

Halomonas alimentaria sp. nov., isolated from jeotgal, a traditional Korean fermented seafood

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A Gram-negative, moderately halophilic bacterial strain, YKJ-16^T, which was isolated from jeotgal, a traditional Korean food, was considered to be a member of the genus *Halomonas*. Cells of strain YKJ-16^T are non-motile and cocci or short rods, unlike most *Halomonas* species. However, chemotaxonomic and phylogenetic analyses demonstrated that strain YKJ-16^T belongs to the genus *Halomonas*. The predominant isoprenoid quinone is ubiquinone-9. The major fatty acids are C_{18:1}ω7c, C_{16:0}, C_{19:0} cyclo ω8c and C_{16:1}ω7c and/or iso C_{15:0} 2OH. The phylogenetic tree showed that strain YKJ-16^T forms a distinct evolutionary lineage within the radiation comprising *Halomonas* species and forms a coherent cluster with *Halomonas halodenitrificans*, *Halomonas cupida* and *Halomonas pacifica*. Levels of 16S rDNA similarity between strain YKJ-16^T and the type strains of other *Halomonas* species are 93.0–96.3%. Levels of DNA–DNA relatedness indicate a taxonomic status of strain YKJ-16^T as a species different from the three species that form the coherent cluster mentioned above. Morphologically, strain YKJ-16^T is also clearly differentiated from the type strains of *H. cupida* and *H. pacifica*. Accordingly, on the basis of the phenotypic characteristics, 16S rDNA sequence analysis and DNA relatedness data, strain YKJ-16^T should be placed in the genus *Halomonas* as a novel species. The name *Halomonas alimentaria* sp. nov. is proposed with strain YKJ-16^T (= KCCM 41042^T = JCM 10888^T) as the type strain.

Keywords: *Halomonas alimentaria*, sp. nov., polyphasic taxonomy, Korean traditional food, jeotgal

INTRODUCTION

The genus *Halomonas* was originally proposed, with the sole species *Halomonas elongata*, to accommodate a group of Gram-negative, rod-shaped and moderately halotolerant strains (Vreeland *et al.*, 1980). The genus *Deleya* was created to accommodate some marine *Alcaligenes* species and *Pseudomonas marina* (Baumann *et al.*, 1983). The species reclassified into the genus *Deleya* appear not to have been compared with *Halomonas elongata*, the sole species of *Halomonas* at

that time. Accordingly, the genera *Deleya* and *Halomonas* were regarded as different genera of the family *Halomonadaceae* (Franzmann *et al.*, 1989) and additional species were assigned to the two genera. The genus *Halovibrio* was created with a single species, *Halovibrio variabilis*, with a vibroid morphology isolated from Great Salt Lake, USA (Fendrich, 1988). Later, these three genera were observed to have similar properties from the results of chemotaxonomic characterization, in which cellular fatty acids, polar lipids and isoprenoid quinones were analysed (Franzmann & Tindall, 1990). The species belonging to the genera *Deleya*, *Halomonas* and *Halovibrio* formed a monophyletic cluster in a phylogenetic tree based on 16S rRNA gene sequences (Dobson *et al.*, 1993; Dobson & Franzmann, 1996). Also, Miller *et al.* (1994) identified the misclassification of *Paracoccus halodenitrificans*,

Abbreviations: ASW, artificial sea water; FAME, fatty acid methyl ester; MA, marine agar; TSA, trypticase soy agar.

The GenBank accession numbers for 16S rDNA sequences of strain YKJ-16^T, *Halomonas canadensis* DSM 6769^T and *Halomonas israelensis* DSM 6768^T are respectively AF211860, AF211861 and AF211862.

the results of 16S rDNA sequence comparison indicating that the species is phylogenetically related to the family *Halomonadaceae*. The genera *Deleya*, *Halomonas* and *Halovibrio* were subsequently unified into a single genus *Halomonas* and the misclassified *Paracoccus halodenitrificans* was transferred to the genus *Halomonas* (Dobson & Franzmann, 1996). There are currently more than 20 validly described *Halomonas* species.

The revised genus *Halomonas* comprises Gram-negative, straight or curved rod-shaped, slightly or moderately halophilic, halotolerant and alkaliphilic bacteria (Berendes *et al.*, 1996; Dobson & Franzmann, 1996). The species assigned to this genus are aerobic but some are facultatively anaerobic in the presence of nitrate (Dobson & Franzmann, 1996). This genus is characterized chemotaxonomically by the presence of major amounts of fatty acids C_{16:1} plus C_{17:0} cyclo, C_{16:0} and C_{18:1} plus C_{19:0} cyclo and ubiquinone 9 (Q-9) as the predominant isoprenoid quinone (Dobson & Franzmann, 1996). This genus is included within the family *Halomonadaceae*, together with two other genera, *Chromohalobacter* and *Zymobacter* (Dobson & Franzmann, 1996).

Recently, a Gram-negative, moderately halophilic bacterial strain, YKJ-16^T, was isolated from jeotgal, a traditional Korean fermented seafood. This organism was considered to be a member of the genus *Halomonas* from the result of 16S rDNA sequence comparison, but its cells were cocci or short rods, unlike most *Halomonas* species. All *Halomonas* species except *Halomonas halodenitrificans* have rod-shaped cells (Dobson & Franzmann, 1996; Kocur, 1984). Accordingly, the aim of this work was to establish the exact taxonomic position of strain YKJ-16^T by additional phenotypic, phylogenetic and genomic characterization. In this study, the type strains of two *Halomonas* species, *Halomonas canadensis* DSM 6769^T and *Halomonas israelensis* DSM 6768^T, the 16S rDNA sequences of which had not been determined at the time of writing, were subjected to 16S rDNA sequencing and then analysed phylogenetically.

METHODS

Bacterial strains and cultural conditions. Strain YKJ-16^T was isolated from jeotgal by the dilution-plating technique on trypticase soy agar (TSA) (BBL) supplemented with (l⁻¹) 24 g NaCl, 7 g MgSO₄ · 7H₂O, 5.3 g MgCl₂ · 6H₂O, 0.7 g KCl and 0.1 g CaCl₂ (artificial sea water; ASW) (pH 7.5). For the investigation of morphological and physiological characteristics, strain YKJ-16^T was cultivated at 30 °C on marine agar (MA) (Difco) or trypticase soy agar (TSA + ASW) and trypticase soy broth (TSB + ASW) supplemented with ASW. Cell mass for the analyses of the cell wall and menaquinones and for DNA extraction was obtained from TSB + ASW culture. The following *Halomonas* species were cultivated in TSB + ASW for DNA extraction: *H. canadensis* DSM 6769^T, *Halomonas cupida* DSM 4740^T, *H. elongata* DSM 2581^T, *H. halodenitrificans* DSM 735^T, *H. israelensis* DSM 6768^T and *Halomonas pacifica* KCTC 2683^T. All strains were cultivated

on a horizontal shaker at 150 r.p.m. and broth cultures were checked for purity before they were harvested by centrifugation. For fatty acid methyl ester (FAME) analysis, strain YKJ-16^T and some reference species were cultivated for 3 d at 30 °C on MA and TSA + ASW. The reference strains included *H. cupida* DSM 4740^T, *H. elongata* DSM 2581^T, *H. halodenitrificans* DSM 735^T and *H. pacifica* KCTC 2683^T.

Morphological and physiological characterization. Cell morphology was examined by phase-contrast microscopy and transmission electron microscopy (TEM). Flagellum type was examined with TEM using cells from exponentially growing culture. The cells were negatively stained with 1% (w/v) phosphotungstic acid and, after air drying, the grids were examined by using a model CM-20 transmission electron microscope (Philips). Catalase activity was determined by bubble production in a 3% hydrogen peroxide solution. Oxidase activity was determined by oxidation of 1% *p*-aminodimethylaniline oxalate. Production of urease was determined as described previously (Cowan & Steel, 1965). Hydrolysis of aesculin, casein, starch, Tween 80, tyrosine and xanthine was determined on MA with concentrations of substrates described previously (Cowan & Steel, 1965; Lanyi, 1987). Tolerance of sodium chloride and growth at various temperatures were tested on TSA + ASW or TSB + ASW. Other physiological tests were performed with the API 20NE system (bioMérieux).

Isolation of DNA. Chromosomal DNA was isolated and purified according to the method described previously (Yoon *et al.*, 1996), with the exception that ribonuclease T1 was used together with ribonuclease A.

Chemotaxonomic characterization. The presence or absence of diaminopimelic acid in the peptidoglycan was determined by the method described by Komagata & Suzuki (1987). Menaquinones were analysed as described previously (Komagata & Suzuki, 1987) using reversed-phase HPLC. For quantitative analysis of cellular fatty acid composition, a loop of cell mass was harvested and FAMES were prepared and identified following the instructions of the Microbial Identification System (MIDI).

Determination of G + C content. The G + C content was determined by the method of Tamaoka & Komagata (1984). DNA was hydrolysed and the resultant nucleotides were analysed by reversed-phase HPLC.

DNA-DNA hybridization. DNA-DNA hybridization was performed between strain YKJ-16^T and the following *Halomonas* strains: *H. cupida* DSM 4740^T, *H. halodenitrificans* DSM 735^T, *H. pacifica* KCTC 2683^T and *H. elongata* DSM 2581^T. DNA-DNA hybridization was performed fluorometrically by the method of Ezaki *et al.* (1989) using photobiotin-labelled DNA probes and microdilution wells.

16S rDNA sequencing and phylogenetic analysis. The 16S rDNA was amplified by PCR using two universal primers as described previously (Yoon *et al.*, 1998). The PCR product was purified by using a QIAquick PCR purification kit (Qiagen). The purified 16S rDNA was sequenced using ABI PRISM BigDye Terminator cycle sequencing ready reaction kit (Applied Biosystems) as recommended by the manufacturer. The purified sequencing reaction mixtures were electrophoresed automatically using an Applied Biosystems model 310 automatic DNA sequencer. The 16S rDNA sequence of strain YKJ-16^T was aligned with 16S rRNA gene sequences of *Halomonas* species and some other related taxa by using the CLUSTAL W software (Thompson *et al.*,

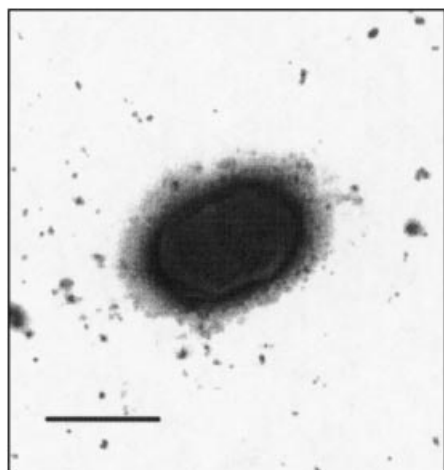


Fig. 1. Transmission electron micrograph of a short, rod-shaped cell of strain YKJ-16^T from exponentially growing culture. Bar, 1 μ m.

1994). 16S rDNA similarity values were calculated from the alignment. Gaps at the 5' and 3' ends of the alignment were omitted from further analyses. Evolutionary distance ma-

trices were calculated by using the algorithm of Jukes & Cantor (1969) with the DNADIST program within the PHYLIP package (Felsenstein, 1993). A phylogenetic tree was constructed by using the neighbour-joining method (Saitou & Nei, 1987) as implemented within the NEIGHBOR program of the same package. The stability of relationships was assessed by a bootstrap analysis of 1000 datasets by using the programs SEQBOOT, DNADIST, NEIGHBOR and CONSENSE of the PHYLIP package.

Nucleotide sequence accession numbers. GenBank and EMBL accession numbers for reference 16S rDNA sequences used in this analysis are given in Fig. 2.

RESULTS

Morphological and physiological characteristics

Strain YKJ-16^T was non-motile. Cells were cocci measuring 0.8–1.2 μ m in diameter or short rods measuring 0.8–1.2 μ m wide and 1.3–1.9 μ m long after 3 d of culture on TSA + ASW and MA. No flagella were found (Fig. 1). Strain YKJ-16^T showed a negative Gram-staining reaction. Colonies were smooth, glistening, circular and low-convex after 3 d of culture. The colour of colonies was cream-yellow on MA and dark yellow on TSA + ASW. No growth occurred on TSA. Strain YKJ-16^T grew on TSA + ASW and MA

Table 1. Differential phenotypic characteristics of strain YKJ-16^T and some *Halomonas* species

Data not obtained in this study were taken from Baumann *et al.* (1983), Kersters & De Ley (1984), Kocur (1984) and Quesada *et al.* (1984). Data in parentheses are those for the type strain from this study or from Baumann *et al.* (1983). All taxa are negative for hydrolysis of starch. +, Positive reaction; –, negative reaction; v, variable reaction; ND, not determined.

Character	Strain YKJ-16 ^T	<i>H. halodenitrificans</i>	<i>H. cupida</i>	<i>H. pacifica</i>
Cell morphology	Cocci or short rods	Cocci or short rods	Straight rods	Straight rods
Flagellation	Absent	Absent	Peritrichous	Peritrichous
Motility	–	–	+	+
Oxidase	+	+	–	+
Catalase	+	+	ND	ND
Reduction of nitrate to nitrite	+	+	v (+)	–
Hydrolysis of				
Aesculin	–	–	+	–
Casein	–	(–)	(–)	(–)
Gelatin	–	–	(–)	(–)
Tween 80	–	–	(–)	(–)
Tyrosine	–	(+)	(+)	(+)
Urea	+	(+)	(+)	(+)
Xanthine	–	(–)	(–)	(–)
Growth at:				
4 °C	+	ND	–	–
40 °C	+	ND	–	+
45 °C	+	ND	–	v (+)
Anaerobic growth	+	+	–	–
G + C content (mol %)	63	64–66	60–63	67–68

Table 2. Cellular fatty acid profiles of strain YKJ-16^T and some *Halomonas* species

Values are percentages of total fatty acids. Fatty acid contents were determined from cells grown on MA and TSA + ASW as shown. Taxa are identified as: 1, strain YKJ-16^T; 2, *H. halodenitrificans* DSM 735^T; 3, *H. cupida* DSM 4740^T; 4, *H. pacifica* KCTC 2683^T; 5, *H. elongata* DSM 2581^T.

Fatty acid	1		2		3		4		5	
	MA	TSA + ASW	MA	TSA + ASW	MA	TSA + ASW	MA	TSA + ASW	MA	TSA + ASW
Saturated fatty acids:										
C _{10:0}	2.4	1.9	2.4	–	3.1	2.8	2.3	2.4	1.9	2.7
C _{10:0} 3OH	0.2	0.2	0.2	–	0.1	0.2	0.2	0.3	0.2	0.9
C _{12:0}	–	–	–	0.6	4.0	3.9	1.5	1.6	3.2	3.6
C _{12:0} 2OH	0.1	0.1	–	–	0.2	0.2	0.1	0.1	0.1	0.1
C _{12:0} 3OH	7.0	5.2	7.2	6.9	8.5	7.1	5.6	5.9	7.1	7.5
C _{14:0}	0.7	1.2	0.2	0.4	0.3	0.2	0.3	0.2	0.2	0.1
C _{15:0}	0.3	0.6	–	0.1	0.1	0.1	0.2	0.2	0.2	0.1
C _{16:0}	18.7	27.0	20.4	24.7	22.0	23.4	25.3	26.0	26.7	24.8
C _{16:0} 3OH	–	–	–	–	–	–	–	–	0.3	0.2
C _{17:0}	0.3	0.2	0.4	0.2	0.5	0.6	0.2	0.4	0.2	0.3
Iso C _{17:0}	–	–	–	–	–	0.1	–	0.3	–	–
C _{17:0} cyclo	1.3	5.1	–	0.2	2.5	0.4	2.9	1.8	5.1	2.4
C _{18:0}	0.2	0.2	0.3	0.2	0.6	0.6	0.3	0.4	0.2	0.3
C _{19:0} cyclo ω8c	7.8	12.9	2.1	0.8	15.5	1.3	18.5	14.3	28.6	12.7
Unsaturated fatty acids:										
C _{17:1} ω8c	–	–	–	–	0.2	0.2	–	–	–	–
C _{18:1} ω7c	41.4	19.4	51.3	43.4	30.7	46.2	29.8	35.3	20.1	38.4
11-Methyl C _{18:1} ω7c	0.4	0.4	–	–	0.3	–	0.5	0.4	0.4	0.1
C _{18:1} ω9c	–	0.2	–	–	–	–	–	–	–	–
C _{20:2} ω6,9c	–	0.2	–	–	0.2	–	0.3	0.2	0.4	0.1
10-Methyl fatty acids:										
C _{19:0}	–	–	–	–	0.3	–	–	–	0.4	0.1
Summed features:*										
3	19.0	24.2	15.7	22.6	10.9	12.1	11.6	9.6	4.7	4.9
7	0.3	0.9	–	–	–	–	–	–	–	–
Unknown fatty acid(s)	–	0.1	–	–	0.3	0.5	0.5	0.6	0.2	0.3

* Summed features represent groups of two or three fatty acids that could not be separated by GLC with the MIDI system. Summed feature 3 contained one or more of C_{16:1} ω7c and/or iso C_{15:0} 2OH. Summed feature 7 contained one or more of an unknown fatty acid of ECL 18-846, C_{19:0} cyclo ω10c and/or C_{19:1} ω6c.

under anaerobic conditions. Strain YKJ-16^T grew optimally in the presence of 1–13% (w/v) NaCl. It grew in the presence of 23% NaCl but not in the presence of 0% or more than 24% NaCl. Strain YKJ-16^T grew at 4 and 45 °C but not at 50 °C. The optimal growth temperature was 30 °C. The optimal pH for the growth was 6.5–7.5 but growth was inhibited at pH 5.0. Strain YKJ-16^T had catalase and oxidase activities. Urea was hydrolysed but no hydrolysis of aesculin, casein, gelatin, starch, Tween 80, tyrosine or xanthine was observed. Nitrate was reduced to nitrite. Indole was not produced and arginine was not deaminated. Acid was not produced from glucose. Physiological properties are summarized in Table 1, together with those of the type strains of *H. halodenitrificans*, *H. cupida* and *H. pacifica*.

Chemotaxonomic characteristics and DNA base composition

Strain YKJ-16^T did not contain any diaminopimelic acid as the diagnostic amino acid in the cell wall peptidoglycan. The predominant isoprenoid quinone found in strain YKJ-16^T was ubiquinone with nine isoprene units (Q-9). The fatty acid patterns of cultures on TSA + ASW and MA were found to be similar for strain YKJ-16^T and some *Halomonas* species, although some fatty acids, notably C_{18:1} ω7c, differed in proportion between the two cultures (Table 2). Strain YKJ-16^T was characterized by having saturated and unsaturated fatty acids and no branched fatty acids. The major fatty acids found in strain YKJ-16^T are C_{18:1} ω7c, C_{16:0}, C_{19:0} cyclo ω8c and C_{16:1} ω7c and/or

halodenitrificans DSM 735^T, *H. pacifica* KCTC 2683^T and *H. elongata* DSM 2581^T.

DISCUSSION

In the course of monitoring micro-organisms present in the Korean fermented seafood jeotgal, we have isolated a large number of bacterial strains and characterized them taxonomically. Gram-positive, endospore-forming bacilli have been observed to predominate, but some Gram-negative bacteria were also found in the jeotgal. Of these isolates, one Gram-negative, coccoid or short rod-shaped strain (YKJ-16^T) attracted our attention and was applied to further taxonomic studies. Phylogenetic analysis based on the 16S rDNA sequence assigns strain YKJ-16^T to the family *Halomonadaceae*, specifically to the genus *Halomonas* (Fig. 2). Strain YKJ-16^T forms a phylogenetic lineage within the evolutionary radiation encompassed by the genus *Halomonas*, particularly within the radiation of a cluster comprising *H. halodenitrificans*, *H. cupida* and *H. pacifica* (Fig. 2). The results obtained from physiological and chemotaxonomic analyses are consistent with the result of the phylogenetic classification. The genus *Zymobacter*, which has been placed in the family *Halomonadaceae* and includes a single species, *Zymobacter palmae*, is the closest phylogenetic neighbour of the genus *Halomonas* (Dobson & Franzmann, 1996). The genera *Halomonas* and *Zymobacter* contain Q-9 as the predominant isoprenoid quinone and have similar fatty acid profiles (Franzmann & Tindall, 1990; Okamoto *et al.*, 1993). However, the two genera are known to be differentiated by the content of fatty acids C_{16:0} and C_{16:1} plus C_{17:0} cyclo (Dobson & Franzmann, 1996). The levels of C_{16:0} in members of the genus *Halomonas* are 15.5–32.0%, whereas the mean level of C_{16:0} in *Zymobacter palmae* is 51% (Franzmann & Tindall, 1990; Okamoto *et al.*, 1993). Members of the genus *Halomonas* contain 7.7–43.1% C_{16:1} plus C_{17:0} cyclo, whereas *Zymobacter palmae* contains less than 0.5% C_{16:1} plus C_{17:0} cyclo (Franzmann & Tindall, 1990; Okamoto *et al.*, 1993). The fatty acid profiles of *Halomonas* species are mirrored by the result of fatty acid analysis of strain YKJ-16^T. Accordingly, strain YKJ-16^T can be differentiated from the genus *Zymobacter* by the composition of diagnostic fatty acids, as represented in Table 2. The genus *Chromohalobacter*, another member of the family *Halomonadaceae*, included only a single species, *Chromohalobacter marismortui*, at the time of writing. *C. marismortui* falls within the phylogenetic radiation comprising the *Halomonas* species, despite the conclusion of Mellado *et al.* (1995) that enough phenotypic differences exist between *C. marismortui* and the *Halomonas-Deleya* complex to support its position as a distinct genus. In our study, *C. marismortui* ATCC 17056^T was found to be most closely related to *H. canadensis* DSM 6769^T and *H. israelensis* DSM 6768^T, with respective levels of 16S rDNA similarity of 98.2 and 96.8%. While this paper was in press, Arahall *et al.* (2001) proposed the

transfer of *H. canadensis* and *H. israelensis* to the genus *Chromohalobacter*. In our opinion, a decision concerning whether *Chromohalobacter* represents a separate genus within the phylogenetic radiation of the genus *Halomonas* or should be included in the genus *Halomonas* should await additional taxonomic data, particularly chemotaxonomic data. Therefore, based on physiological and chemotaxonomic properties and phylogeny, strain YKJ-16^T should be placed in the genus *Halomonas*, despite its cellular morphology, which differs from that of most *Halomonas* species.

Strain YKJ-16^T exhibited the closest phylogenetic affinity to *H. halodenitrificans*, *H. cupida* and *H. pacifica* (Fig. 2). Levels of 16S rDNA similarity of strain YKJ-16^T to *H. cupida* DSM 4740^T, *H. halodenitrificans* ATCC 13511^T and *H. pacifica* DSM 4742^T are respectively 97.0, 97.2 and 97.3%. The cluster containing these species is differentiated from other *Halomonas* species by a high bootstrap resampling value of 99.1%. 16S rDNA similarity values between strain YKJ-16^T and other *Halomonas* species are in the range 93.0–96.3%, indicating that strain YKJ-16^T cannot be assigned to any of these other species (Stackebrandt & Goebel, 1994). Accordingly, comparative taxonomic studies were performed between strain YKJ-16^T and *H. halodenitrificans*, *H. cupida* and *H. pacifica* in order to determine whether strain YKJ-16^T could be considered as a novel species of the genus *Halomonas* or should be assigned to one of these three species. From its morphological and physiological properties, strain YKJ-16^T appears to be most similar to *H. halodenitrificans* (Table 1). However, strain YKJ-16^T and *H. halodenitrificans* DSM 735^T exhibit differences in the proportions of some fatty acids, especially in the proportion of C_{18:1} ω7c on TSA + ASW culture. The level of DNA–DNA relatedness between strain YKJ-16^T and *H. halodenitrificans* DSM 735^T is 13.5%, which is low enough to consider them as different species (Wayne *et al.*, 1987). Strain YKJ-16^T is differentiated morphologically and physiologically from *H. cupida* and *H. pacifica* (Table 1). In particular, the cellular morphology of strain YKJ-16^T is clearly distinguishable from those of the latter two species, which have rod-shaped and peritrichously flagellated cells. Moreover, levels of DNA–DNA relatedness support the position of strain YKJ-16^T as a species different from *H. cupida* and *H. pacifica*. Accordingly, on the basis of differences in some phenotypic characteristics, phylogenetic inference and genetic distinctiveness, strain YKJ-16^T should be placed as a novel species of the genus *Halomonas*, for which the name *Halomonas alimentaria* sp. nov. is proposed.

Description of *Halomonas alimentaria* sp. nov.

Halomonas alimentaria (a.li.men.ta'ri.a. L. adj. *alimentaria* relating to food).

Cells are cocci measuring 0.8–1.2 μm in diameter or short rods measuring 0.8–1.2 μm wide and 1.3–1.9 μm long. Gram-staining reaction is negative. No flagella

are found. Facultatively anaerobic. Colonies are smooth, glistening, circular and low-convex after 3 d of culture. Colour of colonies is cream-yellow on MA and dark yellow on TSA + ASW. Catalase- and oxidase-positive. Urea is hydrolysed. Aesculin, casein, gelatin, starch, Tween 80, tyrosine and xanthine are not hydrolysed. Nitrate is reduced to nitrite. Indole is not produced. Arginine is not deaminated. Acid is not produced from glucose. Optimal NaCl concentration for growth is 1–13% (w/v). Grows in the presence of 23% NaCl. No growth occurs in the presence of 0% or more than 24% NaCl. Growth occurs at 4 and 45 °C but not at 50 °C. Optimal growth temperature is 30 °C. Optimal pH for growth is 6.5–7.5. Growth is inhibited below pH 5.0. The predominant isoprenoid quinone is Q-9. The major fatty acids are C_{18:1}ω7c, C_{16:0}, C_{19:0} cyclo ω8c and C_{16:1}ω7c and/or iso C_{15:0} 2OH. The G + C content is 63 mol% (determined by HPLC). Isolated from the traditional Korean fermented seafood jeotgal.

The type strain is strain YKJ-16^T, which has been deposited at the Korean Culture Center of Microorganisms as KCCM 41042^T and at the Japan Collection of Microorganisms as JCM 10888^T.

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