Pseudoteredinibacter isopora gen. nov., sp. nov., a marine bacterium isolated from the reef-building coral *Isopora palifera*

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A Gram-negative, heterotrophic, marine bacterium, designated strain SW-11^T, was isolated from the reef-building coral *Isopora palifera* in Kenting, Taiwan. Cells were rods and were motile by a single polar flagellum. The strain grew at 10–45 °C (optimum, 30–35 °C), at pH 7.0–8.0 (optimum, pH 7.5) and with 2.0–4.0 % NaCl (optimum, 2.5–3.0 %). The polar lipids comprised phosphatidylethanolamine, phosphatidylglycerol, phosphatidylserine, diphosphatidylglycerol and four unknown phospholipids. Isoprenoid quinones consisted of ubiquinone 9 (78.8 %) and ubiquinone 8 (21.1 %). Major cellular fatty acids were summed feature 3 (C_{16:1}ω7c and/or C_{16:1}ω6c; 22.3 %), C_{17:1}ω8c (13.4 %), summed feature 8 (C_{18:1}ω6c and/or C_{18:1}ω7c; 13.1 %), C_{16:0} (10.3 %) and anteiso-C_{17:1}ω9c (10.0 %). The DNA G + C content was 51.6 mol%. 16S rRNA gene sequence analysis indicated that strain SW-11^T belongs to the class *Gammaproteobacteria* and is a member of the order *Alteromonadales*. Strain SW-11^T shared 93.2 % 16S rRNA gene sequence similarity with *Teredinibacter turnerae* T7902^T and 92.1 % with *Saccharophagus degradans* 2-40^T, and can be further distinguished from these two related strains by distinct patterns of fatty acid content and differences in the polar lipid profile, the ability to utilize different compounds as carbon sources, the ability to degrade various compounds and differences in enzyme activities. The phylogenetic data and those from physiological, morphological and chemotaxonomic characterizations indicate that strain SW-11^T represents a novel species and genus, for which the name *Pseudoteredinibacter isopora* gen. nov., sp. nov. is proposed. The type strain of *Pseudoteredinibacter isopora* is SW-11^T (=BCRC 17935^T =LMG 25246^T).

Corals harbour a diverse array of bacterial associates (reviewed by Brown & Bythell, 2005), some of which are thought to be site- and species-specific (Hong *et al.*, 2009; Chiou *et al.*, 2010; Kvennefors *et al.*, 2010). Coral-associated bacteria are increasingly considered to be important in coral health, and altered bacterial community structures have been linked to both coral disease and

bleaching (Rosenberg *et al.*, 2007; Sampayo *et al.*, 2008; Rypien *et al.*, 2010). Recent research indicates that, although site-specific variations in the bacterial communities of healthy corals are present, host species-specific bacterial associates within a distinct cluster of gammaproteobacteria can be identified that are potentially linked to coral health (Kvennefors *et al.*, 2010). It is important to understand the dynamics of the coral-associated bacterial community structures of healthy and unhealthy corals.

During screening for novel micro-organisms from a coral of the species *Isopora palifera* at Kenting, Taiwan (GPS location: 21° 52' 35" N 120° 43' 29" E), several different

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain SW-11^T is FJ347760.

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

isolates were obtained. This study is focused on one isolate, SW-11^T. Comparative 16S rRNA gene sequence analysis indicated that strain SW-11^T forms an independent branch within the *Gammaproteobacteria*. Accordingly, the aim of the present work was to determine the exact taxonomic position of strain SW-11^T by a polyphasic characterization that included phenotypic and chemotaxonomic properties and detailed phylogenetic analysis based on 16S rRNA gene sequences.

Strain SW-11^T was isolated and maintained on marine 2216 agar (MA; BD Difco) or in marine 2216 broth (MB; BD Difco) and formed semi-translucent colonies after incubation at 30 °C for 2 days. Subcultivation was done on MA at 30 °C for 24–48 h. On this medium, strain SW-11^T was able to grow at 10–45 °C but not at 4 or 50 °C. The strain was preserved at –80 °C as a 20% (v/v) glycerol suspension in MB or by lyophilization with 20% (w/v) skimmed milk. *Saccharophagus degradans* DSM 17024^T and *Teredinibacter turnerae* ATCC 39867^T were obtained from the Deutsche Sammlung von Mikroorganismen und Zellkulturen (DSMZ) and the American Type Culture Collection (ATCC), respectively, and used as reference strains for both phenotypic and genotypic tests. *S. degradans* DSM 17024^T was grown and maintained on MA. *T. turnerae* ATCC 39867^T was grown and maintained on shipworm basal medium (SBM), as described previously (Waterbury *et al.*, 1983; Distel *et al.*, 2002).

The 16S rRNA gene sequence of strain SW-11^T was determined and analysed as described previously (Chen *et al.*, 2001). Analysis of the sequence was performed by using the software package BioEdit (Hall, 1999) and MEGA version 3.1 (Kumar *et al.*, 2004), after multiple alignments by using CLUSTAL_X (Thompson *et al.*, 1997). The distance matrix method was employed (distance options according

to Kimura's two-parameter model; Kimura, 1983), including clustering by the neighbour-joining (Saitou & Nei, 1987) (Fig. 1), maximum-likelihood (Felsenstein, 1981) and discrete character-based maximum-parsimony (Kluge & Farris, 1969) methods. In each case, bootstrap values were calculated based on 1000 replications. The 16S rRNA gene sequence of strain SW-11^T was a continuous stretch of 1406 bp; analysis indicated that strain SW-11^T belonged to the class *Gammaproteobacteria* and was a member of the order *Alteromonadales*. Sequence similarity calculations using BioEdit software (over 1400 bp) indicated that strain SW-11^T was most closely related to *T. turnerae* T7902^T (93.2% gene sequence similarity) and *S. degradans* 2-40^T (92.1%). Lower sequence similarities (<92%) were found with representatives of other related genera shown in Fig. 1. The overall topologies of the phylogenetic trees obtained with the neighbour-joining, maximum-likelihood and maximum-parsimony methods were similar (Fig. 1 and Supplementary Figs. S1 and S2, available in IJSEM Online).

The morphology of the cells was observed by phase-contrast microscopy (Leica DM 2000) and scanning electron microscopy (S-3500N; Hitachi) (Supplementary Fig. S3) using cells grown in MB at 30 °C for 6 h (lag growth phase), 18 h (exponential phase) and 36 h (stationary phase). Motility was tested by the hanging drop method. Flagellar staining was performed using the Spot Test flagella stain (BD Difco). The Gram reaction was tested using the BD Difco Gram stain set and the Ryu non-staining KOH method (Powers, 1995). Accumulation of poly-β-hydroxybutyrate granules was tested by light microscopy after staining cells with Sudan black. Colony morphology was examined using a stereoscopic microscope (SMZ 800; Nikon). Details of cell morphology are given in the species description. The pH range for growth

Fig. 1. Neighbour-joining tree based on 16S rRNA gene sequences showing the phylogenetic relationships between strain SW-11^T and some representatives of the class *Gammaproteobacteria*. Bootstrap values (>50%) based on 1000 replications are shown at branching points. Bar, 0.01 substitutions per nucleotide position.

was determined in R2A broth medium dissolved in artificial seawater (NaCl, 24 g; MgCl₂, 5.1 g; Na₂SO₄, 4 g; CaCl₂, 1.1 g; KCl, 0.7 g; NaHCO₃, 0.2 g; KBr, 0.1 g; H₃BO₃, 0.027 g; SrCl₂, 0.024 g; NaF, 0.003 g; distilled water to 1 l; Lyman & Fleming, 1940) using appropriate biological buffers (glycine/HCl, citrate/Na₂HPO₄, phosphate buffer and glycine/NaOH to adjust the pH to 3.0–4.0, 4.0–8.0, 6.0–8.0 and 9.0–11.0, respectively, at 0.5 pH unit intervals). The pH was adjusted prior to sterilization, and post-sterilization controls revealed only minor changes. The NaCl requirement was determined using R2A broth medium containing 0–15.0 % (w/v) NaCl (at 0.5 % intervals). The temperature for growth was examined at 4, 10, 15, 20, 25, 30, 35, 37, 40, 45 and 50 °C. Growth was determined by measuring turbidity (OD₆₀₀). Anaerobic growth was assessed using the Oxoid AnaeroGen system (Miller *et al.*, 1995).

Catalase, oxidase, DNase and lipase (corn oil) activities and hydrolysis of starch, casein, agar, gelatin and Tweens 20, 40, 60 and 80 were determined using standard methods (Gerhardt *et al.*, 1994). Hydrolysis of chitin was tested using agar medium supplemented with 0.2 % colloidal chitin (Hsu & Lockwood, 1975). Colloidal chitin was prepared according to the description of Monreal & Reese (1969). Hydrolysis of alginate [1 % (w/v) sodium alginate] was examined according to the description of Hosoya *et al.* (2009) and lecithin hydrolysis was tested by the method of Smibert & Krieg (1994). Hydrolysis of CM-cellulose was tested as described by Bowman (2000) using R2A medium dissolved in artificial seawater as the basal medium. Eumelanin production via tyrosinase activity was tested according to Kelly *et al.* (1990). Carbon utilization was tested on basal agar medium supplemented with yeast extract (NaCl, 23.6 g; KCl, 0.64 g; MgCl₂·6H₂O, 4.53 g; MgSO₄·7H₂O, 5.94 g; CaCl₂·2H₂O, 1.3 g; NaNO₃, 0.2 g; NH₄Cl, 0.2 g; Bacto agar, 15 g; yeast extract, 0.05 g; distilled water to 1 l; Choi *et al.*, 2006) containing 0.2 % of the carbon source. Incubation was prolonged for a month and growth was scored as positive when visible colonies were observed. The API 20NE, API ZYM (bioMérieux) and MicroPlate GN2 (Biolog) microtest systems were used to determine biochemical properties, enzyme activities and carbohydrate utilization. API ZYM tests were performed according to the manufacturer's recommendation and the API ZYM strip was read after 4 h of incubation at 30 °C. Because strain SW-11^T required 2–3 % NaCl for optimum growth, the sample was suspended in saline solution (3 % NaCl) for API 20NE and MicroPlate GN2 tests. The results were read after 72 h at 30 °C.

Strain SW-11^T was grown in R2A broth medium dissolved in artificial seawater at 30 °C for 2 days and isoprenoid quinones were extracted and separated as described by Minnikin *et al.* (1984) and analysed by HPLC as described by Collins (1985). The major isoprenoid quinones of strain SW-11^T were ubiquinone 9 (78.8 %) and ubiquinone 8 (21.1 %). The DNA G+C content of strain SW-11^T was estimated as described by Mesbah *et al.* (1989). The

nucleoside mixture was separated by HPLC. The DNA G+C content of strain SW-11^T was 51.6 ± 1.0 mol%.

Biomass of SW-11^T, *T. turnerae* ATCC 39867^T and *S. degradans* DSM 17024^T was obtained after growing the strains in R2A medium dissolved in artificial seawater at 30 °C for 3 days. Fatty acid methyl esters were prepared, separated and identified according to the instructions of the Microbial Identification System (Microbial ID; MIDI) (Sasser, 1990). The major fatty acid constituents (≥ 10 %) of strain SW-11^T were summed feature 3 (C_{16:1}ω7c and/or C_{16:1}ω6c; 22.3 %), C_{17:1}ω8c (13.4 %), summed feature 8 (C_{18:1}ω6c and/or C_{18:1}ω7c; 13.1 %), C_{16:0} (10.3 %) and anteiso-C_{17:1}ω9c (10.0 %) (Table 1). This fatty acid profile was distinct from those of *T. turnerae* ATCC 39867^T and *S. degradans* DSM 17024^T. In contrast to *T. turnerae* ATCC 39867^T and *S. degradans* DSM 17024^T, strain SW-11^T possessed fatty acids C_{17:1}ω8c and anteiso-C_{17:1}ω9c. Furthermore, the quantity of fatty acid C_{16:0} in strain SW-11^T was much smaller than that found in *T. turnerae* ATCC 39867^T and *S. degradans* DSM 17024^T, while the

Table 1. Cellular fatty acid compositions of strain SW-11^T, *T. turnerae* ATCC 39867^T and *S. degradans* DSM 17024^T

Strains: 1, SW-11^T; 2, *T. turnerae* ATCC 39867^T; 3, *S. degradans* DSM 17024^T. All data are from this study. Strains were grown at 30 °C for 3 days in R2A medium dissolved in artificial seawater. Values are percentages of the total fatty acids. Fatty acids that made up <1 % of the total in all three strains are not shown; –, <1 %. For unsaturated fatty acids, the position of the double bond is located by counting from the methyl (ω) end of the carbon chain; *cis* isomers are indicated by the suffix *c*.

Fatty acid	1	2	3
C _{10:0}	3.5	3.2	–
C _{10:0} 3-OH	3.2	1.6	8.3
C _{11:0}	2.5	–	2.4
C _{11:0} 3-OH	4.0	–	–
C _{12:0}	3.0	2.5	3.0
anteiso-C _{12:0}	–	–	8.4
C _{12:0} 3-OH	2.4	4.7	–
C _{12:1} 3-OH	–	–	4.3
anteiso-C _{13:0}	–	–	4.1
C _{14:0}	1.1	4.0	5.1
C _{16:0}	10.3	20.9	28.9
C _{17:0}	5.1	1.3	17.3
C _{17:1} ω6c	1.2	–	–
C _{17:1} ω8c	13.4	–	–
anteiso-C _{17:1} ω9c	10.0	–	–
C _{18:0}	–	4.2	5.1
Summed feature 3*	22.3	18.1	3.4
Summed feature 8*	13.1	36.7	9.9

*Summed features are groups of two or three fatty acids that cannot be separated by GLC using the MIDI system. Summed feature 3 comprises C_{16:1}ω7c and/or C_{16:1}ω6c and summed feature 8 comprises C_{18:1}ω7c and/or C_{18:1}ω6c.

quantity of summed feature 8 ($C_{18:1\omega6c}$ and/or $C_{18:1\omega7c}$) was much smaller than that found in *T. turnerae* ATCC 39867^T and the quantity of summed feature 3 ($C_{16:1\omega7c}$ and/or $C_{16:1\omega6c}$) was much greater than that found in *S. degradans* DSM 17024^T (Table 1).

Polar lipids were extracted and analysed by two-dimensional TLC as described by Ventosa *et al.* (1993). Strain SW-11^T, *T. turnerae* ATCC 39867^T and *S. degradans* DSM 17024^T were grown in R2A broth dissolved in artificial seawater at 30 °C for 2 days. The major cellular phospholipids of strain SW-11^T were phosphatidylethanolamine and phosphatidylglycerol, and the minor polar lipids were phosphatidylserine, diphosphatidylglycerol and four unknown phospholipids (PL1–PL4) (Supplementary Fig. S4). Like its closest relatives *T. turnerae* ATCC 39867^T and *S. degradans* DSM 17024^T, strain SW-11^T had phosphatidylethanolamine and phosphatidylglycerol as major cellular phospholipids. However, diphosphatidylglycerol was present in strain SW-11^T and *S. degradans* DSM 17024^T, but absent from *T. turnerae* ATCC 39867^T. In contrast, an unknown glycolipid was present in *T. turnerae* ATCC 39867^T, but absent from strain SW-11^T and *S. degradans* DSM 17024^T. In addition, the unidentified phospholipids detected in strain SW-11^T were not detected in the two reference strains. These results suggested that there are some differences in the polar lipid profiles of the three strains.

Sensitivity of strain SW-11^T to antibiotics was analysed by the diffusion method on MA. Discs containing the following antibiotics (all from Oxoid; 8 mm diameter) were used: ampicillin (10 µg), chloramphenicol (30 µg), gentamicin (10 µg), kanamycin (30 µg), nalidixic acid (30 µg), novobiocin (30 µg), rifampicin (5 µg), penicillin G (10 U), streptomycin (10 µg) and tetracycline (30 µg). The effects of antibiotics on cell growth were assessed after 3 days of incubation at 30 °C. The strain was considered susceptible when the diameter of the inhibition zone was >13 mm, intermediate at 10–12 mm and resistant at <10 mm, as described by Nokhal & Schlegel (1983).

Detailed results of phenotypic and chemotaxonomic characterization are given in the genus and species descriptions and in Tables 1 and 2. Several phenotypic and chemotaxonomic characteristics can be used to differentiate strain SW-11^T from the related genera *Teredinibacter* and *Saccharophagus*. Strain SW-11^T can be differentiated from *T. turnerae* ATCC 39867^T by the presence of $C_{17:1\omega8c}$ and anteiso- $C_{17:1\omega9c}$ (Table 1) and the absence of glycolipid and aminolipids and the presence of diphosphatidylglycerol and several additional phospholipids (Supplementary Fig. S4). Strain SW-11^T is also distinguished from *T. turnerae* ATCC 39867^T by its colony pigmentation, the ability to grow on Difco MA, the inability to grow at lower NaCl concentrations, its ability to produce indole and to hydrolyse gelatin, corn oil, lecithin and starch, the presence of C14 lipase and cystine arylamidase, the absence of α -galactosidase and β -galactosidase and the utilization of D-mannose and propionic acid as carbon and energy sources. Phenotypic

and chemotaxonomic characteristics such as the presence of $C_{17:1\omega8c}$ and anteiso- $C_{17:1\omega9c}$ (Table 1), the absence of aminolipids and the presence of several additional phospholipids (Supplementary Fig. S4), the smaller cell size, the lower NaCl range for growth, the inability to grow at 4 °C, the ability to produce indole, the absence of eumelanin production, the presence of C14 lipase, valine arylamidase, cystine arylamidase, trypsin, α -chymotrypsin and acid phosphatase, the inability to hydrolyse agar, alginate, chitin or CM-cellulose, the ability to hydrolyse gelatin, corn oil, lecithin and Tweens 40 and 80 and the utilization of D-mannose, acetic acid, propionic acid and succinic acid as carbon and energy sources (Table 2) may be helpful in differentiating strain SW-11^T from *S. degradans* DSM 17024^T.

Strain SW-11^T shares 93.2% 16S rRNA gene sequence similarity with *T. turnerae* T7902^T and 92.1% with *S. degradans* 2-40^T. The suggested lower cut-off of 95% 16S rRNA gene sequence similarity for genera (Yarza *et al.*, 2008; Tindall *et al.*, 2010) seems reasonable, and there are several differential phenotypic and chemotaxonomic characteristics between the novel strain and these two related genera. From the results of 16S rRNA gene sequencing, it appears that strain SW-11^T is distinct from any other genera in the order *Alteromonadales*. Consequently, on the basis of a combination of genotypic and phenotypic differences among strain SW-11^T, *T. turnerae* ATCC 39867^T and *S. degradans* DSM 17024^T, we suggest that strain SW-11^T represents a new genus and species in the order *Alteromonadales*, for which the name *Pseudoteredinibacter isopora* gen. nov., sp. nov. is proposed.

Description of *Pseudoteredinibacter* gen. nov.

Pseudoteredinibacter (Pseu'do.te.re.di'ni.bac'ter. Gr. adj. *pseudes* false; N.L. masc. n. *Teredinibacter* a bacterial generic name; N.L. masc. n. *Pseudoteredinibacter* false *Teredinibacter*).

Cells are Gram-negative, chemoheterotrophic, motile, aerobic rods. The predominant fatty acids are summed feature 3 ($C_{16:1\omega7c}$ and/or $C_{16:1\omega6c}$), $C_{17:1\omega8c}$, summed feature 8 ($C_{18:1\omega6c}$ and/or $C_{18:1\omega7c}$), $C_{16:0}$ and anteiso- $C_{17:1\omega9c}$. The major polar lipids are phosphatidylethanolamine and phosphatidylglycerol. The major respiratory quinones are Q-9 and Q-8. The DNA G + C content of the type strain of the type species is 51.6 mol%. The type species is *Pseudoteredinibacter isopora*.

Description of *Pseudoteredinibacter isopora* sp. nov.

Pseudoteredinibacter isopora (N.L. n. *Isopora* the scientific name of a genus of coral; N.L. gen. n. *isopora* of *Isopora*, referring to the isolation of the type strain from a coral belonging to the genus *Isopora*).

Displays the following properties in addition to those described for the genus. Cells are motile by a single polar

Table 2. Differential characteristics of strain SW-11^T, *T. turnerae* ATCC 39867^T and *S. degradans* DSM 17024^T

Strains: 1, *P. isoporaе* SW-11^T; 2, *T. turnerae* ATCC 39867^T; 3, *S. degradans* DSM 17024^T. Data were acquired in this study except for the DNA G + C contents of *T. turnerae* (range of values for six isolates from Distel *et al.*, 2002) and *S. degradans* DSM 17024^T (data from Ekborg *et al.*, 2005). +, Positive; –, negative; w, weakly positive. All strains are Gram-negative and oxidase- and catalase-positive.

Characteristic	1	2	3
Colony colour	Colourless, semi-translucent	Yellow–brown	Cream
Cell shape	Rods	Pleomorphic rods	Pleomorphic rods
Cell length (µm)	0.7–1.2	3.0–6.0	1.5–3.0
Growth on MA (Difco)	+	–	+
NaCl range for growth (% w/v)	2–4	0.5–4	1–10
pH range for growth	7–8	6–10.5	4.5–10
Temperature range for growth (°C)	10–45	20–35	4–37
Indole production	+	–	–
Eumelanin production	–	–	+
Enzyme activities (API ZYM)			
C14 lipase	+	–	–
Valine arylamidase	+	+	–
Cystine arylamidase	+	–	–
Trypsin	+	+	–
α-Chymotrypsin	+	+	–
Acid phosphatase	+	+	–
α-Galactosidase	–	+	–
β-Galactosidase	–	+	–
Hydrolysis of:			
Agar	–	–	+
Alginate	–	–	+
Chitin	–	–	+
CM-cellulose	–	+	+
Starch	w	–	+
Gelatin	+	–	–
Corn oil	+	–	–
Lecithin	+	–	–
Tweens 40 and 80	+	+	–
Carbon utilization of:			
D-Fructose	–	+	–
D-Mannose	+	–	–
Sucrose	–	+	–
Acetic acid	+	+	–
Propionic acid	+	–	–
Succinic acid	+	+	–
Major fatty acids (≥9.9%)*	SF3, C _{17:1} ω8c, SF8, C _{16:0} , ai-C _{17:1} ω9c	SF8, C _{16:0} , SF3	C _{16:0} , C _{17:0} , SF8
Polar lipids†	PE, PG, PS, DPG, PL1–4	PE, PG, PS, GL, AL1–2, PL5	PE, PG, PS, DPG, AL3, PL6–9
Isolation source	Coral	Endosymbiont of teredinid bivalve	Salt marsh
DNA G + C content (mol%)	51.6	49–51	45.8

*ai, Anteiso-branched; SF3, summed feature 3 (C_{16:1}ω7c and/or C_{16:1}ω6c); SF8, summed feature 8 (C_{18:1}ω6c and/or C_{18:1}ω7c).

†DPG, Diphosphatidylglycerol; PE, phosphatidylethanolamine; PG, phosphatidylglycerol; PS, phosphatidylserine; AL1–3, unknown aminolipids; GL, unknown glycolipid; PL1–9, unknown phospholipids.

flagellum. After 48 h growth on MA at 30 °C, mean cell size is 0.3–0.4 × 0.7–1.2 µm. Colonies are round, entire, convex, colourless and semi-translucent, approximately 0.8–1.0 mm in diameter on MA after 48 h incubation at 30 °C. Grows at 10–45 °C (optimum, 30–35 °C), at pH 7.0–8.0 (optimum, pH 7.5) and with 2.0–4.0% (w/v) NaCl (optimum, 2.5–3.0%). Eumelanin production is not observed. No

accumulation of poly-β-hydroxybutyrate granules. Positive for oxidase, catalase, DNase, lipase (corn oil) and hydrolysis of starch, gelatin, aesculin, lecithin and Tweens 20, 40, 60 and 80. Negative for hydrolysis of agar, alginate, chitin, CM-cellulose and casein. In API 20NE tests, negative for glucose acidification, arginine dihydrolase and urease and assimilation of glucose, mannose, malate, arabinose, mannitol,

gluconate, caprate, adipate, citrate and phenylacetate; positive for nitrate and nitrite reduction, indole production, β -glucosidase, protease and assimilation of *N*-acetylglucosamine and maltose. In the API ZYM system, alkaline phosphatase, C4 esterase, C8 esterase lipase, C14 lipase, leucine arylamidase, valine arylamidase, cystine arylamidase, trypsin, α -chymotrypsin, acid phosphatase and naphthol-AS-BI-phosphohydrolase activities are present, and α -galactosidase, β -galactosidase, β -glucuronidase, α -glucosidase, β -glucosidase, *N*-acetyl- β -glucosaminidase, α -mannosidase and α -fucosidase activities are absent. The following compounds are oxidized in the Biolog GN2 MicroPlate: Tweens 40 and 80, D-arabitol, cellobiose, α -D-glucose, D-mannose, acetic acid, β -hydroxybutyric acid, γ -hydroxybutyric acid, α -ketoglutaric acid, propionic acid, quinic acid, D-saccharic acid, succinic acid, bromosuccinic acid, succinamic acid, glucuronamide, L-alaninamide, D- and L-alanine, L-alanyl glycine, L-asparagine, L-aspartic acid, L-glutamic acid, glycyl L-aspartic acid, glycyl L-glutamic acid, L-histidine, hydroxy-L-proline, L-leucine, L-ornithine, L-phenylalanine, L-proline, L-pyrogutamic acid, D- and L-serine, L-threonine, DL-carnitine, γ -aminobutyric acid, urocanic acid, inosine, uridine, thymidine, phenylethylamine, putrescine, 2-aminoethanol, 2,3-butanediol, glycerol, DL- α -glycerol phosphate, α -D-glucose 1-phosphate and D-glucose 6-phosphate. All other substrates in the GN2 microplate are not oxidized. Utilizes the following compounds as carbon and energy sources: cellobiose, aesculin, D-glucose, D-mannose, acetate, propionate, succinate, glycerol, L-alanine, L-arginine, L-asparagine, L-aspartate, L-glycine, L-glutamic acid, L-histidine, L-leucine, L-lysine, L-phenylalanine, L-proline, L-serine, L-threonine, L-valine and urea. The following compounds are not used as carbon and energy sources: amygdalin, L-arabinose, D-fructose, D-galactose, lactose, maltotriose, maltose, D-ribose, D-salicin, trehalose, xylose, sucrose, citrate, gluconate, lactate, malate, malonate, pyruvate, adonitol, *myo*-inositol, D-mannitol, L-cysteine, L-isoleucine, L-methionine and L-tryptophan. The type strain is sensitive to discs containing rifampicin (5 μ g), kanamycin (30 μ g), nalidixic acid (360 μ g), chloramphenicol (30 μ g), gentamicin (10 μ g), novobiocin (30 μ g), tetracycline (30 μ g), streptomycin (10 μ g) and penicillin (10 U) but is resistant to ampicillin (10 μ g). Minor polar lipids include phosphatidylserine, diphosphatidylglycerol and four unknown phospholipids.

The type strain, SW-11^T (=BCRC 17935^T =LMG 25246^T), was isolated from the coral *Isopora palifera*.

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