The Journal of Microbiology (2010) Vol. 48, No. 2, pp. 160-164
DOI 10.1007/s12275-010-0018-9

Psychroflexus lacisalsi sp. nov., a Moderate Halophilic Bacterium Isolated from a Hypersaline Lake (Hunazoko-Ike) in Antarctica

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(Received January 13, 2010 / Accepted March 31, 2010)

A novel Gram-negative, aerobic, moderate halophilic, and psychrotolerant bacterium, designated as strain H7^T, was isolated from a hypersaline lake located in Skarvsnes, Antarctica. Cells were filaments with varying lengths. Coccoid bodies developed in old cultures. Growth occurred with 0.5-15% (w/v) NaCl (optimum, 5.8-7.0%), at pH 6.0-10.0 (optimum, pH 7.0-8.0), and at 10-28°C (optimum, 25°C). The strain had a G+C content of 34.9 mol%, which is within the range of 32-36 mol% reported for the genus *Psychroflexus*. Chemotaxonomic data (major respiratory quinone: MK-6; major fatty acids: aC$_{15:0}$, iC$_{16:0}$ 3-OH, and aC$_{15:1}$ A) supported the classification of strain H7^T within the genus *Psychroflexus*. Phylogenetic analysis based on 16S rRNA gene sequences indicated that strain H7^T should be assigned to the genus *Psychroflexus* and has a homology with *Psychroflexus salinarum* (98.2%), *P. sediminis* (96.1%), *P. torquis* (95.2%), *P. tropicus* (95.8%), and *P. gondwanense* (92.2%). Strain H7 is not identified as *P. salinarum* because that DNA-DNA hybridization data were 8.5% between strain H7^T and *P. salinarum*. The combination of phylogenetic analysis, DNA-DNA hybridization data, phenotypic characteristics, and chemotaxonomic differences supported the view that strain H7^T represents a novel species of the genus *Psychroflexus*. The name *Psychroflexus lacisalsi* is proposed, and the type strain is H7^T (=JCM 16231^T =KACC 14089^T).

***Keywords*:** *Psychroflexus lacisalsi* sp. nov., novel bacterium, 16S rRNA gene, psychrotolerant, Antarctica

The genus *Psychroflexus* was first proposed by Bowman *et al*. (1998) with two described species, *Psychroflexus gondwanense* and *P. torques* (the type species). *Psychroflexus* has three other published species: *P. salinarum* (Yoon *et al*., 2009), *P. tropicus* (Donachie *et al*., 2004), and *P. sediminis* (Chen *et al*., 2009). This genus is commonly characterized as Gram-negative, aerobic, catalase, and oxidase activity positive, with DNA G+C contents of 32-36 mol% (determined by thermal denaturation). Menaquinone-6 is the major respiratory quinone of this genus; aC$_{15:0}$, aC$_{15:1}\omega$10*c*, iC$_{16:0}$, iC$_{16:0}$ 3-OH, and aC$_{17:0}$ 3-OH are the main fatty acids.

Here, we describe the isolation; morphological, physiological, and biochemical profiles; DNA-DNA hybridization value; and 16S rRNA gene sequence of *Psychroflexus* strain H7^T. We propose that this strain be included under the genus *Psychroflexus* as *Psychroflexus lacisalsi* sp. nov.

Materials and Methods

Isolation of strain H7^T and culture conditions

Water sample was collected from 4 m depth at Lake Hunazoko-Ike, Skarvsnes, Antarctica, on January 2005, by the 45th Japanese Antarctic Research Expedition (JARE-45) [pH 7.6, 19% (w/v) salinity, and 22°C temperature]. A sample was spread on modified Luria-Bertani (LB) agar [per L: 10 g Bacto tryptone (Difco, USA), 5 g Bacto yeast extract (Difco), and 58 g NaCl (pH 7.0)] and incubated at 20°C. Colonies that developed after 20 days were transferred to marine agar 2216 (MA; Difco) and further incubated at 20°C for purification. After primary isolation and purification, the isolate was preserved both on MA at 4°C and in 20% (v/v) glycerol suspended in distilled water at -80°C. Anaerobic growth tests were performed with a commercial anaerobic growth test system (Anaero Pack; Mitsubishi Gas Chemical Co., Tokyo, Japan) on MA at 25°C for 7 days. Unless otherwise indicated, morphological, physiological, and other commercial tests were performed with cells grown at 25°C. The reference strain *P. salinaru m* KCTC 22483^T was obtained from the Korean Collection for Type Cultures (KCTC, Daejeon, Korea) and grown according to KCTC instructions.

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Morphology and physiological characteristics

The morphology of strain H7^T was observed under Olympus BX60-FLA fluorescence microscope (Olympus, Japan) using specific filter sets for 4′,6-diamino-2-phenylindole after 12 and 24 h incubation in marine 2216 broth (MB; Difco). Gram staining was performed according to Halebian *et al*. (1981). The presence of gliding motility was also investigated with cells grown in MB for 24 h (Bernardet *et al*., 2002). Growth at various temperatures (4°C, 10°C, 15°C, 20°C, 25°C, 28°C, and 30°C) was measured on MA. The optimum salinity for the growth of strain H7^T was determined in medium A at pH 8.0 [per L: 1 g glucose, 5 g Bacto peptone (Difco), 2.5 g Bacto yeast extract (Difco)], supplemented with artificial seawater (JIS K-2510) containing (per L) 5.29 g $MgCl_2$, 1.54 g $CaCl_2{\cdot}2H_2O$, 0.04 g $SrCl_2{\cdot}6H_2O$, 1.38 g KCl, 0.40 g $NaHCO_3$, 0.20 g KBr, 0.06 g H_3BO_3, 0.01 g NaF, and 4.09 g Na_2SO_4 at various NaCl concentrations [0.5% (w/v), 5.8% (w/v), and 0.0-20.0% (w/v), at increments of 1.0%], incubated at 120 rpm.

Growth was monitored by measuring the turbidity at 650 nm (OD_{650}) with the use of a spectrophotometer (Beckman Instruments, USA). Growth was scored positive if the OD_{650} value is greater than 0.300. The optimum pH was determined in medium A [5.8% (w/v) NaCl], in the range of pH 5.0-13.0 (at increments of pH 1.0), incubated at 120 rpm. Artificial seawater requirement test was done in medium A with a NaCl concentration of 5.8% (w/v). Yeast extract requirement test was done in medium A [5.8% (w/v) NaCl] supplemented with agar to 1.5% (w/v). Flexirubin-type pigments were checked by flooding colonies with 20% KOH (Cowan and Steel, 2004). Catalase activity was determined by bubble production in 3% hydrogen peroxide solution, and oxidase activity was tested using oxidase reagent (bioMérieux Vitek, France). Nitrate reduction was determined in nitrate broth (Difco) containing 5.8% (w/v) NaCl; standard reagents for reductase were added after 72 h (Cowan and Steel, 2004). Amylase was tested in medium A [5.8% (w/v) NaCl] containing 1% (w/v) starch by flooding inoculated plates with iodine (Cowan and Steel, 2004). Hydrolysis of DNA was checked on DNase test agar with methyl green (Difco) (Cowan and Steel, 2004). Hydrolysis of Tween 80 was tested in medium A containing 1% (w/v) Tween 80 with 5.8% (w/v) NaCl concentration, as described by Cowan and Steel (2004). Hydrolysis of agar was checked on MA as described by Cowan and Steel (2004). Hydrolysis of gelatin and esculin, indole production, and assimilation tests were done in API 20 NE test strip (bioMérieux) for 5 days. Strain H7T was incubated on MA for 3 days and suspended into artificial seawater and then added into API 20 NE test strip. Acidification of carbohydrates in API 50 CH test strip (bioMérieux) was followed over 5 days in CHB/E medium with SL-8 trace elements solution (Atlas, 1997), rather than Cohen-Bazire mineral base and 5.8% (w/v) NaCl. Constitutive enzyme activities were assayed in API ZYM test strip (bioMérieux) according to the manufacturer's instructions.

Chemotaxonomy

Fatty acids were prepared according to the Microbial Identification System (MIDI; Microbial ID) protocol. Fatty acids in whole cells grown on MA (15°C) for 5 days were analyzed as described by Sasser (1997) using the MIDI system. The peaks were integrated and identified by the Microbial Identification software package TSBA 4.0.

Menaquinones were extracted following the procedure of Nishijima *et al*. (1997) and analyzed by high-performance liquid chromatography (HPLC, Waters 600 series, Waters, Japan).

The DNA G+C content was determined by HPLC with replications (n=3) as described by Katayama-Fujimura *et al*. (1984). DNA-GC kit (Yamasa Shoyu Co., Japan) was used as the standard mixture.

16S rRNA gene sequencing and phylogenetic analysis

Genomic DNA was extracted from 48 h cultures in MB using the Wizard® Genomic DNA Purification kit (Promega, USA). A fragment of the 16S rRNA gene was amplified from the Genomic DNA by PCR with DNA polymerase and primers, EUB 27F: 5′-AGAGTTTGAT CMTGGCTCAG-3′ and EUB 1492R: 5′-TACGGYTACCTTGTTAC GACTT-3′ (Lane, 1991), and sequenced in a ABI 3100 DNA sequencer (Applied Biosystems, USA) by using the ABI Prism Big Dye Terminator Cycle Sequencing Ready Reaction kit with primers EUB 27F and SP6. The resulting 16S rRNA gene sequence was compared with sequences obtained from public databases (GenBank/EMBL/DDBJ) to find the most closely related species. Phylogenetic and molecular evolutionary analyses were conducted using MEGA version 4 (Tamura *et al*., 2007) after multiple alignment of sequence data with CLUSTAL X (Thompson *et al*., 1994). Distances were calculated using distance options according to Kimura's two-parameter model (Kimura, 1980), and clustering was performed by the neighbor-joining method (Saitou and Nei, 1987). To evaluate the stability of the generated phylogenetic tree, a bootstrap analysis was performed using a consensus tree based on 1,000 randomly generated trees (Felsenstein, 1985).

Nucleotide sequence accession number

The strain H7^T 16S rRNA gene sequence is available from the GenBank nucleotide database at the National Center for Biotechnology Information website (http://www.ncbi.nlm.nih.gov) under accession number AB381940.

DNA-DNA hybridization

A DNA-DNA homology experiment between strain H7^T and *P. salinarum* KCTC 22483^T was performed using photobiotin-labeled probes in microplate wells, as described by Ezaki *et al*. (1989). A multifunctional microplate reader (GENios, TECAN Austria GmbH, Austria) was used for fluorescence measurements.

Results and Discussion

Morphology and physiological characteristics

Cells of strain H7^T were Gram-negative, aerobic, and straight to slightly curved rods. Colonies were orange pigmented on MA. Flexirubin-type pigments were not present. Catalase and oxidase activities were present; nitrate reductase was expressed in the presence of 5.8% (w/v) NaCl. Indole production (API 20 NE test strip) was negative. Other detailed phenotypic and biochemical characteristics of strain H7 are fully described in the species descriptions.

Additional phenotypic characteristics that served to differentiate the strain H7^T and other related *Psychroflexus* species are shown in Table 1. Data for *P. torquis*, *P. gondwanense*, *P. sediminis*, *P. lacisalsi*, *P. tropicus*, and *P. salinarum* were obtained from incubation on MA at 10°C, 20°C, 25°C, 28°C, 30°C, and 30°C, respectively. Enzyme activity and acid production from different substances, for all type strains, were checked by API ZYM and API 50 CH kits, respectively.

Strain H7^T could be clearly differentiated from its nearest relative, *P. salinarum*, by the presence of gliding motility and higher optimum concentration of NaCl [5.8-7.0% (w/v)]; the presence of enzyme activities such as lipase, cystine arylamidase, trypsin, α-chymotrypsin, α-glucosidase, and β-glucosidase; its inability to grow at 30°C and at less than 10°C; and its inability to hydrolyze Tween 80. The strain could be clearly distinguished from its neighbor *P. sediminis* by using a number of phenotypic properties (Table 1), such as inability to produce acid from maltose and to grow at 30°C, as well as its ability to grow in 15% (w/v) NaCl. Strain H7^T could also be clearly distinguished from *P. torquis* by its ability to hydrolyze gelatin and esculin, to grow at 20°C, to grow (OD_{650}>1, 72 h; data not shown) in medium A [5.8% (w/v) NaCl] in the absence of artificial seawater, and its inability to grow at 4°C.

Menaquinones and fatty acid compositions

MK-6 is the sole respiratory quinone detected for the genus *Psychroflexus*. Fatty acid compositions were characterized by the abundance of branched-chain fatty acids (68%). The major

Table 1. Differential characteristics of *P. lacisalsi* strain H7^T and other *Psychroflexus* species

Strains: 1, *P. lacisalsi* H7^T (from this study); 2, *P. salinarum* ISL-14^T (Yoon *et al*., 2009); 3, *P. tropicus* LA1^T (Donachie *et al*., 2004); 4, *P. torquis* ACAM 623^T (Bowman *et al*., 1998); 5, *P. gondwanensis* ACAM 48^T (Bowman *et al*., 1998); 6, *P. sediminis* YIM-C238^T (Chen *et al*., 2009).

All type strains express alkaline phosphatase.

None express α-mannosidase, α-galactosidase, and α-fucosidase.

+, Positive reaction; –, negative reaction; ND, not detected; V, variable; W, weakly positive reaction; MH, moderately halophilic; SH, slightly halophilic

Characteristic	1	2	3	4	5	6
Gliding motility	+	–	+	+	–	+
Yeast extract requirement	–	ND	ND	+	–	ND
ASW requirement	–	ND	ND	+	–	ND
Nitrate reduction	+	+	+	–	–	+
Salinity requirement	MH	MH	MH	SH	MH	SH
NaCl optimum (%, w/v)	5.8-7.0	2	7.5-10	3	5	2-3
NaCl range (%, w/v)	0.5-15	0-17	1-20	1-8	0-15	0.5-6
Temp. range (°C)	10-28	4-35	4-43	-16-20	-5-30	10-40
Hydrolysis of:						
DNA	–	–	–	+	+	ND
Gelatin	+	+	–	–	V	+
Aesculin	+	+	–	–	+	+
Tween 80	–	+	–	+	+	+
Agar	–	ND	ND	–	–	ND
Starch	+	+	ND	+	+	–
Production of acid from						
Glucose	+	W	–	+	+	–
Maltose	+	W	–	+	+	+
Arabinose	–	–	–	–	+	–
Xylose	–	–	–	–	+	–
D-Mannose	–	W	–	+	+	–
Fructose	–	–	+	–	–	–
Mannitol	–	–	+	–	–	–
Sorbitol	–	–	+	–	–	–
Arabitol	–	ND	+	–	–	–
Glycerol	–	ND	–	V	–	–
Glycogen	+	ND	–	ND	ND	+
Production of acid from						
Potassium 5-Ketogluconate	+	ND	+	ND	ND	–
Enzyme activity						
Lipase (C14)	+	–	+	ND	ND	–
Cystine Arylamidase	+	–	+	ND	ND	+
Trypsin	+	–	+	ND	ND	–
α-Chymotrypsin	+	–	+	ND	ND	–
α-Glucosidase	+	–	+	+	+	–
β-Glucosidase	+	–	+	+	+	–
β-Glucuronidase	–	–	–	–	–	+
G+C content (mol%)	34.9 ±0.0	38.5	35± 0.8	32-33	36	35.8

Table 2. Cellular fatty acid profiles of strain H7^T and related type strains of the genus *Psychroflexus*

Strain: 1, *P. lacisalsi* H7^T (data from this study); 2, *P. salinarum* ISL-14^T (Yoon *et al*., 2009); 3, *P. sediminis* YIM-C238^T (Chen *et al*., 2009); 4, *P. torquis* ACAM 623^T (Bowman *et al*., 1998); 5, *P. tropicus* LA1^T (Donachie *et al*., 2004); 6, *P. gondwanensis* ACAM 48^T (Bowman *et al*., 1998).

Data for *P. lacisalsi* H7^T, *P. torquis* ACAM 623^T and *P. tropicus* LA1^T were determined by Gas Chromatograph-Mass Spectrometer (GC-MS) with cells grown at 15°C. –, not detected.

Fatty acid	1	2[a]	3[a]	4	5	6[b]
$C_{12:0}$	0.5	–	–	–	–	–
$C_{15:0}$	–	1.3	–	1.2	0.6	1.9
$C_{16:0}$	–	0.2	–	0.6	–	1.1
$iC_{13:0}$	–	1.5	0.4	0.7	0.5	1.4
$aC_{13:0}$	0.5	0.4	2.8	–	0.6	–
$iC_{14:1}$ $\omega 9c$	–	–	–	–	–	2.8
$iC_{14:0}$	3.4	**7.1**	**7.8**	1.0	2.7	4.8
$iC_{15:1}$ $\omega 10c$	–	–	2.7	0.4	**11.8**	2.2
$aC_{15:1}$ $\omega 10c$	–	–	**10.7**	**16.9**	**12.9**	**18.4**
$aC_{15:1}$	**17.6**[c]	4.0	–	–	–	–
$iC_{15:1}$	1.7[d]	2.3	–	–	–	–
$iC_{15:0}$	**6.5**	**17.9**	1.6	1.1	**16.7**	2.1
$aC_{15:0}$	**35.8**	**23.7**	**29.4**	**35.2**	**19.3**	**23.0**
$iC_{16:0}$	2.5	7.6	1.9	**6.0**	3.4	–
$C_{12:0}$ 3-OH	1.8	–	–	–	–	–
$iC_{14:0}$ 3-OH	0.5	1.1	1.1	–	0.4	–
$C_{15:0}$ 2-OH	4.1	3.0	4.8	–	2.8	–
$iC_{15:0}$ 3-OH	0.9	2.0	1.4	0.3	2.9	0.9
$C_{15:0}$ 3-OH	–	0.2	1.0	2.5	–	0.9
$C_{16:0}$ 3-OH	**15.2**	**12.2**	**16.1**	**15.4**	**10.1**	**18.5**
$C_{16:0}$ 3-OH	–	0.2	–	1.2	0.4	0.4
$iC_{17:0}$ 3-OH	2.1	**6.3**	4.2	0.2	**10.0**	0.9
$aC_{17:0}$ 3-OH	–	–	–	–	2.1	–
$C_{17:0}$ 3-OH	–	–	–	0.4	–	0.7
$C_{17:0}$ 2-OH	**6.6**	3.7	**6.7**	–	3.9	–
C16:1e	–	–	3.2	–	–	–
C17:1 $\omega 6c$	–	1.0	1.8	–	–	–
C17:1 $\omega 8c$	0.4	–	–	–	–	–
C20:4 $\omega 6c$	–	–	–	2.1	–	–
C20:5 $\omega 3c$	–	–	–	4.9	–	–

Major constituents (>5% of total fatty acids) were shown in bold.

[a] At 30°C. [b] At 10°C. [c] Double bond positions in $aC_{15:1}$ were not determined and fatty acids were $aC_{15:1}$ A. [d] Double bond positions in $iC_{15:1}$ were not determined and fatty acids were $iC_{15:1}$ G. [e] Double bond positions in $C_{16:1}$, fatty acids were either $\omega 6c$ or $\omega 7c$.

fatty acids of strain H7^T were $aC_{15:0}$ (35.8%), $aC_{15:1}$ A (17.6%), and $iC_{16:0}$ 3-OH (15.2%), which are similar with those of the genus *Psychroflexus*. Other components were $C_{12:0}$ (0.5%), $aC_{13:0}$ (0.5%), $iC_{14:0}$ (3.4%), $iC_{15:1}$ G (1.7%), $iC_{15:0}$ (6.5%), $iC_{16:0}$ (2.5%), $C_{12:0}$ 3-OH (1.8%), $iC_{14:0}$ 3-OH (0.5%), $C_{15:0}$ 2-OH (4.1%), $iC_{15:0}$ 3-OH (0.9%), $iC_{17:0}$ 3-OH (2.1%), $C_{17:0}$ 2-OH (6.6%), and $C_{17:1}\omega 8c$ (0.4%) (Table 2). The fatty acid profiles of strain H7 differ considerably from other phylogenetically related *Psychroflexus* bacteria (Table 2). Data for *P. torquis*, *P. gondwanense*, *P. lacisalsi*, *P. tropicus*, *P.*

sediminis, and *P. salinarum* were obtained from incubation on MA at 15°C, 10°C, 15°C, 15°C, 30°C, and 30°C, respectively. *P. torquis* and *P. tropicus* were lacking unbranched monounsaturated fatty acids at 15°C incubation, which were detected in previous studies on the genus *Psychroflexus* (Bowman *et al*., 1998; Donachie *et al*., 2004). *P. sediminis* and *P. salinarum* presented 5% and 1.0% (incubation at 30°C) unbranched monounsaturated fatty acids, respectively. However, strain H7^T was found to present trace amounts (0.4%) of unbranched monounsaturated fatty acids (incubation at 15°C), a deviation from other species of the *Psychroflexus* genus. Furthermore, when compared with *P. salinarum*, the species most closely related to strain H7^T, saturated fatty acids of $C_{15:0}$ (1.3%) were found in *P. salinarum* but not in strain H7^T (Table 2). Other differential fatty acid characteristics are shown in Table 2.

Phylogenetic analysis

An almost-complete 16S rRNA gene sequence (1,451 bp) was determined. The sequence similarities between strain H7^T and the type strains of the members of the genus *Psychroflexus* were 98.2% with *P. salinarum* KCTC 22483^T, 96.1% with *P. sediminis* YIM-C238^T, 95.2% with *P. torquis* LMG 21429^T, 95.8% with *P. tropicus* ATCC BAA-734^T, and 92.2% with *P. gondwanense* ATCC 51278^T. Six strains formed a robust cluster in the phylogenetic tree (bootstrap value, 100%) in which strain H7^T was shown to be most closely related to *P. salinarum* KCTC 22483^T (Yoon *et al*., 2009), and two strains formed a distinct subclade with significant bootstrap support (98%) (Fig. 1). According to the 16S rRNA gene sequence and phylogenetic analysis, strain H7^T fell firmly within the genus *Psychroflexus* in the Cytophaga-Flexibacter-Bacteroides (CFB) group of bacteria (Fig. 1).

G+C content and DNA-DNA hybridization

The G+C content was 34.9±0.0 mol% (determined by HPLC method). DNA-DNA hybridization revealed only 8.5% DNA reassociation between strain H7^T and *P. salinarum* KCTC 22483^T. The value was below the threshold (about 70%) recommended by Wayne *et al*. (1987) for assigning strains to the same species.

Taxonomic conclusion

The G+C content of 34.9 mol% is in the range of 32-36 mol% reported for the genus *Psychroflexus* (Bowman *et al*., 1998). Although phylogenetic analysis based on 16S rRNA gene confirmed strain H7^T to be a member of the genus *Psychro-*

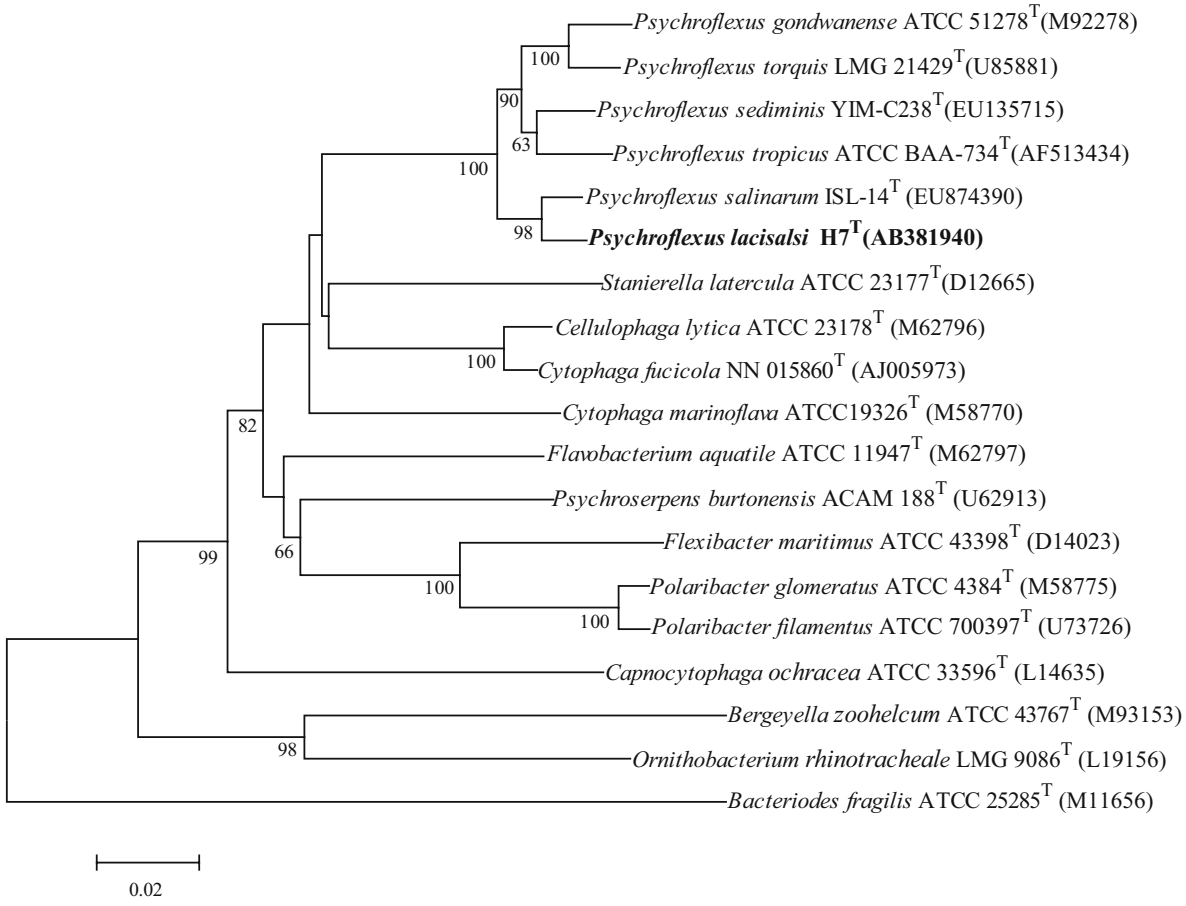

Fig. 1. Phylogenetic tree constructed from a comparative analysis of 16S rRNA gene sequences showing the relationships of *P. lacisalsi* H7^T (bold) with related species. Bootstrap values (expressed as percentages of 1,000 replications) greater than 50% are shown at the branch points. The topology of the tree is based on the neighbor-joining method. GenBank accession no. are shown in parentheses. Bar=0.02 substitutions per nucleotide position.

flexus, the strain can be clearly differentiated from the five closest species according to phylogenetic position, significant distinctions of chemotaxonomic feature (fatty acid profile), and some important physiological reactions (e.g., inability to grow at less than 10°C and more than 28°C) (Table 1). Together with phenotypic and genotypic differences, we conclude that strain H7^T represents a novel species of the genus *Psychroflexus*, for which the name *P. lacisalsi* sp. nov. is proposed.

Description of *P. lacisalsi* sp. nov.

P. lacisalsi (la.ci.sal'si. L. masc. n. lacus, lake; L. adj. salsus, salted, salt; N.L. gen. n. *lacisalsi*, of a salt lake, relating to its isolation from a salt lake) cells are Gram-negative, aerobic, and straight to slightly curved rods 0.3-0.6 μm wide and 1.7-12.0 μm long. Old cultures in MB produce "coccoid bodies". Orange, circular, convex, opaque, entire, smooth, and glistening colonies appear on MA after 3 days at 25°C. Gliding motility is present. Aerobic growth occurs on MA between 10°C and 28°C, but not at 30°C. The optimum temperature is 25°C. The bacterium is moderately halophilic, with an optimum pH of 7.0-8.0; the optimal NaCl concentration is 5.8-7.0% (w/v) in medium A at 25°C. Other species characteristics are as follows: catalase positive, oxidase positive; expresses nitrate reductase in the presence of 5.8% (w/v) NaCl; negative for indole production (API 20 NE test strip). The followings are not utilized as sole carbon sources: *N*-acetyl-glucosamine, adipic acid, L-arbinose, capric acid, D-glucose, malic acid, D-maltose, D-mannitol, D-mannose, phenylacetic acid, potassium gluconate, and trisodium citrate (API 20 NE test strip). The following are expressed: acid phosphatase, alkaline phosphatase, α-chymotrypsin, cystine arylamidase, esterase lipase (C8), α-glucosidase, β-glucosidase, leucine arylamidase, lipase (C14), naphthol-AS-BI-phosphohydrolase, trypsin, and valine arylamidase, express in API ZYM test strip. Acid is produced from starch, esculin ferric citrate, D-glucose, glycerol, glycogen, D-maltose, and potassium 5-ketogluconate (API 50 CH test strip). MK-6 is the sole respiratory quinone. The dominant fatty acids are $aC_{15:0}$ (35.8%), $aC_{15:1}$ A (17.6%), and $iC_{16:0}$ 3-OH (15.2%). The G+C content of the type strain is 34.9 mol% (determined by HPLC).

Type strain H7^T has been deposited in the Korean Agricultural Culture Collection (KACC) and Japan Collection of Microorganisms (JCM). The DDBJ Nucleotide Sequence Database accession number is AB381940.

Type strain H7^T (=KACC 14089^T =JCM 16231^T) was isolated from an Antarctic hypersaline lake.

Acknowledgements

We would like to thank Professor Jean P. Euzéby [Laboratoire de Bactériologie École Nationale Vétérinaire de Toulouse (ENVT) 23, chemin des Capelles B.P. 87614 31076, Toulouse cedex 03, France] for his advice on the Latin name.

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