Rheinheimera nanhaiensis sp. nov., isolated from marine sediments, and emended description of the genus *Rheinheimera* Brettar *et al.* 2002 emend. Merchant *et al.* 2007

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A Gram-negative, facultatively aerobic, oxidase- and catalase-positive, rod-shaped bacterium, designated strain E407-8^T, was isolated from a sediment sample from the South China Sea. Phylogenetic analysis of the 16S rRNA gene sequence revealed that strain E407-8^T was affiliated with the genus *Rheinheimera*, sharing the highest sequence similarity with *Rheinheimera pacifica* KMM 1406^T (97.5 %) and *Rheinheimera aquimaris* SW-353^T (97.4 %) and showing less than 97 % sequence similarity to the type strains of other recognized *Rheinheimera* species. Levels of DNA–DNA relatedness of strain E407-8^T to *R. pacifica* DSM 17616^T and *R. aquimaris* JCM 14331^T were 25.2 % (25.3 % in the duplicate measurement) and 9.4 % (6.5 %), respectively. The bacterium could grow at 10–48 °C (optimum 37 °C) and in the presence of 0–8 % (w/v) NaCl (optimum 0.5–2.5 %). The major cellular fatty acids of strain E407-8^T were summed feature 3 (C_{16:1}ω7c and/or iso-C_{15:0} 2-OH), C_{17:1}ω8c, C_{16:0} and C_{18:1}ω7c. The predominant respiratory quinone was ubiquinone Q-8. The DNA G + C content was 51.0 mol%. Based on the results of our polyphasic taxonomic study, strain E407-8^T represents a novel species in the genus *Rheinheimera*, for which the name *Rheinheimera nanhaiensis* sp. nov. is proposed. The type strain is E407-8^T (=CCTCC AB 209089^T =KACC 14030^T). An emended description of the genus *Rheinheimera* Brettar *et al.* 2002 emend. Merchant *et al.* 2007 is also proposed.

The genus *Rheinheimera*, belonging to the family *Chromatiaceae* in the class *Gammaproteobacteria*, was originally proposed by Brettar *et al.* (2002) for a small group of closely related Gram-negative, flagellated, blue-coloured bacterial strains isolated from seawater samples from different depths of the central Baltic Sea. At the time of writing, the genus *Rheinheimera* contains eight recognized species, *Rheinheimera baltica* (the type species; Brettar *et al.*, 2002), *R. pacifica* (Romanenko *et al.*, 2003), *R. perlucida* (Brettar *et al.*, 2006), *R. aquimaris* (Yoon *et al.*, 2007), *R. chironomi* (Halpern *et al.*, 2007), *R. texasensis* (Merchant *et al.*, 2007), *R. soli* (Ryu *et al.*, 2008) and *R.*

tangshanensis (Zhang *et al.*, 2008). Most *Rheinheimera* species have originated from aquatic (marine or fresh-water) environments, with the exceptions of *R. soli* from a playground soil sample and *R. tangshanensis* from rice-plant root samples, indicating that members of this genus may be widespread in various environments (Ryu *et al.*, 2008; Zhang *et al.*, 2008).

In our recent study on the diversity of protease-producing marine bacteria (Zhou *et al.*, 2009), a protease-producing *Rheinheimera*-like strain, designated E407-8^T, was isolated from a deep-sea sediment sample from the South China Sea. In this paper, based on a polyphasic taxonomic study, strain E407-8^T is proposed to represent a novel *Rheinheimera* species.

A marine sediment sample was collected from station E407 (18° 29.810' N 112° 0.017' E) at a water depth of 1800 m using a core sampler, during the South China Sea Open

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The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain E407-8^T is FJ169968.

A supplementary figure is available with the online version of this paper.

Cruise of R/V *Shiyan 3* in August 2007. Strain E407-8^T was isolated from the sediment sample using the dilution plating technique on a screening medium containing 0.2 % yeast extract (Oxoid), 0.3 % casein, 0.5 % gelatin, 1.5 % agar and artificial seawater (pH 7.0) at 15 °C (Zhou *et al.*, 2009). Strain E407-8^T was able to form clear hydrolytic zones on this medium. The artificial seawater was prepared with synthetic sea salts (Marine Life Reef Salt, QingDao, China) and contained the following approximate ion concentrations (g l⁻¹): Na⁺, 9.1; K⁺, 0.35; Mg²⁺, 1.25; Ca²⁺, 0.43; Sr²⁺, 0.0095; Cl⁻, 17.1; SO₄²⁻, 2.4; Br⁻, 0.06; F⁻, 0.001; HCO₃⁻, 0.145. The isolated strain E407-8^T was routinely cultivated on a solid medium containing 0.5 % tryptone (Oxoid), 0.1 % yeast extract (Oxoid), 1.5 % agar and artificial seawater (hereafter referred to as marine agar) or in a liquid medium containing 0.5 % tryptone, 0.1 % yeast extract and artificial seawater (hereafter referred to as marine broth) at 30 °C and stored at -80 °C in marine broth supplemented with 20 % glycerol.

Cell morphology was observed by transmission electron microscopy (JEM-100CX II) using cells grown in marine broth at 15 or 30 °C for 24 h. The cells were stained with 1 % phosphotungstic acid. Gram-staining was performed using Hucker's staining method (Murray *et al.*, 1994). Growth at 10, 15, 20, 25, 30, 35, 37, 40, 42, 45, 48 and 50 °C was measured in marine broth. Growth at pH 5.0–11.0 (at intervals of 0.5 pH units) was determined in a medium containing 0.5 % tryptone, 0.1 % yeast extract and distilled water at 30 °C. The pH of the medium was adjusted with 1 M NaOH or HCl. The NaCl concentration range (0–9 %, w/v, in increments of 0.5 %) for growth was tested at 30 °C in the same medium used for pH tests with different NaCl concentrations. Anaerobic growth was checked in an anaerobic chamber (Forma 1029; Thermo Electron) in marine broth 2216 (Difco) at 28 °C for 15 days.

Catalase activity was assessed by bubble formation in 3 % (v/v) H₂O₂ solution. Oxidase activity was determined with commercial oxidase test strips (Merck). DNase activity was detected on DNase test agar (Oxoid) prepared using artificial seawater. Hydrolysis of starch, casein and Tweens 40 and 80 was determined on marine agar at 30 °C according to standard methods (Smibert & Krieg, 1994). The ability to utilize various carbohydrates including D-glucose, N-acetyl-D-glucosamine, sucrose, maltose, citrate, xylose, mannose, trehalose, cellobiose, galactose, raffinose, L-arabinose and lactose as sole carbon and energy sources for growth was determined in a basal medium containing 0.054 % NH₄Cl, 3 % NaCl, 0.3 % MgCl₂·6H₂O, 0.2 % K₂SO₄, 0.02 % K₂HPO₄, 0.001 % CaCl₂, 0.0006 % FeCl₃·6H₂O, 0.0005 % Na₂MoO₄·7H₂O, 0.0004 % CuCl₂·2H₂O, 0.6 % Tris and distilled water supplemented with 1 % carbohydrate as described by Shieh *et al.* (2004). Enzyme activities and other physiological and biochemical traits were determined by using API ZYM, API 20E and API 20NE strips (bioMérieux) according to the manufacturer's instructions. Cells for inoculation of API ZYM, API 20E and API 20NE strips were suspended in artificial seawater;

the API ZYM strip was read after 24 h and the API 20E and API 20NE strips were read after 72 h incubation at 30 °C. Antibiotic susceptibility tests were performed using the disc-diffusion method on marine agar and growth inhibition zones were observed after 3 days of incubation at 30 °C. *R. aquimaris* JCM 14331^T obtained from the Japan Collection of Microorganisms and *R. pacifica* DSM 17616^T obtained from the Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH (DSMZ) were used as reference strains in all the above tests.

Genomic DNA of strain E407-8^T was extracted using a bacterial genomic DNA isolation kit (BioTeke). The 16S rRNA gene was amplified by PCR from genomic DNA with primers 27F and 1492R (Lane, 1991). PCR products were purified using the E.Z.N.A. gel extraction kit (Omega Bio-Tek). Purified PCR products were ligated into pMD 18-T vector (TaKaRa) and sequenced at Biosune Inc. (Shanghai, China) using an automated DNA sequencer (Applied Biosystems model 3730). The obtained 16S rRNA gene sequence of strain E407-8^T was compared with those deposited in GenBank using the BLAST program (<http://blast.ncbi.nlm.nih.gov/Blast.cgi>) and further aligned manually with sequences of related taxa retrieved from GenBank using the MEGA software version 4.0 (Tamura *et al.*, 2007). Phylogenetic trees were constructed by the same software, using the neighbour-joining (Saitou & Nei, 1987) and maximum-parsimony (Fitch, 1971) methods and using bootstrap analyses (1000 replications) (Felsenstein, 1985). Evolutionary distances for the neighbour-joining method were computed using the Jukes & Cantor (1969) model. DNA–DNA hybridization experiments between strain E407-8^T and the two closely related type strains *R. aquimaris* JCM 14331^T and *R. pacifica* DSM 17616^T were conducted at the DSMZ by using the methods of De Ley *et al.* (1970) as modified by Huß *et al.* (1983).

The genomic DNA G+C content was determined using HPLC (Mesbah *et al.*, 1989). Respiratory lipoquinone analyses were carried out by the Identification Service of the DSMZ and Dr B. J. Tindall. Cellular fatty acid analyses, from cells grown in marine broth at 30 °C for 24 h, were performed according to the instructions of the Sherlock Microbial Identification System (MIDI) at the Institute of Microbiology and Epidemiology, Academy of Military Medical Sciences, Beijing, PR China.

Phylogenetic analysis based on the 16S rRNA gene sequence revealed that strain E407-8^T was affiliated with the genus *Rheinheimera*. The strain shared the highest 16S rRNA gene sequence similarity with *R. pacifica* KMM 1406^T (97.5 %) and *R. aquimaris* SW-353^T (97.4 %) and 94.7–96.7 % similarity with type strains of other recognized *Rheinheimera* species. The neighbour-joining phylogenetic tree showed that strain E407-8^T clustered with members of the genus *Rheinheimera* and formed an intragenus branch with *R. pacifica* KMM 1406^T with 80 % bootstrap support (Fig. 1). The maximum-parsimony phylogenetic tree showed a similar topology (Supplementary Fig. S1,

Fig. 1. Neighbour-joining phylogenetic tree based on 16S rRNA gene sequences showing the phylogenetic positions of strain E407-8^T, members of other *Rheinheimera* species and representatives of some other related genera. Bootstrap percentages (from 1000 replicates) are indicated at nodes. Bar, 0.02 substitutions per nucleotide position.

available in IJSEM Online). DNA–DNA relatedness between strain E407-8^T and *R. pacifica* DSM 17616^T and *R. aquimaris* JCM 14331^T was 25.2 % (25.3 % in the duplicate measurement) and 9.4 % (6.5 %), respectively. Since strains sharing less than 70 % DNA–DNA relatedness

or less than 97 % 16S rRNA gene sequence similarity are generally considered to belong to separate species (Wayne *et al.*, 1987; Stackebrandt & Goebel, 1994; Stackebrandt *et al.*, 2002), the above genotypic data indicated that strain E407-8^T represents a novel species in the genus *Rheinheimera*.

The DNA G + C content of strain E407-8^T was 51.0 mol%, which was close to the highest G + C content reported for *Rheinheimera* species (50.5 mol%; Yoon *et al.*, 2007). The major fatty acids (>5 %) of strain E407-8^T were summed feature 3 (C_{16:1}ω7c and/or iso-C_{15:0} 2-OH; 21.1 %), C_{17:1}ω8c (14.5 %), C_{16:0} (11.9 %), C_{18:1}ω7c (10.0 %) and C_{17:0} (8.6 %). The fatty acid profile of strain E407-8^T was generally similar to those of other known *Rheinheimera* species, which are characterized by unsaturated fatty acids including C_{16:1}ω7c, C_{17:1}ω8c and C_{18:1}ω7c and the straight-chain fatty acid C_{16:0} as major fatty acid components (Table 1). The dominant respiratory quinone of strain E407-8^T was ubiquinone Q-8 (98 %); minor amounts of Q-7 (2 %) was also detected.

Cells of strain E407-8^T were found to be able to produce prosthecae (Fig. 2), a cellular substructure formed by cytoplasmic extrusion from the cell wall and considered to help bacteria to improve nutrient uptake efficiency by

Table 1. Fatty acid compositions of strain E407-8^T and type strains of other *Rheinheimera* species

Strains: 1, E407-8^T; 2, *R. pacifica* DSM 17616^T; 3, *R. aquimaris* JCM 14331^T; 4, *R. soli* BD-d46^T (data from Ryu *et al.*, 2008); 5, *R. chironomi* K19414^T (Halpern *et al.*, 2007); 6, *R. tangshanensis* JA3-B52^T (Zhang *et al.*, 2008); 7, *R. baltica* OSBAC1^T (Brettar *et al.*, 2002); 8, *R. texasensis* A62-14B^T (Merchant *et al.*, 2007); 9, *R. perlucida* BA131^T (Brettar *et al.*, 2006). Values are percentages of total fatty acids; –, not detected or not reported.

Fatty acid	1	2		3		4	5	6	7	8	9
		This study	Romanenko <i>et al.</i> (2003)	This study	Yoon <i>et al.</i> (2007)						
C _{10:0}	0.2	0.1	—	0.1	—	3.7	1.2	2.2	—	—	—
C _{11:0} 3-OH	2.1	0.4	—	1.5	1.7	4.6	5.5	3.3	—	—	1.2
C _{12:0}	1.3	2.8	—	2.1	3.1	0.5	1.1	—	1.4	2.0	1.1
C _{12:0} 3-OH	3.9	4.7	—	3.6	5.6	9.5	8.5	7.2	5.3	12.8	3.1
C _{13:0} 3-OH	2.7 ^{a*}	1.0 ^a	—	2.1 ^a	3.0 ^a	1.3 ^a	1.9 ^a	—	1.0	—	0.7
C _{14:0}	0.7	1.4	—	0.9	2.1	1.4	0.9	—	2.3	—	1.8
C _{14:0} 3-OH	2.0 ^b	3.8 ^b	—	2.1 ^b	3.4 ^b	0.3 ^b	0.3 ^b	—	1.6	—	0.5
C _{15:0}	2.8	1.0	2.4	3.2	2.7	6.0	6.9	2.1	1.7	—	3.0
C _{15:1} ω8c	4.5	1.3	3.3	3.8	1.4	2.9	2.8	3.0	1.7	—	2.0
C _{16:0}	11.9	19.9	19.1	17.7	25.1	10.8	14.8	7.8	19.5	19.0	17.1
iso-C _{16:0}	3.7	1.5	3.7	2.1	0.7	0.8	1.5	—	0.5	—	1.2
C _{16:1} ω7c	21.1 ^c	28.5 ^c	—	23.4 ^c	13.8 ^c	24.0 ^c	25.8 ^c	33.7	33.6	38.6	33.4
C _{16:1} ω9c	0.6	2.1	25.5	2.1	2.3	0.7	—	—	1.7	—	—
C _{17:0}	8.6	4.1	8.1	8.1	9.3	4.2	5.8	—	3.3	—	3.4
C _{17:1} ω8c	14.5	5.6	11.7	11.6	9.7	12.5	7.6	15.2	5.7	3.8	13.9
C _{18:0}	0.6	1.5	—	0.8	1.5	0.4	0.3	—	0.5	2.0	0.4
iso-C _{18:0}	1.2	0.6	1.3	0.6	—	—	—	—	—	—	—
C _{18:1} ω7c	10.0	15.9	15.7	8.1	11.0	7.1	6.7	13.4	15.9	7.7	12.4

*Reported as: a, summed feature 1 (C_{13:0} 3-OH and/or iso-C_{15:1} H); b, summed feature 2 (C_{14:0} 3-OH and/or iso-C_{16:1} I); c, summed feature 3 (C_{16:1}ω7c and/or iso-C_{15:0} 2-OH). Summed features are groups of two or three fatty acids that cannot be separated by GLC with the MIDI System.

Fig. 2. Transmission electron micrographs of negatively stained cells of strain E407-8^T, showing a single polar flagellum (F) and prosthecae (P). Cells observed were cultivated in marine broth at 15 °C (a, b) and 30 °C (c) for 24 h. Bars, 1 µm.

increasing the cellular surface-to-volume ratio (Hedlund *et al.*, 1997; Van Trappen *et al.*, 2004a; Young, 2006). To the best of our knowledge, this is the first observation of prostheca formation in the genus *Rheinheimera*; members of the class *Gammaproteobacteria* able to produce prosthecae have been reported from the genera *Alteromonas* (Van Trappen *et al.*, 2004a; Chiu *et al.*, 2007; Vandecandelaere *et al.*, 2008), *Glaciecola* (Van Trappen *et al.*, 2004b; Chen *et al.*, 2009), *Pseudidiomarina* (Jean *et al.*, 2006) and *Simiduia* (Shieh *et al.*, 2008).

Other morphological, physiological and biochemical characteristics of strain E407-8^T are given in the species description and in Table 2. Cells of strain E407-8^T were Gram-negative, oxidase- and catalase-positive, flagellated rods (Fig. 2). Consistent with other known *Rheinheimera* species, the strain could grow across broad ranges of temperature (10–48 °C) and NaCl concentration (0–8 %) and could assimilate *N*-acetylglucosamine and hydrolyse gelatin, starch and aesculin. The above phenotypic features supported the assignment of the strain to the genus *Rheinheimera*. There was also a range of phenotypic characteristics that could be used to differentiate strain E407-8^T from recognized *Rheinheimera* species, such as flagellum position and number, prostheca formation,

reduction of nitrate, oxygen requirement, ranges of salt, temperature and pH for growth, enzyme activities, carbohydrate assimilation and DNA G+C content (Table 2).

Taken together, the results of phylogenetic analysis of 16S rRNA gene sequences, DNA–DNA hybridization experiments and analysis of fatty acid profiles and phenotypic characteristics indicate that strain E407-8^T should be assigned to the genus *Rheinheimera* and represents a novel species of the genus, for which the name *Rheinheimera nanhaiensis* sp. nov. is proposed.

Some properties of strain E407-8^T are not in agreement with or were not included in the original and emended descriptions of the genus *Rheinheimera* (Brettar *et al.*, 2002; Merchant *et al.*, 2007), such as facultatively aerobic growth, the ability to produce prosthecae, growth at 48 °C or in 8 % NaCl and the presence of summed feature 3 among the major fatty acids. Similar discrepancies can also be observed for some other *Rheinheimera* species with validly published names, indicating the necessity to emend further the description of the genus, as follows.

Emended description of the genus *Rheinheimera* Brettar *et al.* 2002 emend. Merchant *et al.* 2007

The description is as given by Brettar *et al.* (2002) and Merchant *et al.* (2007) with the following amendments. Cells of some species can produce prosthecae. Growth is aerobic or facultatively aerobic, chemoheterotrophic and occurs at 4–48 °C. Dominant fatty acids are C_{16:1}ω7*c* or summed feature 3 (C_{16:1}ω7*c* and/or iso-C_{15:0} 2-OH), C_{16:0}, C_{17:1}ω8*c* and C_{18:1}ω7*c* (Table 1). Strains do not necessarily need NaCl for growth and cannot tolerate >8 % NaCl.

Description of *Rheinheimera nanhaiensis* sp. nov.

Rheinheimera nanhaiensis (nan.hai.en'sis. N.L. fem. adj. *nanhaiensis* pertaining to NanHai, the Chinese name for the South China Sea, where the type strain was isolated).

Cells are Gram-negative, straight or curved rods (1.0–2.0 µm long and 0.3–0.5 µm wide). Motile by a single polar flagellum. Able to form prosthecae. Facultatively aerobic. Colonies on marine agar are slightly yellow, circular (1.5–2.0 mm in diameter) and convex with smooth surfaces after incubation for 48 h at 30 °C. Oxidase- and catalase-positive. Reduces nitrate to nitrite. Grows at 10–48 °C (optimum, 37 °C), but not at 50 °C. Grows in 0–8 % (w/v) NaCl (optimum, 0.5–2.5 %) and at pH 5.5–10.0 (optimum, pH 7.5–8.5). Hydrolyses starch, gelatin, casein, DNA and Tweens 40 and 80. Able to utilize D-glucose, *N*-acetyl-D-glucosamine, sucrose, trehalose, cellobiose and maltose as sole carbon and energy sources. In API 20NE tests, positive for reduction of nitrate to nitrite, gelatinase, assimilation of D-glucose, *N*-acetylglucosamine and maltose and hydrolysis of aesculin and negative for indole production, arginine dihydrolase, urease, β-galactosidase,

Table 2. Differential characteristics of strain E407-8^T and type strains of other *Rheinheimera* species

Strains: 1, E407-8^T; 2, *R. pacifica* DSM 17616^T (unless indicated, data from Romanenko *et al.*, 2003); 3, *R. aquimaris* JCM 14331^T (Yoon *et al.*, 2007); 4, *R. soli* BD-d46^T (Ryu *et al.*, 2008); 5, *R. chironomi* K19414^T (Halpern *et al.*, 2007); 6, *R. tangshanensis* JA3-B52^T (Zhang *et al.*, 2008); 7, *R. baltica* OSBAC1^T (Brettar *et al.*, 2002); 8, *R. texasensis* A62-14B^T (Merchant *et al.*, 2007); 9, *R. perlucida* BA131^T (Brettar *et al.*, 2006). All strains are Gram-negative and positive for oxidase, assimilation of *N*-acetylglucosamine and hydrolysis of gelatin, starch and aesculin. +, Positive; w, weakly positive; –, negative; ND, not detected or no data available.

Characteristic	1	2	3	4	5	6	7	8	9
Cell morphology*	SR/CR	R	R/C	SR/CR	R	R	R/C	R	R
Cell size (µm)									
Width	0.3–0.5	0.6–0.8	0.3–0.7	0.9–1.5	0.3–0.7	0.4–1.0	0.5–1.5	0.7–0.8	0.6–1.2
Length	1.0–2.0	1.8–2.0	0.3–5.0	2.0–3.5	1.0–2.4	1.3–2.5	0.9–2.5	1.2–2.5	0.9–2.4
Flagella†	S, P	M, P and L	S, P	S, P	S, P	S, P or L	S, P	S, P or M, P and L	S, P
Oxygen requirement‡	FA	A	A	FA	FA	A	A	FA	FA
Catalase	+	+\$	+\$	+	–	+	+	+	+
Nitrate reduction	+	–\$	+\$	+	+	–	–	+	+
Temperature for growth (°C)									
Range	10–48	4–37	4–43	15–35	4–40	10–37	4–30	25–37	4–37
Optimum	37	25–30\$	30–37	25–30	30–37	30	20–25	30–37	20–30
NaCl concentration for growth (% w/v)									
Range	0–8	0–8	0–8	0–4	0–2	0–3	0–6	0–1	0–8
Optimum	0.5–2.5	0.5–2.5\$	1–3	0–1	0.5–1	1	1–3	0	1–3
pH for growth									
Range	5.5–10.0	5.5–10.5\$	5.5–10.5	6.5–8.0	6.5–10.0	6.0–8.5	5.7–10.0	6.5–9.6	5.7–10.0
Optimum	7.5–8.5	8.0–8.5\$	7.0–8.0	7.0–7.5	7.5–8.0	7.0	7.0	7.5–8.0	7.0
API ZYM results									
<i>N</i> -Acetylglucosaminidase	+	+\$	–\$	+	+	ND	–	ND	+
α-Chymotrypsin	+	+\$	–\$	+	+	ND	–	ND	+
Acid phosphatase	+	+\$	+\$	w	+	ND	–	ND	+
Esterase (C4)	+	–\$	+\$	+	+	ND	–	ND	+
β-Glucosidase	–	–\$	–\$	–	–	ND	+	ND	+
Assimilation of:									
D-Glucose	+	+\$	+\$	+	+	+	+	+	–
L-Arabinose	–	+\$	–\$	+	–	+	–	+	–
Maltose	+	+\$	+\$	+	+	–	+	–	–
Citrate	–	+\$	–\$	–	–	–	–	–	–
DNA G + C content (mol%)	51.0	49.6	50.5	49.2	49.9	47.0	48.9	48.2	48.9
Isolation source	Marine sediment	Deep seawater	Seawater	Soil	Chironomid egg mass	Rice roots	Surface seawater	Lake water	Surface seawater

*C, Cocci; CR, curved rods; R, rods; SR, straight rods.

†M, Multiple; S, single; L, lateral; P, polar.

‡A, Aerobic; FA, facultatively aerobic.

\$Result from this study.

acid production from glucose and assimilation of arabinose, mannose, mannitol, gluconate, caprate, adipate, malate, citrate and phenylacetate. In API 20E tests, positive for gelatinase, weakly positive for acid production from sucrose and negative for β-galactosidase, arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase, utilization of citrate, H₂S production, urease, tryptophan deaminase, indole production, the Voges–Proskauer test and acid production from glucose, mannitol, inositol, sorbitol, rhamnose, melibiose, amygdalin and arabinose. With API ZYM strips, the following enzyme activities are

detected: *N*-acetyl-β-glucosaminidase, α-chymotrypsin, trypsin, alkaline and acid phosphatases, esterase (C4), esterase lipase (C8), leucine arylamidase, valine arylamidase and naphthol-AS-BI-phosphohydrolase; activities of α- and β-galactosidase, β-glucuronidase, α- and β-glucosidase, α-mannosidase, β-fucosidase, lipase (C14) and cystine arylamidase are not detected. Susceptible to (µg per disc) chloramphenicol (30), erythromycin (15), gentamicin (10), kanamycin (30) and streptomycin (10), but resistant to ampicillin (10), penicillin G (10), vancomycin (30), lincomycin (2) and tetracycline (30). The respiratory

lipoquinones are Q-8 (98 %) and Q-7 (2 %). The major fatty acids (>5 %) are summed feature 3 (C_{16:1}ω7c and/or iso-C_{15:0} 2-OH), C_{17:1}ω8c, C_{16:0}, C_{18:1}ω7c and C_{17:0}. The DNA G+C content of the type strain is 51.0 mol%.

The type strain is E407-8^T (=CCTCC AB 209089^T =KACC 14030^T), isolated from marine sediments of the South China Sea.

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