Aliidiomarina taiwanensis gen. nov., sp. nov., isolated from shallow coastal water

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A Gram-negative, heterotrophic, aerobic, marine bacterium, designated AIT1^T, was isolated from a seawater sample collected in the shallow coastal region of Bitou Harbour, New Taipei City, Taiwan. Cells grown in broth cultures were straight or slightly curved rods that were motile by means of a single polar flagellum. Strain AIT1^T required NaCl for growth, grew optimally at 30–40 °C and with 1.5–5.0 % NaCl, and was incapable of anaerobic growth by fermentation of glucose or other carbohydrates. The isoprenoid quinones consisted of Q-8 (95.2 %) and Q-9 (4.8 %). The major polar lipids comprised diphosphatidylglycerol, phosphatidylglycerol and phosphatidylethanolamine. The cellular fatty acids were predominantly iso-branched and included iso-C_{17:0} (26.5 %), summed feature 9 (comprising iso-C_{17:1ω9c} and/or 10-methyl C_{16:0}; 25.9 %) and iso-C_{15:0} (20.5 %). The DNA G + C content was 51.5 mol%. Phylogenetic analysis based on 16S rRNA gene sequences showed that strain AIT1^T formed a distinct lineage within the class *Gammaproteobacteria* and was most closely related to members of the genus *Idiomarina* in the family *Idiomarinaceae* (91.5–93.9 % 16S rRNA gene sequence similarity). The phylogenetic data, together with chemotaxonomic, physiological and morphological data, revealed that the isolate should be classified as a representative of a novel species in a new genus in the family *Idiomarinaceae*, for which the name *Aliidiomarina taiwanensis* gen. nov., sp. nov. is proposed. The type strain is AIT1^T (=JCM 16052^T=BCRC 80035^T=NCCB 100321^T).

Halophilic, aerobic, Gram-negative, rod-shaped bacteria belonging to the family *Idiomarinaceae* (Ivanova *et al.*, 2004; Jean *et al.*, 2006), order *Alteromonadales* (Bowman & McMeekin, 2005), class *Gammaproteobacteria*, are unusual in that they contain high levels of iso-branched cellular fatty acids (Ivanova *et al.*, 2004). They can also be distinguished from other members of the order *Alteromonadales* by their poor ability to use carbohydrates as sole carbon and energy sources (Ivanova *et al.*, 2004). Signature nucleotides in the 16S rRNA gene sequences have been defined for the family *Idiomarinaceae*, including those at positions 143 (C or A), 662 (A), 682 (A), 830 (T) and 856 (A) (*Escherichia coli* K12 numbering, accession no. AE000471; Jean *et al.*, 2006).

The family *Idiomarinaceae* formerly comprised the genera *Idiomarina* (Ivanova *et al.*, 2004) and *Pseudidiomarina* (Jean *et al.*, 2006). However, the species of *Pseudidiomarina* were recently reassigned to the genus *Idiomarina* (Taborda *et al.*, 2009) because of the difficulty in differentiating the two genera by phenotypic characteristics. At the time of writing, the genus *Idiomarina* accommodated 16 species, *Idiomarina abyssalis* (Ivanova *et al.*, 2000), *I. baltica* (Brettar *et al.*, 2003), *I. fontislapidosi* (Martínez-Cánovas *et al.*, 2004), *I. loihiensis* (Donachie *et al.*, 2003), *I. ramblicola* (Martínez-Cánovas *et al.*, 2004), *I. seosinensis* (Choi & Cho, 2005), *I. zobellii* (Ivanova *et al.*, 2000), *I. insulalsae*, *I. taiwanensis*, *I. homiensis*, *I. marina*, *I. salinarum*, *I. sediminum* and *I. tainanensis* (Taborda *et al.*, 2009), and *I. donghaiensis* and *I. maritima* (Wu *et al.*, 2009); the latter eight formerly belonged to the genus *Pseudidiomarina*. Members of the genus *Idiomarina* have been isolated from saline habitats with a wide range of salinity, such as coastal and oceanic waters, coastal

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain AIT1^T is HQ537484.

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

sediments, inland hypersaline wetlands, solar salterns and submarine hydrothermal fluids.

During a survey of diversity of heterotrophic marine bacteria, strain AIT1^T was recovered from a seawater sample collected from the shallow coastal region of Bitou Harbour, New Taipei, on the north coast of Taiwan. The sample was diluted 10-fold with sterile NaCl/Tris buffer (30 g NaCl and 0.24 g Tris base, 1 l deionized water; pH 8.0). Aliquots (0.1 ml) of dilutions (10^{-1} to 10^{-3}) were spread on polypeptone-yeast (PY) agar (Shieh *et al.*, 2000) in triplicate and incubated at 30 °C in the dark for 7 days under aerobic conditions. Individual colonies were picked and purified by successive streaking on PY agar. The isolate was maintained at 25 °C in PY stab cultures under aerobic conditions.

Morphological and physiological characterization was carried out following established procedures (Jean *et al.*, 2006). Analysis of cellular fatty acids, isoprenoid quinones and DNA G+C content was carried out using early stationary-phase cells harvested from cultures grown in PY broth or on PY agar at 30 °C for 3 days under aerobic conditions, according to the methods described by Shieh *et al.* (2008). The HPLC apparatus used for analysis of isoprenoid quinones was equipped with an Inertsil ODS-2 column (1.5 × 250 mm; GL Science). Fatty acids were extracted, saponified, esterified and analysed by GC according to the MIDI system (Sasser, 1990) and were identified using the library 2005 supplied in the software package Sherlock Microbial Identification System version 6.0 (MIDI). Polar lipids were analysed using cells grown in marine agar 2216 (Difco) at 30 °C for 3 days under aerobic conditions, according to the methods described by Lin & Shieh (2006). Cluster analysis with the software PC-ORD version 5.1 (McCune & Mefford, 1999) assessed the similarity of the cellular fatty acids of strain AIT1^T and members of the genus *Idiomarina*. Distances were evaluated using the correlation coefficient and clustering was performed using hierarchical agglomerative clustering with group-average linkage (McCune & Mefford, 1999).

For analysis of the 16S rRNA gene sequence, cells were grown in PY broth at 30 °C for 3 days and harvested by centrifugation. Extraction and purification of total genomic DNA and PCR amplification of the 16S rRNA gene were performed according to the methods described by Jean *et al.* (2006). Sequencing, alignment and comparison with reference sequences available in GenBank, calculation of distance matrices and reconstruction of neighbour-joining, maximum-parsimony and maximum-likelihood trees were performed as described by Shieh *et al.* (2004) and Jean *et al.* (2006). The stability of clusters was evaluated by bootstrap analysis of 1000 resamplings.

A nearly complete 16S rRNA gene sequence (1441 nt) was determined for strain AIT1^T. Preliminary sequence comparisons with sequences in GenBank indicated that strain AIT1^T belonged to the order *Alteromonadales* of the class *Gammaproteobacteria* but that it was not closely related to

members of species with validly published names (<94.0 % 16S rRNA gene sequence similarity). The highest sequence similarities (91.5–93.9 %) were observed with the type strains of species in the genus *Idiomarina*. The distant relationship between strain AIT1^T and other species was also evident in the neighbour-joining tree (Fig. 1); strain AIT1^T represented a novel lineage that was an outgroup with respect to the genus *Idiomarinaceae*, which contained two groups, species clusters I and II. Similar results were also observed in the maximum-parsimony and maximum-likelihood phylogenetic trees (data not shown). It should be noted that the species clusters are based on 16S rRNA gene sequences and no data are available for other phylogenetically useful genes such as *groEL*, *rpoB* or *gyrA*. Sequences of strains outside of the family *Idiomarinaceae* had <90 % 16S rRNA gene sequence similarity with strain AIT1^T. On the basis of the phylogenetic analysis using three tree-making algorithms and the low levels of 16S rRNA gene sequence similarity between the isolate and all members of recognized species, strain AIT1^T should be classified as a representative of a novel species in a new genus in the family *Idiomarinaceae*.

Strain AIT1^T exhibited the signature nucleotides that are distinctive for the family *Idiomarinaceae* (Ivanova *et al.*, 2004; Jean *et al.*, 2006): i.e. positions 143 (A), 662 (A), 682 (A), 830 (T) and 856 (A) (Table 1). However, the isolate also exhibited nucleotides at positions 240 (A), 286 (T), 762 (A), 811 (T), 1336 (A) and 1439 (G) that distinguished it from other members of the family *Idiomarinaceae*, which exhibited G, C, T, C, C and T/A at these positions, respectively. These nucleotides may be considered as the signature nucleotides of a new genus in the family *Idiomarinaceae*.

The species clusters I and II in the family *Idiomarinaceae* also exhibited specific nucleotides: for species cluster I, positions 143 (C), 206 (C), 213 (G), 241 (G), 285 (C), 653 (A), 658 (C), 748 (G) and 1439 (T); and for species cluster II, positions 1256 (A), 1279 (G), 1286 (A) and 1439 (A) (Table 1). Thus, analysis of species cluster-specific nucleotides, together with the clear phylogenetic divergence of the species clusters and the low 16S rRNA gene sequence similarities between members of the two species clusters (92.7–95.7 %) are consistent with the previous conclusion that species clusters I and II represent the genera *Idiomarina* and *Pseudidiomarina*, respectively (Jean *et al.*, 2009). However, members of the genus *Pseudidiomarina* have recently been reclassified in the genus *Idiomarina* because of the difficulty in differentiating the two genera based on phenotypic characteristics (Taborda *et al.*, 2009).

The DNA G+C content of strain AIT1^T was 51.5 mol%, which was nearly identical to that for *I. insulisalae* (51.6%), but lower than that for *I. salinarum* CCUG 54359^T (53.9 mol%) and higher than those for the remaining members of the genus *Idiomarina* (45.0–50.4 mol%) (Table 2). The isolate contained Q-8 as the predominant isoprenoid quinone (96.3 %) and Q-9 as a minor quinone

Fig. 1. Unrooted phylogenetic tree derived from neighbour-joining analysis of 16S rRNA gene sequences showing the relationship between strain AIT1^T and type strains of recognized species of the genus *Idiominarina*, together with some other related taxa belonging to the *Gammaproteobacteria*. Bootstrap values (>70 %) based on 1000 replications are shown at branch nodes. Bar, 0.01 substitutions per nucleotide position.

Table 1. Signature nucleotides detected among the 16S rRNA gene sequences of strain AIT1^T and species clusters I and II in the genus *Idiominarina*

Signature nucleotides are shown in bold.

Position	Nucleotide present in:		
	Strain AIT1 ^T	Species cluster I	Species cluster II
143	A	C	A
206	T	C	T
213	A	G	A
240	A	G	G
241	A	G	A
285	T	C	T
286	T	C	C
653	C	A	C
658	T	C	T
662	A	A	A
682	A	A	A (T)
748	A	G	A
762	A	T	T
811	T	C	C
830	T	T	T
856	A	A	A
1256	C	C	A
1279	A	A	G
1286	T	T	A
1336	A	C	C
1439	G	T	A

(3.7 %). All recognized members of the genus *Idiominarina* also contain Q-8 as the predominant isoprenoid quinone, but Q-9 has not been previously reported and some members contain Q-7 as the minor quinone (Table 2). The major polar lipids of strain AIT1^T were diphosphatidylglycerol, phosphatidylglycerol and phosphatidylethanolamine, which is typical of the family *Idiominarinaceae* (Taborda *et al.*, 2009). Strain AIT1^T was similar to other members of the family *Idiominarinaceae* in that it contained iso-C_{17:0}, summed feature 9 (comprising iso-C_{17:1}ω₉c and/or 10-methyl C_{16:0}) and iso-C_{15:0} as the major cellular fatty acids (Table 2 and Supplementary Table S1, available in IJSEM Online). However, iso-C_{17:0} and summed feature 9 were much more abundant in the isolate than in the reference strains (52.4 % vs 17.8–36.7 %) and the isolate could also be distinguished by the presence of iso-C_{15:0} 3-OH (2.2 %), and the absence of iso-C_{13:0} and iso-C_{13:0} 3-OH. Moreover, cluster analysis of the fatty acids (Fig. 2) differentiated strain AIT1^T from all other members of the family *Idiominarinaceae*. The cluster analysis also divided the family *Idiominarinaceae* into four groups, one comprising species cluster I (group II) and the others comprising species cluster II (groups I, III and IV).

Strain AIT1^T was mesophilic, halophilic and Gram-negative and produced light brown, circular, convex and non-luminescent colonies on PY agar. Carbohydrate fermentation tests in PY-carbohydrate stab media (Shieh *et al.*, 2000) showed that the isolate did not ferment any of the test carbohydrates (D-arabinose, L-arabinose, cellobiose, dulcitol,

Table 2. Characteristics useful for differentiating strain AIT1^T from recognized members of the genus *Idiomarina*

Strains: 1, *Aliidiomarina taiwanensis* sp. nov. AIT1^T; 2, *I. abyssalis* ATCC BAA-312^T; 3, *I. baltica* DSM 15154^T; 4, *I. fontislapidosi* DSM 16139^T; 5, *I. loihiensis* DSM 15497^T; 6, *I. ramblicola* DSM 16140^T; 7, *I. seosinensis* JCM 12526^T; 8, *I. zobellii* ATCC BAA-313^T; 9, *I. donghaiensis* 908033^T; 10, *I. homiensis* DSM 17923^T; 11, *I. insulalsae* CVS-6^T; 12, *I. marina* PIM1^T; 13, *I. maritima* 908087^T; 14, *I. salinarum* CCUG 54359^T; 15, *I. sediminum* LMG 24046^T; 16, *I. tainanensis* PIN1^T; 17, *I. taiwanensis* PIT1^T. Data for columns 2–8, 10, 11, 14 and 15 were taken from Taborda *et al.* (2009), for columns 9 and 13 from Wu *et al.* (2009), for columns 12 and 16 from Jean *et al.* (2009) and for column 17 from Jean *et al.* (2006). All strains are positive for oxidase. +, Positive; –, negative/not detected/trace amount detected (<1 %); ND, no data available.

Characteristic	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
Motility	+	+	+	+	+	+	+	+	+	+	+	–	+	ND	–	–	–
Monotrichous flagella	+	+	+	+	+	+	+	+	–	+	+	–	+	ND	–	–	–
NaCl (%)																	
Optimum	1.5–5.0	3–6	3–6	3–5	7.5–10.0	3–5	7–10	3–6	3	3–5	5	2–5	3	2–3	1–8	2–5	1–4
15 %	–	+	–	+	+	+	+	–	–	+	+	+	+	–	+	+	–
Temperature optimum (°C)	30–40	20–22	30–40	32	30	32	30–35	20–22	37	25–30	37–40	30–35	37	30–37	30–40	30–35	30–35
Growth at:																	
4 °C	+	+	–	+	+	–	+	+	–	+	–	–	–	+	–	–	–
40 °C	+	–	+	+	+	+	+	–	+	+	+	+	+	+	+	+	+
45 °C	+	–	+	+	+	–	–	–	+	+	+	–	+	–	–	–	–
Optimum pH	8	ND	ND	ND	ND	ND	ND	ND	8–9	ND	7.5–8.0	7–8	8–9	7–8	8–9	7–8	8
Growth at pH 6	–	+	+	+	ND	+	+	+	–	+	+	+	–	+	–	+	ND
Hydrolysis of:																	
Aesculin	–	–	–	+	–	+	+	–	–	+	–	–	–	–	ND	–	+
Casein	–	ND	ND	+	ND	+	ND	ND	+	–	–	–	+	–	–	–	–
Tween 80	–	–	+	+	+	+	+	–	+	+	–	–	+	+	+	–	+
Enzymes																	
DNase	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	–	+
Gelatinase	+	+	+	+	+	+	+	+	+	+	+	+	+	–	+	+	+
Catalase	+	+	+	+	+	+	+	+	+	+	+	+	+	+	–	+	+
H ₂ S production	–	ND	+	+	ND	+	ND	ND	+	+	ND	–	–	ND	–	–	–
Nitrate reduction	+	+	–	–	–	–	+	–	–	+	–	–	–	+	–	–	+
Acid production from:																	
D-Arabinose	–	–	–	–	–	–	–	ND	–	–	+	–	ND	–	–	–	–
D-Xylose	–	–	–	–	–	–	–	ND	–	–	+	–	ND	–	–	–	–
API ZYM																	
Alkaline phosphatase	–	+	+	+	+	+	+	+	+	+	+	+	+	+	ND	+	+
Esterase (C4)	–	+	+	+	+	+	+	+	+	+	+	+	+	+	ND	+	+
Esterase lipase (C8)	–	+	+	+	+	+	+	+	+	+	+	+	+	+	ND	+	+
Lipase (C14)	–	–	–	–	–	–	–	–	+	–	–	+	+	–	+	+	+
Leucine arylamidase	–	+	+	+	+	+	+	+	+	+	+	+	+	+	ND	+	+
Valine arylamidase	+	–	+	+	–	–	–	–	+	+	–	+	+	–	ND	+	+
Cystine arylamidase	+	–	+	–	–	–	–	–	+	+	–	+	+	–	ND	+	+
Trypsin	+	–	–	–	–	–	–	–	+	+	+	+	+	+	ND	+	+
α-Chymotrypsin	+	–	+	+	–	+	–	+	+	+	+	+	+	+	ND	+	+
Acid phosphatase	+	+	+	ND	+	ND	+	+	+	+	+	+	+	–	ND	+	+
Fatty acids (%)																	
iso-C _{13:0}	–	1.4	–	–	1.8	1.4	–	1.6	2.2	1.7	1.0	1.3	1.6	1.6	3.2	1.7	4.6
iso-C _{13:0} 3-OH	–	3.7	2.9	3.2	3.9	3.5	3.3	4.7	5.2	3.8	2.5	3.3	5.0	5.0	4.0	4.0	3.8
iso-C _{15:0}	20.5	22.2	33.4	26	28.2	21.5	24.6	30.5	22.9	21.9	16.7	17.0	26.8	34.1	28.4	21.4	37.8
iso-C _{15:0} 3-OH	2.2	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
iso-C _{17:0}	26.5	11.4	13.3	10.2	13.5	14.4	12.4	12.6	23.1	8.6	15.3	18.2	15.4	19.9	11.6	21.0	14.4
Summed feature 9*	25.9	13.4	8.2	6.6	11.3	16.1	10.1	5.2	12.5	10.4	10.2	16.6	11.6	11.8	11.4	15.7	8.3
Quinones																	
Major	Q-8	Q-8	Q-8	Q-8	Q-8	Q-8	Q-8	Q-8	Q-8	Q-8	Q-8	Q-8	Q-8	Q-8	Q-8	Q-8	Q-8

Table 2. cont.

Characteristic	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
Minor	Q-9	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	Q-7	ND	ND	ND	Q-7	ND
DNA G + C content (mol%)	51.5	50.4	49.7	46.0	47.4	48.7	45.0	48.0	45.5	45.1	51.6	46.6	45.2	53.9	50.0	46.9	49.3

*Summed features represent two or three fatty acids that cannot be separated by the Microbial Identification System. Summed feature 9 consisted of iso-C_{17:1}ω₉c and/or 10-methyl C_{16:0}.

D-fructose, D-galactose, D-glucose, *myo*-inositol, lactose, maltose, D-mannitol, D-mannose, melezitose, melibiose, raffinose, D-ribose, D-sorbitol, sucrose, trehalose and D-xylose). No growth was observed in CM media, which contain glucose or other carbohydrates as sole carbon and energy sources, although these media have been shown to support the growth of various other marine bacteria (Shieh *et al.*, 2003, 2004). Endospores were not found. Neither sporulation nor endospore-like structures were ever observed by phase-contrast microscopy and spore staining. Poly-β-hydroxybutyrate-like granules were not observed. Strain AIT1^T was susceptible to (μg per disc, unless otherwise stated) carbenicillin (100), cephalothin (30), chloramphenicol (30), colistin (10), erythromycin (15), gentamicin (10), nalidixic acid (30), novobiocin (30), penicillin G (10 U), polymyxin B (300 U) and tetracycline (30), intermediately susceptible to ampicillin (10), kanamycin (30), neomycin (30) and streptomycin (10), and resistant to oxacillin (1) and vancomycin (30). The negative reactions for alkaline

phosphatase, esterase (C4), esterase lipase (C8) and leucine arylamidase with the API ZYM tests enabled strain AIT1^T to be distinguished from the recognized members of the family *Idiomarinaceae* for which comparative data were available. Additional characteristics useful for distinguishing strain AIT1^T are listed in Table 2.

On the basis of phylogenetic, chemotaxonomic and physiological data, strain AIT1^T should be classified as a representative of a novel species in a new genus in the family *Idiomarinaceae* for which the name *Aliidiomarina taiwanensis* gen. nov., sp. nov. is proposed.

Description of *Aliidiomarina* gen. nov.

Aliidiomarina (A.li.i.di.o.ma.ri'na. L. pronoun. *alius* other, another; N.L. n. *Idiomarina* a name of a bacterial genus; N.L. fem. n. *Aliidiomarina* the other *Idiomarina*).

Belongs to the family *Idiomarinaceae* in the class *Gamma-proteobacteria*. Cells are heterotrophic, Gram-negative

Fig. 2. Cluster analysis of cellular fatty acids of strain AIT1^T and type strains of recognized species of the genus *Idiomarina*. Strains: 1, *Aliidiomarina taiwanensis* sp. nov. AIT1^T; 2, *I. abyssalis* ATCC BAA-312^T; 3, *I. baltica* DSM 15154^T; 4, *I. fontislapidosi* DSM 16139^T; 5, *I. loihiensis* DSM 15497^T; 6, *I. ramblicola* DSM 16140^T; 7, *I. seosinensis* JCM 12526^T; 8, *I. zobellii* ATCC BAA-313^T; 9, *I. donghaiensis* 908033^T; 10, *I. homiensis* DSM 17923^T; 11, *I. insulalsae* CVS-6^T; 12, *I. marina* PIM1^T; 13, *I. maritima* 908087^T; 14, *I. salinarum* CCUG 54359^T; 15, *I. sediminum* LMG 24046^T; 16, *I. tainanensis* PIN1^T; 17, *I. taiwanensis* PIT1^T. Raw data are provided in Supplementary Table S1, available in IJSEM Online (strains are numbered according to the legend).

rods and motile by means of a single polar flagellum. Chemo-organotrophic and capable of respiratory, but not fermentative, metabolism. Mesophilic and halophilic. Oxidase- and catalase-positive. The major fatty acids are iso-branched and include iso-C_{17:0}, summed feature 9 (comprising iso-C_{17:1ω9c} and/or 10-methyl C_{16:0}) and iso-C_{15:0}. The minor cellular fatty acids include iso-C_{15:0} 3-OH. C_{13:0} and iso-C_{13:0} 3-OH are not detected. Q-8 is the major isoprenoid quinone and Q-9 is a minor quinone. The major polar lipids are diphosphatidylglycerol, phosphatidylglycerol and phosphatidylethanolamine. The genus-specific nucleotide positions in the 16S rRNA gene (*E. coli* K12 numbering) include positions 240 (A), 286 (T), 762 (A), 811 (T), 1336 (A) and 1439 (G). The DNA G+C content is approximately 51–52 mol%. The type species is *Aliidiomarina taiwanensis*.

Description of *Aliidiomarina taiwanensis* sp. nov.

Aliidiomarina taiwanensis (tai.wan.en'sis. N.L. fem. adj. *taiwanensis* pertaining to Taiwan, where the type strain was isolated).

Has the following characteristics in addition to those given for the genus. Cells are approximately 1.5–2.8 µm long and 0.5–0.8 µm wide. After incubation on PY agar at 30 °C for 7 days, colonies are approximately 4–6 mm in diameter, light brown, circular, convex and non-luminescent, with entire edges. Endospores are absent. Poly-β-hydroxybutyrate is not accumulated. Nitrate is reduced to nitrite, but not to nitrous oxide or nitrogen. NaCl is required for growth: grows with 0.5–10 % NaCl (optimum 1.5–5.0 %), but not with 0 or 12.5 % NaCl. Grows at 4–45 °C (optimum 30–40 °C), but not at 50 °C, and at pH 7–9, but not at pH 6 or 10. Arginine dihydrolase, lysine decarboxylase and ornithine decarboxylase are absent. Indole is produced. H₂S is not produced from thiosulphate. DNA and gelatin are hydrolysed, but aesculin, agar, casein, starch, Tween 80 and urea are not. With API ZYM, positive for acid phosphatase, valine arylamidase, cystine arylamidase, α-chymotrypsin, naphthol-phosphohydrolase and trypsin. With API 50CH, oxidizes *N*-acetylglucosamine, starch, L-arabinose, erythritol, D-fructose, L-fucose, D-galactose, D-glucose, glycerol, glycogen, maltose, D-mannitol, D-mannose, potassium gluconate, D-ribose, sucrose and trehalose. With GN2 MicroPlates, oxidizes acetic acid, *N*-acetyl-D-galactosamine, *N*-acetyl-D-glucosamine, L-asparagine, L-aspartic acid, bromosuccinic acid, dextrin, D-fructose, L-fucose, α-D-glucose, D-glucose 6-phosphate, D-gluconic acid, D-glucosaminic acid, L-glutamic acid, glycogen, glycyl L-aspartic acid, L-histidine, *p*-hydroxyphenylacetic acid, inosine, DL-lactic acid, maltose, D-mannitol, D-mannose, D-psicose, pyruvic acid methyl ester, L-serine, sucrose, trehalose, thymidine, turanose and uridine.

The type strain, AIT1^T (=JCM 16052^T=BCRC 80035^T=NCCB 100321^T), was isolated from shallow coastal

seawater of Bitou Harbour, New Taipei City, Taiwan. The DNA G+C content of the type strain is 51.5 mol%.

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