.3	0.2	0.2
C16:0	22.1	23.3	21.7
C17:0	0.3	0.3	0.3
C17:0 cyclo	0.3	–	–
C18:0	–	0.2	0.3
C19:0 cyclo $\omega 8c$	0.6	0.1	0.1
Unsaturated fatty acids			
C15:1$\omega 6c$	0.1	–	–
C15:1$\omega 8c$	–	tr	–
C16:1$\omega 5c$	–	0.1	0.1
C17:1$\omega 6c$	–	0.1	0.1
C17:1$\omega 8c$	–	0.2	0.2
Iso-C17:1$\omega 8c$	0.1	–	–
C18:1$\omega 5c$	0.1	0.1	0.1
C18:1$\omega 7c$	43.5	48.5	51.4
C20:1$\omega 7c$	–	–	0.1
Branched fatty acids			
Iso-C11:0	0.1	0.1	0.1
Iso-C17:0	0.1	0.1	0.1
Hydroxy fatty acids			
C10:0 3OH	0.3	0.2	0.3
C11:0 3OH	0.1	0.1	0.1
C12:0 2OH	Tr	0.1	0.2
C12:0 3OH	9.4	6.3	7.1
C12:1 3OH	0.1	Tr	0.1
Summed feature 3[a]	12.3	12.6	9.6

All data, including that for *H. anticariensis* DSM 16096^T, were obtained in this study. Values are percentages of total fatty acids; fatty acids that accounted for less than 0.1% total fatty acids in both strains are not shown

[a] Summed feature 3 consisted of $C_{16:1}$ $\omega 7c$/iso-$C_{16:1}$2-OH. Tr, trace; –, not detected

were similar to those reported for *H. anticariensis* DSM 16096^T (Martínez-Cánovas et al. 2004). The G+C contents of the strains YIM 93003^T and YIM 94343^T were as 63.4 and 64.0 mol%, respectively.

Phylogenetic analysis

The almost complete 16S rRNA gene sequences of strain YIM 93003^T (1474 bp) and YIM 94343^T (1561 bp) were determined in this study. The GenBank accession numbers of the 16S rRNA gene sequences of strains YIM 93003^T and YIM 94343^T are HQ832735 and HQ832736, respectively. Alignment data showed that strains YIM 93003^T and YIM 94343^T had the highest level of 16S rRNA gene sequence similarity with respect to members of the *Gammaproteobacteria*, in particular with respect to members of the genus *Halomonas*. In the phylogenetic tree based on the neighbor-joining algorithm, strains YIM 93003^T and YIM 94343^T clustered together with the type strain of *H. anticariensis* DSM 16096^T (Fig. 1); this relationship was supported by all of the tree-making methods used in this study (Fig. 1, Figs. S2, S3). The 16S rRNA gene sequences indicated that the closest relative strain with YIM 93003^T and YIM 94343^T was the type strain *H. anticariensis* DSM 16096^T (97.5 and 97.4% sequence similarity, respectively). Levels of the 16S rRNA gene sequences similarity between strains YIM 93003^T, YIM 94343^T and the other *Halomonas* species were less than 97%, ranging from 96.7 [*Halomonas rifensis* HK31^T (HM026177)] to 91.9% [*Halomonas magadiensis* 21M1^T (X92150)], and the similarity between strains YIM 93003^T and YIM 94343^T was 99.4%. The results of the 16S rRNA gene sequence comparisons clearly demonstrated that strains YIM 93003^T and YIM 94343^T were two members of the genus *Halomonas*. DNA–DNA relatedness were studied by using the optical renaturation method on a UV–Vis spectrophotometer (model UV1601; Shimadzu) under optimal hybridization conditions. The DNA–DNA hybridization relatedness values were expressed as the means of the three values. The DNA–DNA hybridization values for strains YIM 93003^T and YIM 94343^T, YIM 93003^T and DSM 16096^T, YIM 94343^T and DSM 16096^T were 38.1 ± 3.0, 18.3 ± 4.7, and 20.8 ± 4.6%, respectively, which are well below the 70% cut-off point recommended for assignment of strains to the same genomic species (Wayne et al. 1987), thus suggesting that the strains YIM 93003^T and YIM 94343^T should be considered as two different genomic species of the genus *Halomonas.*

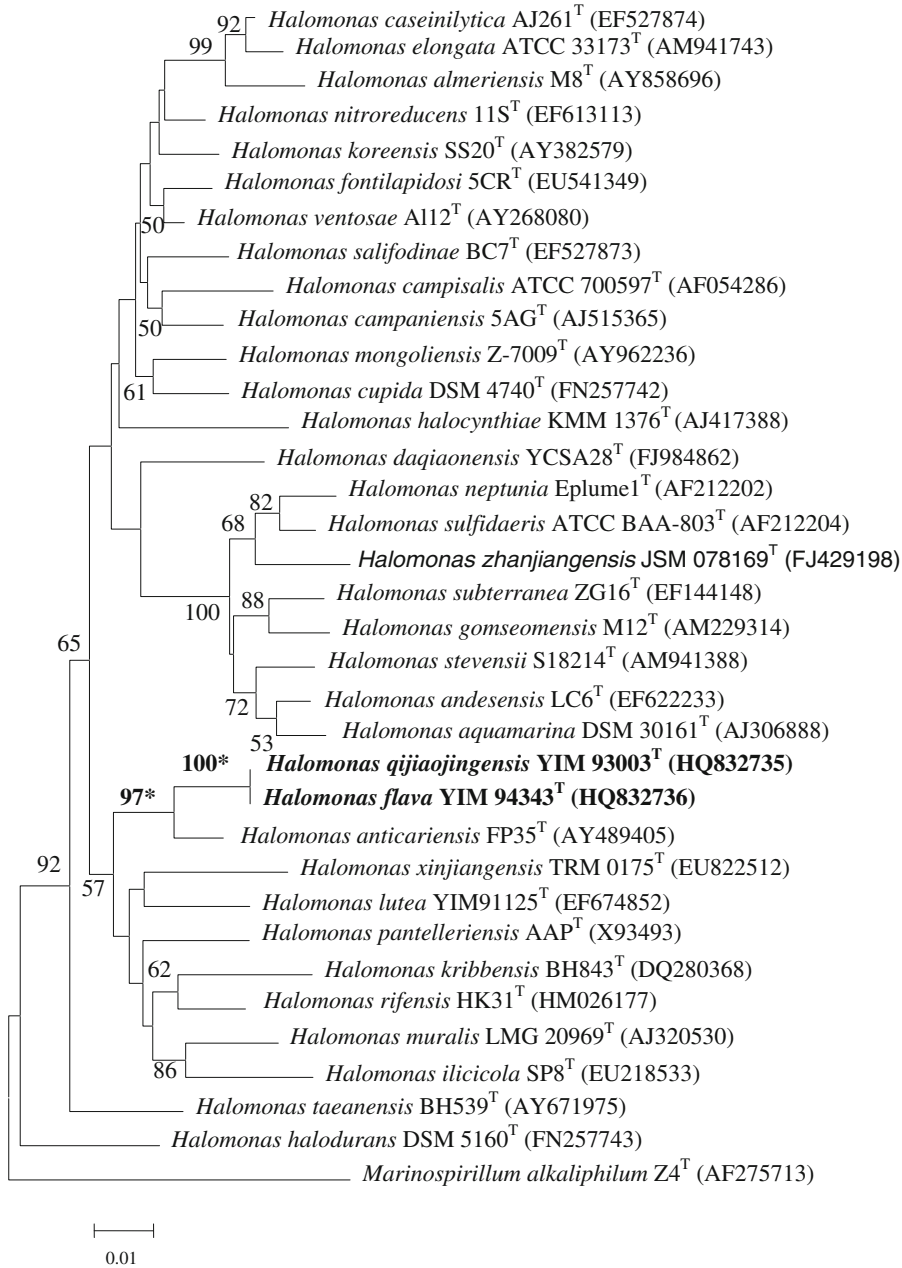

Fig. 1 Neighbor-joining phylogenetic tree, based on 16S rRNA gene sequences, showing the position of strains YIM 93003^T and YIM 94343^T among species of genus *Halomonas*. The sequence of *Marinospirillum alkaliphilum* Z4^T (AF275713) was used as an outgroup. *Asterisks* indicate branches of the tree that were also found using the maximum-likelihood (Felsenstein 1981) and maximum-parsimony (Fitch 1971) tree-making algorithms. Numbers on branch nodes are bootstrap values (1000 resamplings, only values over 50% are given). *Bar*, 0.01 substitution per 100 nucleotide positions

Taxonomic conclusion

The combination of phylogenetic, chemotaxonomic and phenotypic data indicated that strains YIM 93003^T and YIM 94343^T were two members of the genus *Halomonas*. However on the basis of phenotypic, phylogenetic differences (Table 1) and the DNA–DNA hybridization values between these novel strains and previously described species *H. anticariensis* DSM 16096^T within the genus *Halomonas*, the

strains YIM 93003^T and YIM 94343^T should be considered to represent two different novel species of the genus *Halomonas*, for which the names *Halomonas qijiaojingensis* sp. nov., and *Halomonas flava* sp. nov., are proposed.

Description of *Halomonas qijiaojingensis*

Halomonas qijiaojingensis (qi.jiao'jing.en'sis. N.L. fem. adj. *qijiaojingensis* pertaining to Qijiaojing Lake, Xinjiang Province, north-west China, where the sample from which the type strain was isolated and was collected).

Cells are aerobic, Gram-negative rods (0.4–0.7 × 1.8–2.8 μm), not motile. Colonies on TSA medium are circular with entire margins, convex, smooth and yellow, and approximately 1–2 mm in diameter after incubation at 37°C for 2 days. The type strain grow well on the TSA medium. Growth ranges for temperature, pH, and NaCl are 20–40°C, pH 6–9 and 0.5–23% (w/v) NaCl, with optimal growth at 37°C, pH 7.5, and 5–7% (w/v) NaCl. Nitrate is reduced. Oxidase- and catalase-positive. Hydrolyzes urea, while aesculin, gelatin, casein, ONPG, starch and, Tweens 20, 40, 60, and 80 are not hydrolyzed. Poly-β-hydroxyalkanoates, exopolysaccharide, H_2S, indole production, methyl red and Voges–Proskauer tests give negative results. Oxidation/fermentation of D-glucose; respiration in fumarate, nitrate and nitrite; and DNAse activity all give negative results. Utilizes D-galactose, L-arabinose, citrate, dulcitol, glycerol, D-glucose, D-mannitol, D-xylose, maltose, sodium citrate, D-sorbitol, sucrose, trehalose, xylitol as sole carbon sources; inositol, lactose, L-rhamnose, raffinose are not utilized. Utilizes alanine, DL-α-alanine, glutamic acid, histidine, hypoxanthine, L-arginine, L-asparagine, L-threonine, lysine, ornithine, phenylalanine, proline, tyrosine, valine, xanthine as sole nitrogen sources; DL-methionine, glycine are not utilized. In the API 50 CHB system, acid is produced from D-adonitol, D-fructose, D-fucose, D-glucose, glycerol, maltose, D-mannose, sucrose, trehalose, D-turanose, but not from *N*-acetylglucosamine, aesculin, amygdalin, arbutin, D-arabinose, L-arabinose, D-arabitol, L-arabitol, cellobiose, dulcitol, erythritol, L-fucose, D-galactose, gentiobiose, glycogen, inositol, inulin, D-lactose, D-lyxose, D-mannitol, melezitose, melibiose, methyl α-D-glucopyranoside, methyl α-D-mannopyranoside, methyl β-D-xylopyranoside, potassium gluconate, potassium 2-ketogluconate, potassium 5-ketogluconate, raffinose, -ribose, rhamnose, salicin, D-sorbitol, sorbose, starch, D-tagatose, xylitol, D-xylose and L-xylose. In the API ZYM system, alkaline phosphatase and α-glucosidase give positive results; acid phosphatase, *N*-acetyl-β-glucosaminidase, arylamidase, α-chymotrypsin, cystine arylamidase, esterase (C4), esterase lipase (C8), α-fucosidase, α-galactosidase, β-galactosidase, β-glucuronidase, β-glucosidase, leucine arylamidase, lipase (C14), α-mannosidase, naphthol-AS-BI-phosphohydrolase, trypsin, valine arylamidase are negative. The type strain is sensitive to the following antibiotics (μg per disc, unless indicated otherwise): amikacin (30), ampicillin (10), chloramphenicol (30), ciprofloxacin (5), gentamicin (10), norfloxacin (10), tobramycin (10), sulfamethoxazole (23.75). Resistance is exhibited only to vancomycin (30), erythromycin (15), penicillin G (10 Iu/disc) and clindamycin (3). Q-9 is the predominant ubiquinone. The major cellular fatty acids (>10%) are C18:1ω7*c* (43.5%), C16:0 (22.1%) and Summed feature 3 (C16:1 ω7*c*/iso-C15:02-OH) (12.3%). The DNA G+C content is 63.4 mol%.

The type strain, YIM 93003^T (= CCTCC AB 208133^T = KCTC 22228^T), was isolated from Qijiaojing Lake, Xinjiang province, north-west China.

Description of *H. flava*

Halomonas flava (fla.va. L. fem. adj. flava, yellow, reflecting the colour of colonies).

Cells are aerobic, Gram-negative rods (0.4–0.5 × 1.7–2.4 μm), not motile. Colonies on TSA medium are circular with entire margins, convex, smooth and yellow, and approximately 1–1.5 mm in diameter after incubation at 37°C for 2 days. The type strain grows well on TSA medium. Growth ranges for temperature, pH and NaCl are 20–40°C, pH 6–9 and 0.5–23% (w/v) NaCl, with optimal growth at 37°C, pH 7.5 and 5–7% (w/v) NaCl. Nitrate is reduced. Oxidase- and catalase-positive. Hydrolyezs aesculin, while casein, gelatin, ONPG, starch, urea and Tweens 20, 40, 60 and 80 are not hydrolysed. Poly-β-hydroxyalkanoates, exopolysaccharide, H_2S, indole production and methyl red tests give negative results. Positive for Voges-Proskauer test. Oxidation/fermentation of D-glucose; respiration in fumarate, nitrate

and nitrite; DNAse activity each give negative results. Utilizes dulcitol, glycerol, D-glucose, L-arabinose, D-mannitol, maltose, sodium citrate, D-sorbitol, sucrose, trehalose, xylitol as sole carbon sources; D-galactose, D-xylose, inositol, lactose, L-rhamnose, raffinose are not utilized. Utilizes alanine, citrate, glutamic acid, histidine, hypoxanthine, L-arginine, L-asparagine, L-threonine, lysine, ornithine, phenylalanine, proline, tyrosine, valine, xanthine as sole nitrogen sources; DL-methionine, glycine, DL-α-alanine are not utilized. In the API 50 CHB system, acid is produced from aesculin, L-arabinose, arbutin, cellobiose, D-fructose, D-glucose, glycerol, D-mannitol, D-mannose, D-ribose, salicin, sucrose, D-tagatose, trehalose, but not from amygdalin, D-adonitol, D-arabinose, D-arabitol, L-arabitol, dulcitol, erythritol, D-fucose, L-fucose, D-galactose, gentiobiose, glycogen, inositol, inulin, D-lactose, D-lyxose, maltose, melezitose, melibiose, methyl α-D-glucopyranoside, methyl α-D-mannopyranoside, methyl *β*-D-xylopyranoside, *N*-acetylglucosamine, potassium gluconate, potassium 2-ketogluconate, potassium 5-ketogluconate, raffinose, rhamnose, D-sorbitol, sorbose, starch, D-turanose, D-xylose, xylitol and L-xylose. In the API ZYM system, acid phosphatase, alkaline phosphatase, α-glucosidase, *β*-glucosidase give positive results; *N*-acetyl-*β*-glucosaminidase, α-chymotrypsin, cystine arylamidase, esterase (C4), esterase lipase (C8), α-fucosidase, α-galactosidase, *β*-galactosidase, *β*-glucuronidase, leucine arylamidase, lipase (C14), α-mannosidase, naphthol-AS-BI-phosphohydrolase, trypsin, valine arylamidase are negative. The type strain is sensitive to the following antibiotics (μg per disk, unless indicated otherwise): amikacin (30), ampicillin (10), chloramphenicol (30), ciprofloxacin (5), erythromycin (15), gentamicin (10), penicillin G (10 Iu/disc), norfloxacin (10), sulfamethoxazole (23.75). Resistance is exhibited only to tobramycin (10), vancomycin (30) and clindamycin (3). Q-9 is the predominant ubiquinone. The major cellular fatty acids (>10%) are C18:1*ω*7*c* (48.5%), C16:0 (23.3%) and Summed feature 3 (C16:1 *ω*7*c*/iso-C15:02-OH) (12.6%). The DNA G+C content is 64.0 mol%.

The type strain, YIM 94343^{T} (=CCTCC AB 2010382^{T} =KCTC 23356^{T}), was isolated from Qijiaojing Lake, Xinjiang province, north-west China.

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