Ekhidna lutea gen. nov., sp. nov., a member of the phylum *Bacteroidetes* isolated from the South East Pacific Ocean

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A novel aerobic, heterotrophic bacterium, designated BiosLi39^T, was isolated from the South East Pacific Ocean. Cells were Gram-negative gliding rods forming yellow colonies on marine agar. The isolate was oxidase-, catalase- and alkaline phosphatase-positive and β -galactosidase-negative. Strain BiosLi39^T grew at 20–37 °C (optimum 30 °C), at pH 7.0–9.0 (optimum pH 8.0) and with 20–60 g NaCl l⁻¹ (optimum 30–50 g NaCl l⁻¹). The fatty acids (>1 %) comprised iso-C_{14:0}, iso-C_{15:1} G, iso-C_{15:0}, anteiso-C_{15:0}, C_{15:1} G, C_{15:0}, iso-C_{15:0} 2-OH, iso-C_{16:1} G, iso-C_{16:0}, iso-C_{16:0} 3-OH, iso-C_{16:0} 2-OH, iso-C_{17:0} 3-OH, C_{17:0} 2-OH and three unidentified components with equivalent chain lengths of 17.87, 18.10 and 18.71. A significant proportion of the hydroxylated fatty acids are amide-linked. The lipid pattern indicated the presence of phosphatidylethanolamine, two unidentified aminolipids and three unidentified polar lipids. The strain contained menaquinone 7 as the sole respiratory lipoquinone and did not produce flexirubin-type pigments. The G+C content of the genomic DNA was 37.2 mol%. Comparative 16S rRNA gene sequence analysis indicated that strain BiosLi39^T was distantly related to all of the representatives of the phylum *Bacteroidetes*. Its closest relative was *Marinoscillum furvescens* IFO 15994^T, with which it shared 92.5 % 16S rRNA gene sequence similarity. On the basis of genotypic, phenotypic and chemotaxonomic characteristics, we propose a novel genus and species, *Ekhidna* gen. nov., sp. nov., with type strain BiosLi39^T (=DSM 19307^T =CIP 109600^T =OBB 398^T).

Members of the phylum *Bacteroidetes* have a worldwide distribution in marine and terrestrial ecosystems. They are particularly common and abundant in many freshwater and marine systems (Kirchman, 2002). Although all of the cultured strains of this group are Gram-negative chemoheterotrophs, they display a high degree of biological diversity with respect to their biochemical and physiological properties and chemotaxonomic characteristics, which is also reflected in their genotypic diversity.

The taxonomy of this large group of bacteria, formerly classified as the group *Cytophaga-Flavobacterium-Bacteroides*

(Olsen *et al.*, 1994), has a long history of nomenclatural modifications and large sections are in need of taxonomic clarification. As an example, the differentiation between members of the genera *Cytophaga*, *Flavobacterium* and *Flexibacter* has been problematic because of the numerous phenotypic similarities between the representatives and because delineation relied for a long time mainly on the presence or absence of gliding motility, a feature that is now considered as a common ancestral property that may be lost by some organisms in the course of their evolution. The taxonomy of the phylum *Bacteroidetes* has been partially clarified by rRNA similarity studies (Paster *et al.*, 1985; Gherna & Woese, 1992; Nakagawa & Yamasato, 1993, 1996; Bernardet *et al.*, 1996; Nakagawa *et al.*, 2002) and chemotaxonomic analyses (Dees *et al.*, 1985; Nakagawa & Yamasato, 1993, 1996).

During the last decade, many novel taxa belonging to this phylum have been characterized. In parallel, the general application of polyphasic taxonomy has led to taxonomic re-evaluation or reclassification of misclassified taxa

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Abbreviation: ECL, equivalent chain length.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain BiosLi39^T is AM746475.

A graph showing the effect of temperature on the maximum growth rate of strain BiosLi39^T is available with the online version of this paper.

(Vandamme *et al.*, 1994; Bernardet *et al.*, 1996; Nakagawa & Yamasato, 1996; Johansen *et al.*, 1999; Suzuki *et al.*, 2001; Sakamoto *et al.*, 2002). Nevertheless, the phylogenetic positions of many taxa are still not clear-cut (Suzuki *et al.*, 2001; Bernardet *et al.*, 2002) and the boundaries of classes and families, as well as the phenotypic and genotypic characteristics of these taxonomic levels, are still not well defined. In this study, a novel marine member, strain BiosLi39^T, of the phylum *Bacteroidetes* is described.

In November–December 2004, seawater samples were collected in the oligotrophic waters of the South East Pacific Gyre (28° 32.176' S 104° 18.480' W) during the BIOSOPE oceanographic cruise. A sample collected at a depth of 5 m (21 °C, 35.9 ‰ salinity) was used to inoculate marine broth (MB; Difco), which was incubated at 25 °C. The enrichment was spread on marine agar (MA; Difco). Strain BiosLi39^T was isolated from a yellow colony by repeated streaking on MA. Stock cultures were stored at –80 °C in MB supplemented with 5 % (v/v) DMSO or 35 % (v/v) glycerol.

The almost-complete 16S rRNA gene sequence (1368 bp) of the strain was obtained from a single colony as described elsewhere (Agogu *et al.*, 2005); both strands were sequenced. The sequence was compared with those in available databases using BLAST (Altschul *et al.*, 1990) and aligned with its nearest neighbours using CLUSTAL X (Thompson *et al.*, 1997). The alignment was refined manually using SEAVIEW (Galtier *et al.*, 1996) based on an alignment generated in parallel with the RDP II sequence aligner (http://rdp8.cme.msu.edu/cgis/seq_align.cgi) before calculating identity percentages from 1325 unambiguously aligned nucleotides for a similarity matrix. Phylogenetic reconstructions were represented graphically using PHYLIP version 3.67 (<http://evolution.genetics.washington.edu/phylip/getme.html>) on the basis of evolutionary distances (neighbour-joining method with Jukes and Cantor corrections) (Saitou & Nei, 1987) and maximum likelihood (Felsenstein, 1981). The robustness of the inferred topologies was assessed by bootstrap analyses (Felsenstein, 1985) based on 1000 resamplings for the neighbour-joining method and 100 replications for the maximum-likelihood method. A phylogenetic tree reconstructed with the maximum-likelihood method is shown in Fig. 1. The 16S rRNA gene sequence analysis revealed that strain BiosLi39^T belonged to the phylum *Bacteroidetes*. Within this lineage, strain BiosLi39^T formed a separate lineage within a robust cluster also containing *Marinoscillum furvescens* IFO 15994^T (formerly described as '[*Microscilla*] *furvescens*'; Lewin, 1969) and *Marinoscillum pacificum* MRN461^T, and high bootstrap values for this relationship were observed. The same relationships were recovered in a phylogenetic tree reconstructed with the neighbour-joining method (data not shown). Strain BiosLi39^T shared 92.5 and 91.1 % 16S rRNA gene sequence similarity with *M. furvescens* IFO 15994^T and *M. pacificum* MRN461^T, respectively. Other close phylogenetic neighbours were members of the genus *Roseivirga* (90.0–91.0 %), *Fabibacter halotolerans*

UST030901-097^T (89.5 %), *Marivirga tractuosa* IFO 15989^T (89.0 %) and *Marivirga sericea* IFO 15983^T (89.1 %). Such low levels of 16S rRNA gene sequence similarity between strain BiosLi39^T and its nearest neighbours indicated that the isolate represented a novel genus within the phylum *Bacteroidetes*.

The DNA G+C content was determined by the Identification Service of the DSMZ (Braunschweig, Germany), by HPLC analysis of deoxyribonucleosides as described by Mesbah *et al.* (1989). The DNA G+C content of strain BiosLi39^T was 37.2 mol%, which was within the range typically reported for aerobic members of the phylum *Bacteroidetes*.

Colonies of strain BiosLi39^T were smooth, creamy and shiny with entire edges and bright yellow when grown on MA. After 4 days at 25 °C, colonies were 0.5 mm in diameter. Morphological characteristics of the cells were determined by light microscopy (AX70; Olympus) and transmission electron microscopy (H-7500; Hitachi) with negative staining using uranyl acetate (Raguns *et al.*, 1997). Gliding motility was determined using the hanging-drop method on cells grown at 30 °C in low nutrient medium [0.1 % (w/v) marine broth solidified with 1 % agar], as described by Bernardet *et al.* (2002). Cells of strain BiosLi39^T were Gram-negative, non-spore-forming, gliding, thin straight rods, 2.0–6.0 µm in length and 0.3–0.5 µm in width in mid-exponential phase. Longer cells were observed during late stationary phase. The presence of flexirubin-type pigments was investigated by flooding colonies with 20 % KOH and then with acid, as described elsewhere (Reichenbach, 1989; Bernardet *et al.*, 2002); a negative reaction that is characteristic of the absence of flexirubin was observed. The non-diffusive bright yellow colour was probably produced by carotenoid pigments, but no attempt was made to characterize them further.

To analyse respiratory quinones and polar lipids, strain BiosLi39^T was grown on MA at 30 °C for 5 days and checked for purity. Analyses of isoprenoid quinones and polar lipids were carried out by the Identification Service of the DSMZ by the two-stage method (Tindall, 1990a, b), using chloroform/methanol/water (65:25:4) in the first dimension and chloroform/methanol/acetic acid/water (80:12:15:4) in the second dimension and with phosphatidylethanolamine serving as an internal reference point. Menaquinone 7 was the only respiratory quinone (100 %). Phosphatidylethanolamine was the only phospholipid and five other unidentified polar lipids, two containing amino groups, were also present (Fig. 2). It should be noted that the R_f values of the unidentified lipids need to be documented by means of an image of the chromatogram in order to allow comparison with any future work. Phosphosphingolipids were not produced. The presence of phosphatidylethanolamine as the sole predominant diglyceride-based phospholipid, together with an array of various amino acid-based lipids, is typical of polar lipid patterns of most aerobic members of the phylum *Bacteroidetes*.

Fig. 1. Maximum-likelihood dendrogram based on 16S rRNA gene sequences showing the phylogenetic relationships between strain BiosLi39^T and some related taxa. Bootstrap values (>50%) based on 100 replicates are shown at branch nodes. Bar, 0.02 substitutions per nucleotide position.

The determination of the whole-cell fatty acid composition of strain BiosLi39^T was performed on cultures grown at 30 °C for 72 h on MA. This analysis was initially carried out at the DSMZ according to the standard protocol of the Microbial Identification System (MIDI Inc., 2001). Extracts were analysed using a Hewlett Packard model HP6890A gas chromatograph equipped with a flame-ionization detector, as described by Kämpfer & Kroppenstedt (1996). However, a number of peaks were not identified and further studies were undertaken using the two-stage method of Labrenz *et al.* (1998) that detects fatty acids with ester links (stage 1) and ester and non-ester (amide) links (stage 2). Fatty acid peaks were initially identified using the MIDI system using

the TSBA 5.0 peak-naming table and checked by mass spectrometry using a Varian CP-3800 GC coupled to a Varian 320-MS mass spectrometer and fitted with a Varian CP-8400 auto-sampler. The presence of unsaturated fatty acids was confirmed by bromination (Brian & Gardner, 1968), the presence of 3-OH fatty acids by the presence of dominant peaks at m/z 103 and the presence of 2-OH fatty acids by the presence of peaks at m/z $M^+ - 59$ and m/z 90. The fatty acids are reported in Table 1, with a differentiation between only ester-linked fatty acids and both ester-linked and amide-linked fatty acids. Briefly, the following observations were made. Summed feature 3 (iso-C_{15:0} 2-OH and/or C_{16:1}ω7c) was shown by mass spectrometry and the fact that it was not affected by bromination suggested that it comprises iso-C_{15:0} 2-OH. The fact that increased levels of this fatty acid and a number of the other 2-OH and 3-OH fatty acids were released in higher concentrations only after hydrolysis under conditions that released amide-linked fatty acids is consistent with the presence of amide-linked 2-OH and 3-OH fatty acids being present in capnine-like compounds (Godchaux & Leadbetter, 1984). This is also consistent with polar lipid patterns where lipids that do not stain with any of the 'normal' spray reagents have R_f values similar to authentic capnine derivatives in the same solvent systems (B. J. Tindall, unpublished), although further structural work is needed to clarify the structure of the lipids labelled L1, L2 and L3 (Fig. 2). Amide-linked 3-OH fatty acids have also been shown to be present in the aminolipids of *Flavobacterium johnsoniae* (*Cytophaga johnsonae*) (Kawazoe *et al.*, 1991). A fatty acid with an equivalent chain length (ECL) of 16.863 was identified by the peak-naming table as C_{17:1}ω6c, but was clearly a C_{16:0} 2-OH fatty acid, which was tentatively identified as iso-C_{16:0} 2-OH on the basis of its ECL (this fatty acid is not included in the peak-naming tables of the MIDI system that were available). A peak with an ECL of 14.814 was not identified by the MIDI system, but was shown to be a C_{15:1} isomer by mass spectrometry. Preliminary structural elucidation suggests that the double bond in this compound is located at the same position as in

Fig. 2. Thin-layer chromatogram of the polar lipids of strain BiosLi39^T. AL, unidentified aminolipid; L, unidentified polar lipid; PE, phosphatidylethanolamine. TLC was performed on silica gel thin layers using chloroform/methanol/water (65:25:4) in the first dimension and chloroform/methanol/acetic acid/water (80:12:15:4) in the second dimension and with phosphatidylethanolamine serving as an internal reference point.

Table 1. Whole-cell fatty acid profiles of strain BiosLi39^T and its closest phylogenetic neighbours

Strains: 1, *Ekhidna lutea* gen. nov., sp. nov. BiosLi39^T; 2, *Marinoscillum furvescens* DSM 4134^T (Seo *et al.*, 2009); 3, *Marinoscillum pacificum* MRN 461^T=JCM 1406^T (Seo *et al.*, 2009). Column A shows only ester-linked fatty acids. Column B shows both ester-linked fatty acids and amide-linked fatty acids. Values in bold represent hydroxy fatty acids that are ester- and amide-linked. tr, Trace; –, not detected/not reported.

Fatty acid (%)	1		2	3
	A	B		
iso-C _{14:0}	1.6	1.0	–	–
C _{14:0}	–	–	1.5	1.1
C _{14:0} 2-OH	–	–	3.9	2.6
iso-C _{15:1} G	29.3	23.4	tr	3.2
iso-C _{15:0}	32.7	27.9	19.8	8.5
anteiso-C _{15:0}	3.0	2.2	–	–
C _{15:1} G*	0.0	2.5	–	–
C _{15:0}	3.5	2.8	tr	0.9
iso-C _{15:0} 2-OH†	6.8	12.3	–	–
C _{15:0} 2-OH	0.3	0.5	tr	1.5
iso-C _{16:1} G	4.6	5.0	–	–
iso-C _{16:0}	2.8	2.5	1.9	3.2
C _{16:1} ω5c	–	–	21.6	28.5
C _{16:0}	1.8	0.9	2.6	3.5
iso-C _{16:0} 3-OH	1.6	1.5	–	–
iso-C _{16:0} 2-OH‡	0.8	1.4	–	–
C _{16:0} 2-OH	–	–	tr	1.2
C _{16:0} 3-OH	–	–	1.2	1.9
iso-C _{17:0}	–	–	tr	1.0
C _{17:1} ω6§	–	–	tr	1.8
iso-C _{17:0} 3-OH	4.0	7.3	4.1	9.8
C _{17:0} 2-OH	0.6	1.3	–	–
C _{17:0} 3-OH	1.2	0.7	tr	1.0
Summed features				
3	–	–	34.8	22.2
4	–	–	tr	1.0
Unknown ECLs				
14.959	–	–	1.3	1.1
17.87	0.0	3.2	–	–
18.10	2.2	1.3	–	–
18.71	3.0	2.2	–	–

*Not identified by the MIDI system.

†Identified as summed feature 3 (iso-C_{15:0} 2-OH and/or C_{16:1}ω7c) by the MIDI system.

‡Identified as C_{17:1}ω6c by the MIDI system.

§May be incorrectly identified by the MIDI system.

||Summed features represent two or three fatty acids that cannot be separated by the Microbial Identification System. Summed feature 3 consisted of iso-C_{15:0} 2-OH and/or C_{16:1}ω7c. Summed feature 4 consisted of iso-C_{17:1} I and/or anteiso-C_{17:1} B.

the compounds identified as iso-C_{15:1} G and iso-C_{16:0} G, which suggests that they are part of a (chemically) homologous series. The novel fatty acid that is not listed

in the MIDI Sherlock peak-naming table is labelled C_{15:1} G. This information, together with the absence of significant quantities of unsaturated fatty acids with alternative stereochemistry of the double bond, indicates that C_{15:1} G exists in strain BiosLi39^T, together with appropriate enzymes and genes. Further work on the identification of these fatty acids is in progress.

Unless stated otherwise, physiological characterization of strain BiosLi39^T was performed in triplicate in MB in the dark and aerobically under agitation. Growth was routinely monitored by measuring the increase in optical density at 600 nm using a spectrophotometer. Cell numbers were determined by flow cytometry in order to calculate calibration curves. Growth rates were calculated using linear regression analysis with five to nine points along the logarithmic portions of the resulting growth curves. Growth was tested at 9, 15, 20, 25, 30, 33, 37, 40 and 44 °C on MB medium. The novel isolate was mesophilic and grew at 20–37 °C (optimum 30 °C; Supplementary Fig. S1, available in IJSEM Online). No growth was observed at 15 and 40 °C. Growth at pH 4.0–10.0 (at intervals of one pH unit) was tested at 30 °C in MB after adjustment to the required pH as described elsewhere (Alain *et al.*, 2002). The pH range for growth was rather narrow (pH 7.0–9.0) with a marked optimum at pH 8.0, which is close to that of seawater. Growth with 2, 5, 10, 20, 30, 40, 50, 60, 70 and 90 g NaCl l⁻¹ was tested at 30 °C in MB. Growth was observed with 20–60 g NaCl l⁻¹ (optimum 30–50 g NaCl l⁻¹) and no growth was observed at 10 and 70 g NaCl l⁻¹. This experiment demonstrated that strain BiosLi39^T is a general marine-type halophile.

Strain BiosLi39^T was found to be aerobic. Conventional phenotypic tests including those for oxidase, catalase and nitrate reductase were performed according to standard methods (Smibert & Krieg, 1994). The isolate was catalase- and oxidase-positive and did not reduce nitrate. Biochemical tests were performed at 30 °C using the API ZYM system (bioMérieux), according to the manufacturer's instructions, using cells swabbed from the surface of MA and suspended in half-strength artificial seawater (Sigma). Supplementary biochemical tests were also performed using the API 20NE system (bioMérieux), according to the manufacturer's instructions. Substrate utilization was investigated as described elsewhere (Alain *et al.*, 2008). In summary, negative reactions were observed for gelatinase, urease, arginine dihydrolase, indole- and β-galactosidase production and a positive reaction was observed for glucose fermentation. Strain BiosLi39^T was able to hydrolyse aesculin, but not agar, cellulose (filter paper), gelatin or urea. Strain BiosLi39^T produced alkaline phosphatase, esterase (C4), esterase lipase (C8), cystine arylamidase, leucine arylamidase, valine arylamidase, trypsin, α-chymotrypsin, acid phosphatase and naphthol-AS-BI-phosphohydrolase, but not lipase (C14), α-fucosidase, α-galactosidase, β-galactosidase, α-glucosidase, β-glucosidase, α-mannosidase or N-acetyl-β-glucosaminidase. Strain BiosLi39^T assimilated citric acid, malic acid and phenylacetic acid and grew on yeast extract and peptone.

Antibiotic sensitivity tests were performed with susceptibility discs (Bio-Rad) or filter-paper discs impregnated with different antibiotics on MA at 30 °C for 1 week. Susceptibility was scored for zone diameters more than 10 mm. Strain BiosLi39^T was sensitive to vancomycin, rifampicin, tetracycline, penicillin, polymyxin B and ciprofloxacin and was resistant to oxacillin.

Strain BiosLi39^T is most closely phylogenetically related to members of the genus *Marinoscillum*, family 'Flexibacteraceae', and more distantly related to members of the genera *Roseivirga*, *Fabibacter*, *Reichenbachiella* and *Fulvivirga*, family 'Flammeovirgaceae'. Characteristics that differentiate strain BiosLi39^T from representatives of these genera are given in Table 2. In brief, in addition to phylogenetic distance, strain BiosLi39^T can be distinguished from its closest relatives by a number of genotypic and phenotypic features, including gliding motility, colony pigmentation, fatty acid profile, some enzyme activities, inability to degrade some high-molecular-mass compounds and genomic DNA G+C content. The value of the chemotaxonomic data in differentiating a new genus from the genera most closely related to strain BiosLi39^T is limited because there is a need for comprehensive studies on these and related taxa and on the identity of some fatty acids previously reported. Nevertheless, major differences can be observed in the fatty acid profile of strain BiosLi39^T and those of its two closest relatives.

In conclusion, in view of all the above-mentioned distinctive features, we propose that strain BiosLi39^T be assigned to a novel genus and species, for which the name *Ekhidna lutea* gen. nov., sp. nov. is proposed.

Description of *Ekhidna* gen. nov.

Ekhidna (E'khid.na. N.L. fem. n. *Ekhidna* a sea nymph-dragon of Greek mythology producing slime, referring to the creaminess and smoothness of the colonies).

Cells are Gram-negative, non-spore-forming, rod-shaped and motile by gliding. Aerobic and chemoorganoheterotrophic. Mesophilic. Neutrophilic. Grow best at NaCl concentrations close to marine salinity. Oxidase-, catalase- and alkaline phosphatase-positive. The predominant quinone is MK-7. The fatty acid profile comprises exclusively ester-linked fatty acids (iso-C_{14:0}, iso-C_{15:1} G, iso-C_{15:0}, anteiso-C_{15:0}, C_{15:0}, iso-C_{16:1}, iso-C_{16:0}, iso-C_{16:0} 3-OH, unknown ECL 18.10 and unknown ECL 18.71) and ester- and amide-linked fatty acids (iso-C_{15:1} G, iso-C_{15:0} 2-OH, iso-C_{16:0} 2-OH, iso-C_{17:0} 3-OH, C_{17:0} 2-OH and unknown ECL 17.87). The polar lipid pattern comprises phosphatidylethanolamine, two unidentified aminolipids and three unidentified polar lipids. The R_f values of the unidentified compounds are shown in Fig. 2. Affiliated to the phylum *Bacteroidetes* (16S rRNA gene sequence analysis). The DNA G+C content is 37.2 mol%. The type species is *Ekhidna lutea*.

Description of *Ekhidna lutea* sp. nov.

Ekhidna lutea (lu'te.a. L. fem. adj. *lutea* gold yellow, the colour of the colonies on marine agar).

In addition to the characters described for the genus, displays the following characteristics. Colonies on MA medium are smooth, convex, brilliant with entire edges and intensely yellow. Flexirubin-type pigments are not

Table 2. Characteristics differentiating strain BiosLi39^T from closely related taxa

Taxa: 1, *Ekhidna lutea* sp. nov. BiosLi39^T; 2, *Marinoscillum furvescens* LMG 13023^T; 3, *Marinoscillum pacificum* MRN 461^T; 4, *Roseivirga ehrenbergii* KMM 6017^T; 5, *Fabibacter halotolerans* UST030701-097^T; 6, *Reichenbachiella agariperforans* KMM 3525^T; 7, *Fulvivirga kasyanovii* KMM 6220^T. Data were taken from Lau *et al.* (2006), Nedashkovskaya *et al.* (2003, 2005, 2007), Seo *et al.* (2009) and this study. A, Apricot; B, brown; O, orange; P, pink; Y, yellow; +, positive; −, negative; ND, not determined.

Characteristic	1	2	3	4	5	6	7
Gliding motility	+	+	+	−	+	+	+
Pigmentation	Y	O	A	P	P	O	PB
Flexirubin	−	−	−	−	−	+	−
Conditions for growth							
Range (% NaCl)	2–6	0.4–9.3	0.4–5.4	1–8	0–12	1–6	0–10
Range (°C)	20–37	15–45	15–40	4–39	12–36	4–35	12–44
β-Galactosidase	−	−	−	+	+	ND	+
Hydrolysis of:							
Agar	−	−	−	−	−	+	−
Gelatin	−	+	−	+	−	+	+
Production of:							
Indole	−	−	+	−	−	−	−
Acid from glucose	−	−	−	−	+	−	−
16S rRNA gene sequence similarity with strain BiosLi39 ^T (%)	100	92.5	91.1	91.0	89.5	89.3	88.8
DNA G+C content (mol%)	37.2	44.0	41.5	40.2	42.5	44.5	59.9

produced. Grows on yeast extract and peptone. Grows at 20–37 °C (optimum 30 °C), at pH 7.0–9.0 (optimum pH 8.0) and with 20–60 g NaCl l⁻¹ (optimum 30–50 g NaCl l⁻¹). Positive for oxidase, catalase and alkaline phosphatase, but negative for β -galactosidase, gelatinase, urease and arginine dihydrolase. Does not reduce nitrate. Does not produce indole. Hydrolyses aesculin, but not agar, cellulose (filter paper), gelatin or urea. Does not produce acid from glucose. Produces esterase (C4), esterase lipase (C8), cystine arylamidase, leucine arylamidase, valine arylamidase, trypsin, α -chymotrypsin, acid phosphatase and naphthol-AS-BI-phosphohydrolase, but not lipase (C14), α -fucosidase, α -galactosidase, β -galactosidase, α -glucosidase, β -glucosidase, α -mannosidase or *N*-acetyl- β -glucosaminidase. Assimilates citric acid, malic acid and phenylacetic acid. The DNA G+C content of the type strain is 37.2 mol%.

The type strain, BiosLi39^T (=DSM 19307^T =CIP 109600^T =OBB 398^T), was isolated from marine waters of the South East Pacific Gyre.

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