Ruegeria conchae sp. nov., isolated from the ark clam *Scapharca broughtonii*

Jina Lee,[1]† Tae Woong Whon,[1]† Na-Ri Shin,[1] Seong Woon Roh,[1] Jandi Kim,[1] Seong-Kyu Park,[1] Min-Soo Kim,[1] Kee-Sun Shin,[2] Jung-Sook Lee,[2] Keun Chul Lee,[2] Young-Ok Kim[3] and Jin-Woo Bae[1]

Correspondence
Jin-Woo Bae
baejw@khu.ac.kr

[1]Department of Life and Nanopharmaceutical Sciences and Department of Biology, Kyung Hee University, Seoul 130-701, Republic of Korea

[2]Korean Collection for Type Cultures (KCTC), Biological Resource Center (BRC), Korea Research Institute of Bioscience and Biotechnology (KRIBB), 125 Gwahak-ro, Yuseong-gu, Daejeon 305-806, Republic of Korea

[3]Biotechnology Research Division, National Fisheries Research and Development Institute (NFRDI), Gijang, Busan 619-705, Republic of Korea

A slightly halophilic, Gram-negative, strictly aerobic, non-motile rod, designated TW15^T, was isolated from an ark clam in South Korea. Growth occurred at 10–37 °C, with 1–5 % (w/v) NaCl and at pH 7.0–10.0. Optimal growth occurred at 25–30 °C, with 2 % (w/v) NaCl and at pH 8.0. Strain TW15^T exhibited both oxidase and catalase activities. The major fatty acids of strain TW15^T were summed feature 8 (consisting of $C_{18:1}\omega7c$ and/or $C_{18:1}\omega6c$) and 11-methyl $C_{18:1}\omega7c$. The predominant isoprenoid quinone was ubiquinone-10 (Q-10). The polar lipids of strain TW15^T comprised phosphatidylcholine, phosphatidylglycerol, diphosphatidylglycerol, an unidentified phospholipid, an unidentified aminolipid and five unidentified lipids. Phylogenetic analysis based on 16S rRNA gene sequences indicated that strain TW15^T was most closely related to *Ruegeria lacuscaerulensis* DSM 11314^T (98.0 % 16S rRNA gene sequence similarity). DNA–DNA relatedness with closely related strains was $<52\pm3$ %. The DNA G+C content was 55.7 mol%. On the basis of phenotypic, genotypic and phylogenetic data, strain TW15^T represents a novel species of the genus *Ruegeria*, for which the name *Ruegeria conchae* sp. nov. is proposed. The type strain is TW15^T (=KACC 15115^T =JCM 17315^T).

The genus *Ruegeria* was first introduced by Uchino *et al.* (1998) to accommodate Gram-negative, aerobic, oxidase- and catalase-positive, non-phototrophic bacteria. At the time of writing, eight species of the genus *Ruegeria* have been identified: *Ruegeria lacuscaerulensis*, *R. pomeroyi* (Yi *et al.*, 2007), *R. mobilis* (Muramatsu *et al.*, 2007), *R. atlantica* (Uchino *et al.*, 1998), *R. scottomollicae* (Vandecandelaere *et al.*, 2008), *R. marina* (Huo *et al.*, 2011), *R. faecimaris* (Oh *et al.*, 2011) and *R. halocynthiae* (Kim *et al.*, 2012). *Ruegeria gelatinovorans* and *Ruegeria algicola* have been reclassified as *Thalassobius gelatinovorus* (Arahal *et al.*, 2005) and *Marinovum algicola* (Martens *et al.*, 2006), respectively, and two species of the genus *Silicibacter*, *Silicibacter lacuscaerulensis* and *Silicibacter pomeroyi*, have been transferred to the genus *Ruegeria* (Yi *et al.*, 2007). *R. pelagia* (Lee *et al.*, 2007) has been reported as a later heterotypic synonym of *R. mobilis* (Lai *et al.*, 2010). All species of the genus *Ruegeria* have been isolated from marine environments with the exception of *R. lacuscaerulensis*, which was isolated from a geothermal lake (Petursdottir & Kristjansson, 1997).

Strain TW15^T was isolated from an ark clam (*Scapharca broughtonii*) in the South Sea of Korea. Ark clams inhabit mud flats from the intertidal zone to a depth of 50 m and are farmed in large quantities for food. After being harvested from an ark clam farm, one ark clam was flash-frozen and then preserved at −80 °C until use. Homogenized tissue was suspended in sterilized PBS, serially diluted and cultured on marine agar 2216 (MA; Difco) at 25 °C for 3 days. A pure culture was obtained after at least three subcultivations on MA and was stored as a suspension in 40 % glycerol at −80 °C.

The 16S rRNA gene sequence of strain TW15^T was amplified by colony PCR using PCR Pre-Mix (iNtRon Biotechnology) with two universal bacterial primers:

†These authors contributed equally to this work.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain TW15^T is HQ171439.

Two supplementary figures are available with the online version of this paper.

forward primer 8F (5′-AGAGTTTGATCCTGGCTCAG-3′) and reverse primer 1492R (5′-GGYTACCTTGTTACGA CTT-3′). After purification using a QIAquick PCR Purification kit (Qiagen), sequencing was performed using a BigDye Terminator Cycle Sequencing Ready Reaction kit (Applied Biosystems), according to the manufacturer's instructions. To obtain a nearly full-length 16S rRNA gene sequence, the sequence fragments were assembled in SeqMan (DNASTAR). Comparison of the 16S rRNA gene sequence of strain TW15^T with sequences in the EzTaxon Server (Chun *et al.*, 2007) clearly showed that the isolate was most closely related to members of the genus *Ruegeria* and exhibited 98.0 % 16S rRNA gene sequence similarity to *R. lacuscaerulensis* DSM 11314^T, 97.8 % to *R. atlantica* DSM 5823^T, 97.5 % to *R. halocynthiae* MA1-6^T, 96.9 % to *R. pomeroyi* DSM 15171^T, 96.2 % to *R. faecimaris* HD-28^T, 95.7 % to *R. mobilis* DSM 23403^T, 95.7 % to *R. scottomollicae* CCUG 55858^T and 95.0 % to *R. marina* JCM 16262^T. Multiple sequence alignment of the 16S rRNA gene sequences of strain TW15^T and members of closely related species was carried out using CLUSTAL W (Thompson *et al.*, 1994) and the phylogenetic relationships were determined using MEGA5 (Tamura *et al.*, 2011). The neighbour-joining (Saitou & Nei, 1987), maximum-parsimony (Kluge & Farris, 1969) and maximum-likelihood (Felsenstein, 1981) methods were used to determine phylogenetic distances from 1000, 1000 and 300 random bootstrap replicates, respectively. The results of the phylogenetic analysis showed that strain TW15^T belongs to a cluster with other members of the genus *Ruegeria* (Fig. 1).

Based on the results of phylogenetic analysis, the following strains were used as reference strains for comprehensive analysis: *R. lacuscaerulensis* DSM 11314^T, *R. atlantica* DSM 5823^T, *R. pomeroyi* DSM 15171^T, *R. faecimaris* HD-28^T, obtained from the original isolator (Oh *et al.*, 2011), *R. marina* JCM 16262^T, *R. mobilis* DSM 23403^T, *R. halocynthiae* MA1-6^T, obtained from the original isolator (Kim *et al.*, 2012), and *R. scottomollicae* CCUG 55858^T. Growth at 4, 10, 15, 25, 30, 37, 40, 45 and 55 °C was tested in triplicate in marine broth 2216 (MB; Difco). Growth with 0, 1, 2, 3, 4, 5, 8, 10, 12, 15 and 20 % (w/v) NaCl was determined in triplicate in MB that comprised all of the constituents except NaCl and was supplemented with appropriate concentrations of NaCl. Growth at pH 4.0–12.0 (in increments of one pH unit) was examined in triplicate at 30 °C in MB with the pH adjusted with the following buffers: 10 mM MES (pH 4–6), 10 mM TAPS (pH 7–9) and 10 mM Na_2HPO_4 (pH 10–11). The conditions for growth of strain TW15^T were 10–37 °C, 1–5 % (w/v) NaCl and pH 7.0–10.0 and for optimal growth were 25–30 °C, 2 % (w/v) NaCl and pH 8.0. Based on the requirement of NaCl for growth, strain TW15^T was defined as a slight halophile (Ventosa & Nieto, 1995).

Unless stated otherwise, all tests used to characterize strain TW15^T were performed under optimal conditions. Morphological, physiological and biochemical analyses were conducted after cultivation for 72 h at 30 °C in MB or on MA. Gram-staining was carried out using a Gram-staining kit (bioMérieux), according to the manufacturer's instructions, and cells were observed by light microscopy (Eclipse 50*i*; Nikon). Motility was examined according to the method of Tittsler & Sandholzer (1936) on semi-solid agar medium consisting of 0.3 % beef extract, 1 % pancreatic digest of casein, 0.5 % sodium chloride and

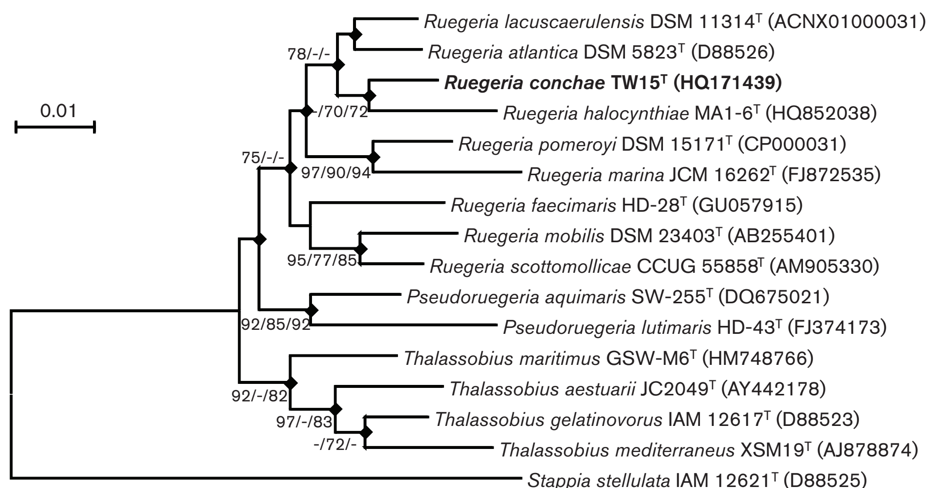

Fig. 1. Consensus 16S rRNA gene sequence phylogenetic tree constructed using the neighbour-joining, maximum-parsimony and maximum-likelihood algorithms, showing the position of strain TW15^T in the genus *Ruegeria*. Bootstrap values (⩾70 %) based on 1000, 1000 and 300 replicates for the neighbour-joining, maximum-parsimony and maximum-likelihood algorithms, respectively, are shown at branch nodes. Filled diamonds indicate that the corresponding nodes were recovered with all three algorithms. *Stappia stellulata* IAM 12621^T was used as an outgroup. Bar, 0.01 substitutions per nucleotide.

0.4 % agar. Cell morphology was observed by light microscopy and energy-filtering transmission electron microscopy (Libra 120; Carl Zeiss) (Fig. S1, available in IJSEM Online). For transmission electron micrography, a single colony of the isolate was suspended in 500 μl sterile PBS buffer. Copper grids with 200-mesh carbon-coated Formvar were floated on a droplet of the suspension, negatively stained with 2 % uranyl acetate for 10 s, washed with deionized water two or three times and air-dried. Catalase activity was determined by bubble production in 3 % (v/v) hydrogen peroxide. Oxidase activity was determined using 1 % (w/v) tetramethyl-*p*-phenylenediamine (bioMérieux). Hydrolysis of casein and starch was examined on MA supplemented with 0.5 % (w/v) soluble starch (Junsei) or skim milk agar (Difco), respectively. For the investigation of susceptibility to antibiotics, paper discs were impregnated with antibiotics as follows (μg per disc unless otherwise stated): ampicillin (10), chloramphenicol (100), gentamicin (30), kanamycin (30), novobiocin (5), penicillin G (20 U), polymyxin B sulfate (100 U), streptomycin (50) and tetracycline (30). Enzyme activities were determined using the API ZYM and API 20 NE systems (bioMérieux), according to the manufacturer's instructions. Sole carbon source assimilation was tested using the API 50 CH system with AUX medium (bioMérieux) containing 2 % NaCl, according to the manufacturer's instructions. Acid production from carbohydrate was determined using the API 50 CHB/E system (bioMérieux), according to the manufacturer's instructions. Strain TW15^T was a catalase- and oxidase-positive, non-motile, Gram-negative rod (0.3–0.5 μm long and 0.5–1.0 μm wide). Strain TW15^T did not hydrolyse casein or starch. Strain TW15^T was sensitive to ampicillin, chloramphenicol, kanamycin, novobiocin, penicillin G, polymyxin B sulfate, streptomycin and tetracycline, but resistant to gentamicin. The biochemical characteristics of strain TW15^T distinguished it from the members of the genus *Ruegeria* (Table 1).

Genomic DNA of strain TW15^T and the reference strains was extracted for genotypic analysis as described by Rochelle *et al.* (1992). The DNA G + C content of strain TW15^T was determined by whole-genome sequencing using 454 GS FLX Titanium pyrosequencing (Roche). To determine the genetic distances between strain TW15^T and the reference strains, DNA–DNA hybridization was carried out using a genome-spotted microarray with reciprocal analysis (Bae *et al.*, 2005; Chang *et al.*, 2008). The DNA G + C content of strain TW15^T was 55.7 mol% (Lee *et al.*, 2011), which is in the range for the genus *Ruegeria*. The DNA–DNA relatedness of strain TW15^T with *R. lacuscaerulensis* DSM 11314^T, *R. halocynthiae* MA1-6^T and *R. atlantica* DSM 5823^T was 52 ± 3, 37 ± 3 and 48 ± 3 %, respectively. These values are below the threshold of 70 % (Wayne *et al.*, 1987), which indicated that strain TW15^T represented a distinct genospecies.

For the analysis of cellular fatty acids, strains TW15^T, *R. lacuscaerulensis* DSM 11314^T, *R. halocynthiae* MA1-6^T and *R. atlantica* DSM 5823^T were cultured at 30 °C on MA for 3 days. The physiological ages of strain TW15^T and the reference strains were standardized to the exponential phase. The cellular fatty acids were saponified, methylated and extracted according to the protocol of the Sherlock Microbial Identification System (MIDI, 1999). The extracted cellular fatty acids were analysed by GC (Hewlett Packard 6890) and identified using the Microbial Identification software Sherlock version 4.0 (Sasser, 1990) and the TSBA40 database. The isoprenoid quinone composition of strain TW15^T was analysed by TLC according to the method of Hiraishi *et al.* (1996). The polar lipids of strain TW15^T were extracted using the procedure described by Xin *et al.* (2000) and separated using two-dimensional TLC on 20 × 20 cm silica gel glass plates (Merck). The two solvents used for separation were chloroform/methanol/water (65 : 25 : 4, by vol.) for the first dimension and chloroform/methanol/acetic acid/water (80 : 12 : 15 : 4, by vol.) for the second dimension. To identify the phospholipids, phosphatidylglycerol, phosphatidylcholine, phosphoethanolamine and diphosphatidylglycerol were obtained from Sigma. The reference compounds and the phospholipids of strain TW15^T were separated using one-dimensional TLC on 20 × 20 cm silica gel glass plates with chloroform/acetic acid/methanol/water (50 : 6 : 6 : 1, by vol.) and detected with Zinzadze reagent. The major cellular fatty acids (>10 % of the total) of strain TW15^T were summed feature 8 (consisting of $C_{18:1}\omega7c$ and/or $C_{18:1}\omega6c$) and 11-methyl $C_{18:1}\omega7c$. The fatty acid compositions of strain TW15^T, *R. lacuscaerulensis* DSM 11314^T, *R. halocynthiae* MA1-6^T and *R. atlantica* DSM 5823^T are given in Table 2. The predominant quinone of strain TW15^T was ubiquinone-10 (Q-10), which is in accordance with the genus *Ruegeria*. The polar lipid profile of strain TW15^T consisted of an unidentified aminolipid, phosphatidylcholine, phosphatidylglycerol, diphosphatidylglycerol, an unidentified phospholipid and five unidentified lipids (Fig. S2). Glycolipids were not detected. Phosphatidylcholine and phosphatidylglycerol have also been detected in other species of the genus *Ruegeria* (Kim *et al.*, 2012; Oh *et al.*, 2011). Taking into account the differences in its polar lipid composition, such as diphosphatidylglycerol, strain TW15^T could be distinguished from other members of the genus *Ruegeria*.

The results of the phenotypic, genotypic and phylogenetic analysis indicate that strain TW15^T represents a novel species of the genus *Ruegeria*, for which the name *Ruegeria conchae* sp. nov. is proposed.

Description of *Ruegeria conchae* sp. nov.

Ruegeria conchae (con′chae. L. gen. n. *conchae* of/from a bivalve, shellfish).

Cells are slightly halophilic, strictly aerobic, Gram-negative, non-motile rods (0.3–0.5 μm long and 0.5–1.0 μm wide). Colonies are yellow, circular with entire margins and 1.0–2.5 mm in diameter after incubation for 3 days on MA at

Table 1. Differential characteristics of strain TW15^T and members of the genus *Ruegeria*

Strains: 1, *Ruegeria conchae* sp. nov. TW15^T (this study); 2, *R. lacuscaerulensis* DSM 11314^T (Petursdottir & Kristjansson, 1997); 3, *R. atlantica* DSM 5823^T (Uchino *et al.*, 1998); 4, *R. mobilis* DSM 23403^T (Muramatsu *et al.*, 2007); 5, *R. pomeroyi* DSM 15171^T (González *et al.*, 2003); 6, *R. scottomollicae* CCUG 55858^T (Vandecandelaere *et al.*, 2008); 7, *R. faecimaris* HD-28^T (Oh *et al.*, 2011); 8, *R. marina* JCM 16262^T (Huo *et al.*, 2011); 9, *R. halocynthiae* MA1-6^T (Kim *et al.*, 2012). Data are from the sources listed, except where marked. +, Positive; w, weakly positive; −, negative; ND, no data available.

Characteristic	1	2	3	4	5	6	7	8	9
Motility	−	−	−	+	+	+	−	−	−
Growth at:									
4 °C	−	−	−*	−	−	+	w	−	−
40 °C	−	+	−*	−	+	w	−	+	−
Optimum growth temperature (°C)	25–30	45	20–30*	25–30	30*	20*	30	35–37	30
pH range	7–10	6.5–8.5†	6–11†	5–11†	ND†	5–9	5.0–9.5	6.5–9.0	5.5–10.5
NaCl range (%)	1–5	1.5–7†	3–10†	0–10†	1.5–7†	1–15	0.5–7	0–7.5	0.5–6
DNA G+C content (mol%)	55.7	66	55–58	58.5	68	61	57.9	63.5	58.6
Hydrolysis of:‡									
Aesculin ferric citrate	w	w	+	w	w	w	w	w	+
Gelatin	−	−	−	−	+	−	+	−	w
Acid production from:‡									
Glycerol	−	−	w	−	−	+	−	−	−
Erythritol	+	−	−	−	−	+	w	−	−
D-Arabinose	−	−	−	+	−	−	−	−	−
L-Arabinose	−	−	−	+	−	−	−	−	−
D-Ribose	−	−	−	−	−	−	−	−	+
D-Xylose	−	−	−	w	+	−	−	−	−
L-Xylose	−	−	−	−	+	−	−	−	−
D-Adonitol	−	−	−	−	+	+	−	−	−
Methyl β-D-xyloside	−	−	−	−	+	+	+	+	−
D-Galactose	−	−	−	−	−	+	+	−	−
D-Glucose	−	−	−	w	w	−	−	+	−
D-Fructose	+	−	−	+	+	−	−	−	w
D-Mannose	+	−	−	−	−	−	−	−	+
L-Sorbose	−	−	−	−	−	−	−	−	w
Dulcitol	−	+	+	−	−	−	−	−	−
Inositol	+	−	w	−	+	−	−	−	−
D-Mannitol	+	−	w	−	−	+	−	−	−
D-Sorbitol	−	−	w	−	−	+	−	+	−
Methyl α-D-mannoside	−	+	−	−	−	−	+	−	−
Methyl α-D-glucoside	+	w	−	−	−	+	−	−	−
N-Acetylglucosamine	−	−	−	−	−	+	+	−	−
Amygdalin	−	−	+	−	−	−	−	−	−
Arbutin	+	−	−	−	w	+	−	−	−
Aesculin	+	+	+	+	w	+	+	−	+
Salicin	+	−	−	−	−	+	−	−	−
Cellobiose	−	w	−	+	−	−	−	−	−
Maltose	+	+	−	−	−	−	−	−	−
Lactose	+	−	−	−	−	+	−	−	−
Sucrose	−	+	−	−	−	−	−	−	−
Trehalose	−	+	−	−	−	−	−	−	−
Melezitose	−	+	−	−	−	−	+	−	−
Raffinose	−	−	w	−	−	−	−	−	−
Glycogen	−	−	+	+	−	w	+	−	−
Xylitol	+	+	+	−	−	+	+	−	−
Gentiobiose	+	−	−	+	−	+	−	−	−
D-Lyxose	−	+	−	−	−	−	−	−	−
D-Tagatose	−	+	−	−	+	−	w	+	+
D-Fucose	−	+	−	−	−	w	−	−	−

Table 1. cont.

Characteristic	1	2	3	4	5	6	7	8	9
D-Arabitol	−	+	−	−	−	−	−	−	−
Gluconate	+	−	−	−	−	−	−	−	−
5-Ketogluconate	+	−	−	−	−	+	+	+	+
Enzyme activities:‡									
Esterase (C4)	+	+	+	+	+	+	+	+	−
Valine arylamidase	−	−	−	w	−	−	w	w	−
Acid phosphatase	+	+	−	w	−	w	+	w	w
Naphthol-AS-BI-phosphohydrolase	w	w	w	+	−	w	+	w	w
β-Galactosidase	w	+	−	−	−	−	w	−	−

*Data from Oh *et al.* (2011).

†Data from Muramatsu *et al.* (2007).

‡Data for the reference strains (*R. lacuscaerulensis* DSM 11314T, *R. atlantica* DSM 5823T, *R. mobilis* DSM 23403T, *R. pomeroyi* DSM 15171T, *R. scottomollicae* CCUG 55858T, *R. faecimaris* HD-28T, *R. marina* JCM 16262T and *R. halocynthiae* MA1-6T) were taken from this study.

Table 2. Cellular fatty acid compositions of strain TW15T and its closest phylogenetic neighbours

Strains: 1, *Ruegeria conchae* sp. nov. TW15T; 2, *R. lacuscaerulensis* DSM 11314T; 3, *R. atlantica* DSM 5823T; 4, *R. halocynthiae* MA1-6T. All data were taken from this study. tr, Trace (<0.5 %); −, not detected.

Fatty acid (%)	1	2	3	4
Straight-chain				
$C_{10:0}$	3.2	3.06	2.73	3.01
$C_{11:0}$	−	tr	−	−
$C_{12:0}$	3.64	2.65	3.17	2.95
$C_{14:0}$	−	−	tr	−
$C_{16:0}$	5.52	3.19	11.48	5.97
$C_{17:0}$	tr	tr	−	tr
$C_{18:0}$	2.7	4.83	3.31	2.43
Unsaturated				
$C_{14:1}\omega5c$	−	tr	−	tr
$C_{17:1}\omega8c$	0.56	−	−	−
$C_{18:1}\omega9c$	0.53	−	−	−
Hydroxy				
$C_{10:0}$ 3-OH	−	1.4	tr	tr
$C_{12:0}$ 3-OH	5.21	4.39	5.26	5.6
$C_{16:0}$ 2-OH	5.47	−	3.45	9.29
iso-$C_{17:0}$ 3-OH	−	tr	tr	−
$C_{18:1}$ 2-OH	0.5	−	−	tr
anteiso-$C_{15:0}$	0.25	−	−	−
$C_{16:0}$ N alcohol	tr	tr	tr	tr
11-Methyl $C_{18:1}\omega7c$	15.23	2.56	8.92	8.91
Summed features*				
3	−	−	0.51	tr
8	56.33	75.4	59.72	60.53

*Summed features represent two or three fatty acids that cannot be separated by the Microbial Identification System. Summed feature 3 consisted of $C_{16:1}\omega7c$ and/or iso-C_{15} 2-OH. Summed feature 8 consisted of $C_{18:1}\omega7c$ and/or $C_{18:1}\omega6c$.

30 °C. Growth occurs at 10–37 °C (optimum 25–30 °C), with 1–5 % (w/v) NaCl (optimum 2 %) and at pH 7.0–10.0 (optimum pH 8.0). Starch and casein are not hydrolysed. Positive for catalase and oxidase. Susceptible to ampicillin, chloramphenicol, kanamycin, novobiocin, penicillin G, polymyxin B sulfate, streptomycin and tetracycline, but resistant to gentamicin. With API ZYM and API 20 NE, positive for alkaline phosphatase, acid phosphatase, esterase (C4), esterase lipase (C8) and leucine arylamidase, weakly positive for hydrolysis of aesculin ferric citrate, naphthol-AS-BI-phosphohydrolase, β-galactosidase and α-glucosidase, but negative for lipase (C14), valine arylamidase, cystine arylamidase, trypsin, α-chymotrypsin, α-galactosidase, β-glucuronidase, *N*-acetyl-β-glucosaminidase, α-mannosidase, α-fucosidase, reduction of nitrates to nitrites, production of indole, fermentation of D-glucose, L-arginine dihydrolase, urease and protease. With API 50 CH, assimilates glycerol, D-ribose, D-xylose, D-glucose, D-mannose, inositol, maltose, trehalose, melezitose, D-arabitol and gluconate, but not erythritol, D-arabinose, L-arabinose, L-xylose, D-adonitol, methyl β-D-xyloside, D-galactose, D-fructose, L-sorbose, L-rhamnose, dulcitol, D-mannitol, D-sorbitol, methyl α-D-mannoside, methyl α-D-glucoside, *N*-acetylglucosamine, amygdalin, arbutin, aesculin, salicin, cellobiose, lactose, melibiose, sucrose, inulin, raffinose, glycogen, xylitol, gentiobiose, turanose, D-lyxose, D-tagatose, D-fucose, L-fucose, L-arabitol, 2-ketogluconate or 5-ketogluconate. With API 50 CHB/E, produces acid from erythritol, D-fructose, D-mannose, inositol, D-mannitol, methyl α-D-glucoside, arbutin, aesculin, salicin, maltose, lactose, xylitol, gentiobiose, gluconate and 5-ketogluconate, but not from glycerol, D-arabinose, L-arabinose, D-ribose, D-xylose, L-xylose, D-adonitol, methyl β-D-xyloside, D-galactose, D-glucose, L-sorbose, L-rhamnose, dulcitol, D-sorbitol, methyl-α-D-mannoside, *N*-acetylglucosamine, amygdalin, cellobiose, melibiose, sucrose, trehalose, inulin, melezitose,

raffinose, starch, glycogen, turanose, D-lyxose, D-tagatose, D-fucose, L-fucose, D-arabitol, L-arabitol or 2-ketogluconate. The major fatty acids are summed feature 8 (consisting of $C_{18:1}\omega7c$ and/or $C_{18:1}\omega6c$) and 11-methyl $C_{18:1}\omega7c$. The predominant ubiquinone is Q-10. The polar lipids are an unidentified aminolipid, phosphatidylcholine, phosphatidylglycerol, diphosphatidylglycerol, an unidentified phospholipid and unidentified lipids.

The type strain is $TW15^T$ (=KACC 15115^T =JCM 17315^T), which was isolated from an ark clam from the South Sea of Korea. The DNA G+C content of the type strain is 55.7 mol%.

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