Paracoccus isopora sp. nov., isolated from the reef-building coral *Isopora palifera*

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A bacterial strain, designated SW-3^T, was isolated from the reef-building coral *Isopora palifera*, from Southern Taiwan, and was characterized by using a polyphasic taxonomic approach. Cells of strain SW-3^T were Gram-reaction-negative, aerobic, rod-shaped and motile by means of monopolar flagella and formed cream-white colonies. Phylogenetic analyses based on 16S rRNA gene sequences showed that strain SW-3^T belonged to the genus *Paracoccus* and its most closely related neighbours were *P. aestuarii* B7^T, *P. homiensis* DD-R11^T, *P. marinus* KKL-A5^T, *P. denitrificans* DSM 413^T and *P. zeaxanthinifaciens* R-1512^T, with sequence similarities of 96.8, 96.6, 96.1, 95.8 and 94.9%, respectively. Strain SW-3^T exhibited optimal growth at 25–30 °C and pH 9–10 and in 3–5% (w/v) NaCl. The predominant cellular fatty acid was summed feature 8 (C_{18:1}ω7c and/or C_{18:1}ω6c; 75%). The major respiratory quinone was Q-10. The polar lipid profile consisted of a mixture of diphosphatidylglycerol, phosphatidylglycerol, phosphatidylcholine and several uncharacterized polar lipids. The DNA G + C content of strain SW-3^T was 63.7 mol%. The results of physiological and biochemical tests allowed clear phenotypic differentiation of this isolate from recognized species of the genus *Paracoccus*. It is evident from the genotypic, phenotypic and chemotaxonomic data that strain SW-3^T represents a novel species of the genus *Paracoccus*, for which the name *Paracoccus isopora* sp. nov. is proposed. The type strain is SW-3^T (=LMG 25205^T =BCRC 17967^T).

The genus *Paracoccus*, first proposed by Davis *et al.* (1969), belongs to the family *Rhodobacteraceae* of the order *Rhodobacterales* in the class *Alphaproteobacteria* of the phylum *Proteobacteria*. At the time of writing, the genus *Paracoccus* comprised 30 recognized species. Members of the genus *Paracoccus* are metabolically versatile and are widely distributed, having been isolated from a variety of different environments, including soil (Siller *et al.*, 1996; Tsubokura *et al.*, 1999), a bioreactor (La *et al.*, 2005), activated sludge (Liu *et al.*, 2006), root nodules (Deng *et al.*, 2010), cornetfish (Kim *et al.*, 2010) and the marine environment (Berry *et al.*, 2003; Kim *et al.*,

2006). In addition to this, at least one species of the genus *Paracoccus* has been identified as an occasional pathogen of humans (Daneshvar *et al.*, 2003; Wallet *et al.*, 2010). The aim of the present study was to determine the taxonomic position of a *Paracoccus*-like isolate, designated strain SW-3^T, which was isolated from the reef-building coral *Isopora palifera*, collected off the coast of Southern Taiwan.

A 50 g sample of coral was collected in a sterile bag from the Kenting coast, Pingtung County, Southern Taiwan (21° 56' 29" N 120° 44' 70" E), at a depth of 3–8 m, stored at 4 °C and transported to the laboratory within 3–4 h. The coral sample was ground and plated on marine agar 2216 (MA; BD Difco) by using a standard dilution plating method. After incubation of the plates at 25 °C for 5 days, a pure culture of strain SW-3^T was obtained from a single colony. The strain was preserved at –80 °C in a suspension containing 20% (v/v) glycerol in marine broth 2216 (MB; BD Difco) or by lyophilization with 20% (w/v) skimmed

Abbreviations: DPG, diphosphatidylglycerol; PC, phosphatidylcholine; PG, phosphatidylglycerol.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain SW-3^T is FJ593906.

One supplementary figure and one supplementary table are available with the online version of this paper.

milk. Five type strains, *Paracoccus zeaxanthinifaciens* JCM 21774^T, *Paracoccus aestuarii* JCM 15119^T, *Paracoccus marinus* NBRC 100637^T, *Paracoccus homiensis* KACC 11518^T and *Paracoccus denitrificans* BCRC 12285^T, were obtained from their respective culture collections and used as reference strains for phenotypic and genotypic tests.

The bacterial cells were observed by phase-contrast microscopy (DM 2000; Leica) in the lag, exponential and stationary phases of growth to ascertain their morphology. Cell motility was tested by using the hanging-drop and semi-solid agar methods. Spot Test Flagella Stain (BD Difco) was used for flagellum staining. The Gram Stain Set S kit (BD Difco) and Ryu non-staining KOH method (Powers, 1995) were used to test the Gram reaction. Poly- β -hydroxybutyrate granule accumulation was observed under light microscopy after staining of the cells with Sudan Black. Colony morphology was examined using a stereoscopic microscope (SMZ 800; Nikon). The optimum pH range for growth was examined in MB using glycine/HCl, citrate/Na₂HPO₄, phosphate or glycine/NaOH buffers to adjust the media to pH 3–4, 4–8, 6–8 or 9–11, respectively, in pH unit intervals of 1. The pH was adjusted prior to sterilization and post-sterilization tests revealed only minor changes in the pH. Tolerance to 0, 0.5, 1, 2, 3, 4 and 5 % (w/v) NaCl was tested on NaCl-free MB, prepared according to the formula of the BD Difco medium, with the NaCl concentration altered as required. Cell growth was measured at 4–45 °C in MB. For all tests, growth was determined by measuring the turbidity (OD₆₀₀) of the cultures. Anaerobic cultivation was performed on MA using the Oxoid AnaeroGen system.

Extraction of genomic DNA, PCR amplification and sequencing of the 16S rRNA gene were carried out as

previously described (Chen *et al.*, 2001). The 16S rRNA gene sequence of strain SW-3^T was obtained using a DNA sequencer (ABI Prism 310; Applied Biosystems). The almost-complete 16S rRNA gene sequence (1426 nt) of strain SW-3^T was compared against those of related species available from the EzTaxon server (Chun *et al.*, 2007), the Ribosomal Database Project (Maidak *et al.*, 2001) and the GenBank database (<http://blast.ncbi.nlm.nih.gov/Blast.cgi>). After multiple alignments of the data were performed in CLUSTAL_X (Thompson *et al.*, 1997), analysis of the sequence data was performed by using the software package BioEdit (Hall, 1999) and MEGA version 3.1 (Kumar *et al.*, 2004). Distances, corrected according to Kimura's two-parameter model (Kimura, 1983), were calculated and clustering was performed using the neighbour-joining method (Saitou & Nei, 1987). Maximum-likelihood (Felsenstein, 1981) and maximum-parsimony (Kluge & Farris, 1969) trees were also reconstructed by using the treeing algorithms in the PHYLIP software package (Felsenstein, 1993). In each case, bootstrap values were calculated based on 1000 replications. A comparison of the 16S rRNA gene sequence of strain SW-3^T with those of members of genera of the order *Rhodobacterales* in the class *Alphaproteobacteria* showed that the strain fell within the radiation occupied by the genus *Paracoccus* (Fig. 1). In the phylogenetic tree based on the neighbour-joining algorithm, strain SW-3^T formed a coherent clade with species of the genus *Paracoccus*. A similar topology was obtained in phylogenetic trees reconstructed using the maximum-parsimony and maximum-likelihood algorithms (Fig. 1). According to pairwise sequence comparisons, strain SW-3^T was most closely related to *P. aestuarii* B7^T (96.8 % 16S rRNA gene sequence similarity), *P. homiensis* DD-R11^T (96.6 %), *P. marinus* KKL-A5^T (96.1 %), *P. denitrificans* DSM 413^T (95.8 %) and

Fig. 1. Neighbour-joining phylogenetic tree based on 16S rRNA gene sequences showing the position of strain SW-3^T and closely related species of the genus *Paracoccus*. Numbers at nodes are bootstrap percentages (>50 %) based on the neighbour-joining (above nodes) and maximum-parsimony (below nodes) tree-making algorithms. Filled circles indicate branches of the tree that were also recovered using the maximum-likelihood and maximum-parsimony tree-making algorithms. Open circles indicate that the corresponding nodes were also recovered in the tree generated with the maximum-parsimony algorithm. *Pelagibaca bermudensis* HTCC 2601^T was used as an outgroup. Bar, 0.01 substitutions per nucleotide position.

P. zeaxanthinifaciens R-1512^T (94.9%). 16S rRNA gene sequence similarities between strain SW-3^T and other species with validly published names within the order *Rhodobacterales* were <95.7%.

The DNA G + C content of strain SW-3^T was estimated as described by Mesbah *et al.* (1989). The nucleoside mixture was separated by means of HPLC. The DNA G + C content of strain SW-3^T was 63.7 ± 1.0 mol%. Isoprenoid quinones were purified by the methods outlined in Minnikin *et al.* (1984) and analysed by HPLC as described by Collins (1985). The major isoprenoid quinone of strain SW-3^T was Q-10.

Biomasses of strains SW-3^T, *P. aestuarii* JCM 15119^T, *P. homiensis* KACC 11518^T, *P. marinus* NBRC 100637^T, *P. denitrificans* BCRC 12285^T and *P. zeaxanthinifaciens* JCM 21774^T were obtained after growing the strains on MA at 30 °C for 3 days under aerobic conditions. Fatty acid methyl esters were prepared, separated and identified according to the instructions for the Microbial Identification System (MIDI) (Sasser, 1990). The predominant fatty acid constituent of strain SW-3^T was summed feature 8 (C_{18:1}ω7c and/or C_{18:1}ω6c; 75.0%). The fatty acid profile of strain SW-3^T was similar to that of other members of the genus *Paracoccus*; however, there were differences in the proportions of some components (Table 1). The fatty acid profile of strain SW-3^T showed a pattern distinct from *P. denitrificans* BCRC 12285^T. In contrast with the other five strains, *P. denitrificans* BCRC 12285^T possessed fatty acids C_{11:0} 2-OH, anteiso-C_{12:0},

anteiso-C_{13:0} and C_{18:1}ω9c. Furthermore, the quantity of fatty acid C_{16:0} in *P. denitrificans* BCRC 12285^T was relatively higher (16.2%) and the quantity of fatty acid summed feature 8 (C_{18:1}ω7c and/or C_{18:1}ω6c) was relatively lower (57.1%) than the other reference strains.

Polar lipids were extracted and analysed by two-dimensional TLC according to the methods of Lechevalier *et al.* (1977). Strain SW-3^T exhibited a complex polar lipid profile consisting of diphosphatidylglycerol (DPG), phosphatidylglycerol (PG), phosphatidylcholine (PC), an unidentified aminolipid (AL1), two unidentified glycolipids (GL1 and GL2) and four unidentified phospholipids (PL1–4) (see Supplementary Fig. S1, available in IJSEM Online). Its closest relatives, *P. aestuarii* JCM 15119^T, *P. homiensis* KACC 11518^T, *P. marinus* NBRC 100637^T, *P. denitrificans* BCRC 12285^T and *P. zeaxanthinifaciens* JCM 21774^T, exhibited very similar polar lipid profiles all having DPG, PG, PC, unidentified aminolipid AL1 and unidentified phospholipids PL1 and PL2. However, unidentified glycolipid GL1 was present in strain SW-3^T, *P. homiensis* KACC 11518^T, *P. marinus* NBRC 100637^T and *P. zeaxanthinifaciens* JCM 21774^T but was absent in *P. aestuarii* JCM 15119^T and *P. denitrificans* BCRC 12285^T. Also, unidentified phospholipid PL4 was detected in strains SW-3^T, *P. aestuarii* JCM 15119^T, *P. homiensis* KACC 11518^T, *P. marinus* NBRC 100637^T and *P. denitrificans* BCRC 12285^T but was not detected in *P. zeaxanthinifaciens* JCM 21774^T. Although there are some differences between the polar lipid profiles of strain SW-3^T and its closest

Table 1. Cellular fatty acid composition of strain SW-3^T and related species of the genus *Paracoccus*

Strains: 1, SW-3^T; 2, *P. marinus* NBRC 100637^T; 3, *P. aestuarii* JCM 15119^T; 4, *P. homiensis* KACC 11518^T; 5, *P. zeaxanthinifaciens* JCM 21774^T; 6, *P. denitrificans* BCRC 12285^T. All strains were grown on MA agar at 30 °C for 3 days. Values are percentages of the total fatty acids. Fatty acids that make up <1% of the total are not shown. For unsaturated fatty acids, the position of the double bond is located by counting from the methyl (ω) end of the carbon chain.

Fatty acid	1	2	3	4	5	6
C _{10:0} 3-OH	4.1	5.2	8.8	4.1	7.8	4.3
C _{11:0} 2-OH	—	—	—	—	—	1.1
C _{12:0}	—	1.6	—	—	—	—
anteiso-C _{12:0}	—	—	—	—	—	3.2
anteiso-C _{13:0}	—	—	—	—	—	1.5
C _{14:0}	—	1.2	—	—	—	—
C _{16:0}	1.5	4.4	1.8	—	2.1	16.2
C _{18:0}	10.2	7.2	8.6	4.4	6.0	4.9
C _{18:0} 3-OH	—	—	—	—	1.9	—
C _{18:1} ω9c	—	—	—	—	—	1.4
C _{18:1} ω7c 11-methyl	1.1	—	—	5.1	—	—
C _{19:0} cyclo ω8c	3.3	—	—	—	—	—
Summed features*						
2	—	—	5.6	1.7	5.4	3.6
3	—	—	—	—	2.8	1.2
8	75.0	79.9	74.7	80.4	72.8	57.1

*Summed features are groups of two or three fatty acids that cannot be separated by GLC using the MIDI system. Summed feature 2 comprises C_{14:0} 3-OH and/or iso-C_{16:1} I, 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.

relatives, the similarities among them suggest they belong to the same genus.

Strain SW-3^T was examined for a broad range of phenotypic properties. Activities of catalase, oxidase, DNase and lipase and hydrolysis of starch, casein and Tweens 20, 40, 60 and 80 were determined according to standard methods (Gerhardt *et al.*, 1994; MacFaddin, 2000). Hydrolysis of 1% (w/v) sodium alginate was tested on MA (Hosoya *et al.*, 2009). Hydrolysis of chitin was tested using agar medium supplemented with 0.2% colloidal chitin (Hsu & Lockwood, 1975). The commercially available API 20 NE and API ZYM (bioMérieux) and the MicroPlate GN2 (Biolog) microtest systems were used to determine the biochemical properties, enzyme activities and carbohydrate utilization pattern of strain SW-3^T. API ZYM tests were performed according to the manufacturer's recommendation and results were read after 4 h of incubation at 37 °C. Because strain SW-3^T required 3–5% NaCl for optimal growth, for MicroPlate GN2 and API 20 NE tests, the bacterial sample was suspended 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). The results of the API 20 NE and MicroPlate GN2 tests were read after 72 h of incubation at 30 °C.

Sensitivity to antibiotics was tested by spreading cells (0.5 McFarland standard) on MA and using discs containing the following antibiotics (µg per disc): ampicillin (10), chloramphenicol (30), gentamicin (10), kanamycin (30), nalidixic acid (30), novobiocin (30), penicillin G (10), rifampicin (5), streptomycin (10), sulphamethoxazole (23.75) plus trimethoprim (1.25) and tetracycline (30). The effects of the antibiotics on cell growth were assessed after 3 days of incubation at 30 °C. The diameter of the antibiotic discs was 8 mm. The strain was considered to be susceptible when the diameter of the inhibition zone was >13 mm, intermediately susceptible at 10–12 mm and resistant at <10 mm as described by Nokhal & Schlegel (1983).

The physiological, biochemical and morphological characteristics of strain SW-3^T are given in the species description, Table 2 and Supplementary Table S1. Examination of phenotypic and genotypic characteristics revealed many common traits between the novel strain and its closest relatives, *P. aestuarii* JCM 15119^T, *P. homiensis* KACC 11518^T, *P. marinus* NBRC 100637^T, *P. denitrificans* BCRC 12285^T and *P. zeaxanthinifaciens* R-1512^T. All strains were Gram-reaction-negative, heterotrophic, aerobic, oxidase- and catalase-positive and had a large proportion of C_{18:1ω7c} and/or C_{18:1ω6c}. The predominant respiratory quinone of all the strains was Q-10 and

Table 2. Differential characteristics of strain SW-3^T and related species of the genus *Paracoccus*

Strains: 1, SW-3^T; 2, *P. marinus* NBRC 100637^T; 3, *P. aestuarii* JCM 15119^T; 4, *P. homiensis* KACC 11518^T; 5, *P. zeaxanthinifaciens* JCM 21774^T; 6, *P. denitrificans* BCRC 12285^T. All listed characteristics were obtained in this study except for the DNA G + C contents of taxa 2–6, which were obtained from the following sources: Khan *et al.* (2008), for *P. marinus* KKL-A5^T; Roh *et al.* (2009), for *P. aestuarii* B7^T; Kim *et al.* (2006), for *P. homiensis* DD-R11^T; Berry *et al.* (2003), for *P. zeaxanthinifaciens* R-1512^T and Liu *et al.* (2008), for *P. denitrificans* DSM 413^T. +, Positive; –, negative; w, weakly positive. All strains were Gram-reaction-negative and oxidase- and catalase-positive.

Characteristic	1	2	3	4	5	6
Colony colour	Creamy white	Creamy white	Dull orange	Deep yellow	Deep orange	Creamy white
Motility	+	–	–	+	–	–
NaCl range for growth (%)	0–12	1–4	0–4	0–14	3–8	0–7
pH range for growth	7–10	6–9	8–10	5–9	6–9	6–8
Temperature range for growth (°C)	4–40	10–35	15–37	10–40	10–40	10–40
Poly-β-hydroxybutyrate accumulation	–	–	+	–	+	+
Arginine dihydrolase	–	+	–	–	w	–
β-Galactosidase	+	–	+	+	+	–
Hydrolysis of:						
Gelatin	–	+	–	+	w	–
Aesculin	+	–	+	+	+	–
Tween 20	+	–	+	–	+	–
Tween 40	+	–	–	–	–	–
Tween 60	+	+	–	–	–	–
Tween 80	+	–	+	–	+	–
Starch	–	–	–	+	–	–
DNA	+	–	–	+	+	+
Polar lipids:						
Unidentified glycolipid GL1	+	+	–	+	+	–
Unidentified phospholipid PL4	+	+	+	+	–	+
DNA G + C content (mol%)	63.7	69.0	62.0	63.0	67.6	66.5

the DNA G+C contents ranged from 62 to 69 mol%. Strain SW-3^T, however, could be clearly differentiated from these species by its ability to grow at a lower temperature (Table 2) and by its inability to utilize DL-lactic acid as a sole carbon source (Supplementary Table S1). Strain SW-3^T could also be differentiated from *P. marinus* NBRC 100637^T by its cell motility, its ability to grow in higher NaCl concentrations and to hydrolyse Tweens 20, 40 and 80, the presence of DNase and β -galactosidase activities, its inability to hydrolyse gelatin and the absence of arginine dihydrolase. Some features differentiated strain SW-3^T from *P. aestuarii* JCM 15119^T, including colony colour, cell motility, a higher NaCl range for growth, the absence of poly- β -hydroxybutyrate accumulation and the ability to hydrolyse Tweens 40 and 60 and DNA. Strain SW-3^T also presented several phenotypic characteristics that differentiated it from *P. homiensis* KACC 11518^T, including a difference in colony colour and the ability to hydrolyse gelatin, starch and Tweens 20, 40, 60 and 80. Other phenotypic properties distinguished strain SW-3^T from *P. zeaxanthinifaciens* JCM 21774^T, such as a difference in colony colour, motility, a higher NaCl range for growth, the absence of poly- β -hydroxybutyrate accumulation, the ability to hydrolyse Tweens 40 and 60, the inability to hydrolyse gelatin and the absence of arginine dihydrolase. In addition, strain SW-3^T could be differentiated from *P. denitrificans* BCRC 12285^T by its motility, its ability to grow in higher NaCl concentrations and hydrolyse aesculin, Tweens 20, 40, 60 and 80, the absence of poly- β -hydroxybutyrate accumulation and the presence of β -galactosidase activity.

Cells of strain SW-3^T were Gram-reaction-negative, rod-shaped, mesophilic, motile by means of a single polar flagellum, catalase- and oxidase-positive and respired with oxygen as the terminal electron acceptor. Cells of strain SW-3^T were able to utilize a wide variety of organic compounds as carbon and energy sources, contained Q-10 as the major quinone and summed feature 8 (C_{18:1}ω7c and/or C_{18:1}ω6c; 75.0%) as the predominant cellular fatty acid and contained 3-hydroxyl fatty acids with C_{10:0} 3-OH predominating. The DNA G+C content of strain SW-3^T was 63.7%mol. These characteristics are consistent with the emended description of the genus *Paracoccus* (Katayama *et al.*, 1995); however, strain SW-3^T was motile and halophilic, whereas most members of the genus *Paracoccus* are non-motile and non-halophilic. Only four known species of the genus *Paracoccus* exhibit motility, *P. versutus*, *P. carotinifaciens*, *P. chinensis* and *P. homiensis*, and, with the exception of *P. homiensis*, these species are all non-halophilic. Strain SW-3^T and *P. homiensis* present several other phenotypic differences, as described above, therefore, strain SW-3^T can be regarded as a member of the genus *Paracoccus*, distinct from other recognized species of the genus.

Strain SW-3^T occupied a distinct position within the genus *Paracoccus*, based on 16S rRNA gene sequence comparisons, and possessed a unique combination of chemotaxonomic and biochemical characteristics (Tables 1 and 2). Taken together, these results suggest that strain SW-3^T represents a novel species of the genus *Paracoccus*, for which the name *Paracoccus isopora* sp. nov. is proposed.

Description of *Paracoccus isopora* sp. nov.

Paracoccus isopora (i.so.por'ae. N.L. gen. n. *isopora* of *Isopora*, a genus of coral, from which the strain was isolated).

Cells are Gram-reaction-negative, aerobic, rod shaped (0.5–0.7 × 0.7–1.5 μm) and motile by means of monopolar flagella. Colonies are a creamy white colour, circular and convex with entire edges and are ~0.6–0.8 mm in diameter on MA after 48 h of incubation at 30 °C. Growth occurs at 4–40 °C (optimum 25–30 °C), pH 7–10 (optimum pH 9–10) and in 0–12% (w/v) NaCl (optimum 3–5%). Negative for poly- β -hydroxybutyrate granule accumulation. Positive for oxidase, catalase and DNase activities and hydrolysis of aesculin and Tweens 20, 40, 60 and 80. Negative for lipase activity (hydrolysis of corn oil) and hydrolysis of casein, starch, alginate and chitin. In API 20 NE tests: positive for aesculin hydrolysis and β -galactosidase activity; negative for nitrate reduction, indole production, gelatin hydrolysis, D-glucose fermentation and arginine dihydrolase and urease activities. In API ZYM tests: positive for alkaline phosphatase, C4 esterase, C8 esterase lipase, C14 lipase, leucine arylamidase, valine arylamidase, acid phosphatase, naphthol-AS-BI-phosphohydrolase, α - and β -galactosidase, α - and β -glucosidase, α -mannosidase and α -fucosidase activities; negative for cystine arylamidase, trypsin, α -chymotrypsin, β -glucuronidase and N-acetyl- β -glucosaminidase activities. The following compounds are utilized as sole carbon sources in the GN2 microplate: dextrin, Tweens 40 and 80, L-fucose, D-galactose, gentiobiose, α -D-glucose, α -lactose, lactulose, maltose, D-mannitol, sucrose, trehalose, turanose, pyruvic acid methyl ester, succinic acid monomethyl ester, α -, β and γ -hydroxybutyric acid, 2,3-butanediol and glycerol. All other substrates in the GN2 microplate are not utilized. Sensitive to rifampicin, nalidixic acid, kanamycin, chloramphenicol, gentamicin, novobiocin, streptomycin, tetracycline, ampicillin, penicillin G and sulphamethoxazole plus trimethoprim. The predominant cellular fatty acid is summed feature 8 (C_{18:1}ω7c and/or C_{18:1}ω6c). The major respiratory quinone is Q-10. The polar lipids are DPG, PG, PC, an unidentified aminolipid (AL1), two unidentified glycolipids (GL1 and GL2) and four unidentified phospholipids (PL1–4).

The type strain, SW-3^T (=LMG 25205^T = BCRC 17967^T), was isolated from a reef-building coral, *Isopora palifera*, collected off the coast of Southern Taiwan. The DNA G+C content of the type strain is 63.7 mol%.

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