Streptomyces glycovorans sp. nov., *Streptomyces xishensis* sp. nov. and *Streptomyces abyssalis* sp. nov., isolated from marine sediments

Ying Xu,[1]† Jie He,[1]† Xin-Peng Tian,[2]† Jie Li,[2] Ling-Ling Yang,[1] Qiong Xie,[3] Shu-Kun Tang,[1] Yi-Guang Chen,[4] Si Zhang[2] and Wen-Jun Li[1,5]

Correspondence
Wen-Jun Li
wjli@ynu.edu.cn
Qiong Xie
xieqiong@gmail.com

[1]The Key Laboratory of Microbial Diversity in Southwest China, Ministry of Education and Laboratory for Conservation and Utilization of Bio-Resources, Yunnan Institute of Microbiology, Yunnan University, Kunming 650091, PR China

[2]Key Laboratory of Marine Bio-resources Sustainable Utilization, RNAM Center for Marine Microbiology, Guangdong Key Laboratory of Marine Materia Medica, South China Sea Institute of Oceanology, Chinese Academy of Sciences, Guangzhou 510301, PR China

[3]State Key Lab of Space Medicine Fundamentals and Application, China Astronaut Research and Training Center, Beijing 100094, PR China

[4]College of Biology and Environmental Sciences, Jishou University, Jishou 416000, PR China

[5]Key Laboratory of Biogeography and Bioresource in Arid Land, Chinese Academy of Science, Xinjiang Institute of Ecology and Geography, Chinese Academy of Sciences, Ürumqi 830011, PR China

Strains YIM M 10366^T, YIM M 10378^T and YIM M 10400^T were isolated from marine sediments collected from the Xisha Islands in the South China Sea. All three isolates were able to grow optimally at pH 7.0, 28–37 °C and 0–3 % (w/v) NaCl. Comparison of 16S rRNA gene sequences showed that these strains are members of the genus *Streptomyces*, exhibiting moderately high 16S rRNA gene sequence similarities of 97.0–98.8 % to members of the most closely related *Streptomyces* species. Morphological characteristics, physiological characteristics and compositions of whole-cell sugars and phospholipids are consistent with the diagnostic characteristics of the genus *Streptomyces*, but still allowed differentiation amongst the three strains and their neighbours. Based on 16S rRNA gene sequence analysis, DNA–DNA relatedness, phenotypic characteristics and chemotaxonomic data, strains YIM M 10366^T, YIM M 10378^T and YIM M 10400^T were identified as members of three novel species of the genus *Streptomyces*, for which the names *Streptomyces glycovorans* sp. nov. (type strain YIM M 10366^T =DSM 42021^T =CCTCC AA2010005^T), *Streptomyces xishensis* sp. nov. (type strain YIM M 10378^T =DSM 42022^T =CCTCC AA 2010006^T) and *Streptomyces abyssalis* sp. nov. (type strain YIM M 10400^T =DSM 42024^T =CCTCC AA 2010008^T) are proposed.

Abundant actinobacteria are distributed throughout the marine environment, from shallow waters to the deep sea, and have generated strong interest as sources of novel bioactive substances (Takizawa *et al.*, 1993; Mincer *et al.*, 2002; Stach *et al.*, 2003). Around 70–80 % of presently known bioactive metabolites that originate from actinomycetes were isolated from members of the genus *Streptomyces*, and this is also true for marine environments (Pathom-aree *et al.*, 2006). We have isolated and deposited many actinobacterial strains that were isolated from the South China Sea and described two new marine actinomycete genera and one novel species (Tian *et al.*, 2009a, b, c). In this study, strains YIM M 10366^T, YIM M 10378^T and YIM M 10400^T were isolated from marine sediment samples collected from the South China Sea. Data from the present taxonomic study indicate that

†These authors contributed equally to this work.

Abbreviations: DPG, diphosphatidylglycerol; PE, phosphatidylethanolamine; PG, phosphatidylglycerol; PI, phosphatidylinositol; PIM, phosphatidylinositol mannosides; PME, phosphatidylmethylethanolamine.

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of strains YIM M 10366^T, YIM M 10378^T and YIM M 10400^T are HQ585117, HQ585118 and HQ585121, respectively.

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

these strains represent three novel species of the genus *Streptomyces*.

Marine sediment samples were collected from the Xisha Islands in the South China Sea in September 2009. Strain YIM M 10366^T was isolated from a sample collected at 17° 33′ 35.661″ N 110° 22′ 47.058″ E at a depth of 778 m. The sample was processed by using the dilution-plating method. The culture was obtained from modified Gauze no. 1 medium [20 g soluble starch, 1 g KNO_3, 0.5 g K_2HPO_4, 0.05 g $MgSO_4.7H_2O$, 0.5 g NaCl, 0.01 g $FeSO_4.7H_2O$, 25 mg cycloheximide, 15 g agar, pH 7.2–7.4, per litre artificial seawater (containing, per litre distilled water: 24.530 g NaCl, 5.200 g $MgCl_2$, 4.090 g Na_2SO_4, 1.160 g $CaCl_2$, 0.201 g $NaHCO_3$, 0.101 g KBr, 0.027 g H_3BO_3)] after growth at 28 °C for 30 days. Strains YIM M 10378^T and YIM M 10400^T were isolated from two deep-sea sediment samples, collected at 17° 27′ 34.988″ N 110° 28′ 46.641″ E at a depth of 1198 m and at 17° 59′ 48.135″ N 114° 34′ 16.668″ E at a depth of 3587 m, respectively, by using the dilution/heat method described previously by Jensen *et al.* (2005) on Gauze no. 1 medium after incubation at 28 °C for 20 days. All three isolates were further cultivated on modified 2216E medium [per litre distilled water: 1 g peptone, 1 g yeast extract, 0.01 g $FeSO_4.7H_2O$, 4 g $(NH_4)_2SO_4$, 0.1 g $CaCO_3$, 15 g agar, pH 7.2–7.4] at 28 °C and maintained as glycerol suspensions (20 %, v/v) at −80 °C. Biomass for chemical and molecular studies was collected by cultivation in TSB medium in flasks on a rotary shaker at 120 r.p.m. at 28 °C for 1 week and harvested by centrifugation at 5000 r.p.m., washed twice with distilled water and then freeze-dried.

Morphological properties were examined by light microscopy (BH-2; Olympus) and scanning electron microscopy (Philips XL30; ESEM-TMP) with 14-day-old cultures on ISP medium 2 modified with 50 % artificial seawater instead of distilled water. Cultural characteristics were determined by using ISP media (Shirling & Gottlieb, 1966) and Czapek's, potato-glucose and nutrient agars (Dong & Cai, 2001) at 28 °C for 7, 15 and 30 days. The colours of both substrate and aerial mycelium and soluble pigments produced were determined by comparison with chips from the colour charts of the ISCC–NBS (Kelly, 1964).

The morphological properties of strains YIM M 10366^T, YIM M 10378^T and YIM M 10400^T were consistent with their assignment to the genus *Streptomyces* (see Fig. S1, available in IJSEM Online). Strains YIM M 10366^T, YIM M 10378^T and YIM M 10400^T formed, respectively, yellow–white, white and moderate yellow aerial mycelia that did not change colour when grown on ISP 2 medium, while the colour of the aerial mycelium of *Streptomyces nanshensis* SCSIO 01066^T (Tian *et al.*, 2009b), the closest phylogenetic neighbour of the novel strains (see below), varied from white to olive-green. Strain YIM M 10366^T formed white and yellow aerial mycelium on Czapek's and ISP 2 agars, respectively, and no aerial mycelium was observed on ISP 3, ISP 5, potato-glucose or nutrient agars. Strain YIM M 10378^T formed white aerial mycelium on all media tested. Aerial mycelium of strain YIM M 10400^T grown on different media was white (Czapek's agar, ISP 3 and nutrient agar), moderate yellow (ISP 2 agar), yellowish white (ISP 5 agar) or strong yellow (potato-glucose agar). Strains YIM M 10366^T, YIM M 10378^T and YIM M 10400^T could be distinguished from each other by using a battery of cultural characteristics (Table S1).

Growth at 4, 12, 28, 37, 45, 50, 55 and 65 °C, pH 4.0–10.0 (at intervals of 1.0 pH unit) and 0, 1, 3, 5, 7, 10, 12, 15, 20 and 25 % (w/v) NaCl was tested for 4 weeks by using Czapek's medium as the basal medium. Oxidase activity was determined from the oxidation of tetramethyl-*p*-phenylenediamine. Catalase activity was determined with 3 % H_2O_2, and bubble production was identified as a positive reaction. Antibiotic susceptibility was examined as described by Groth *et al.* (2004) using antibiotic discs on ISP 2 agar medium incubated at 28 °C for 7 days by the disc-diffusion plate method (Bauer *et al.*, 1966); the concentration of antibiotic was 10 μg per disc. Other phenotypic characteristics were tested by following the standard procedures of Tindall *et al.* (2007). Detailed differential physiological and biochemical properties of strains YIM M 10366^T, YIM M 10378^T and YIM M 10400^T are summarized in the species descriptions and Table 1.

Amino acids in cell-wall hydrolysates were analysed by HPLC after precolumn derivatization with *o*-phthalaldehyde (Tang *et al.*, 2009). Whole-cell sugars were detected by HPLC after precolumn derivatization with 1-phenyl-3-methyl 5-pyrazolone (Hasegawa *et al.*, 1983). Polar lipids were extracted according to Xin *et al.* (2000) and were identified by two-dimensional TLC as described by Tindall (1990). Menaquinones were collected following Collins (1994) and then analysed by HPLC (Tamaoka *et al.*, 1983). Cellular fatty acids were determined by using the Sherlock Microbial Identification System (MIDI) according to the manufacturer's instructions. Fatty acid methyl esters were then analysed by using the Microbial Identification software package (Sherlock version 4.0; MIDI database, TSBA40). The G+C content of genomic DNA was determined by using the HPLC method (Mesbah *et al.*, 1989).

Cell-wall hydrolysates of strains YIM M 10366^T, YIM M 10378^T and YIM M 10400^T contained LL-diaminopimelic acid, which suggested that they belong to cell-wall type I (Lechevalier & Lechevalier, 1970). Whole-cell hydrolysates of all three isolates contained glucose, galactose, mannose and ribose. Strains YIM M 10366^T and YIM M 10378^T also contained xylose and an unknown component, while strain YIM M 10400^T contained two other unknown components. All three isolates contained five major phospholipids: phosphatidylglycerol (PG), diphosphatidylglycerol (DPG), phosphatidylmethylethanolamine (PME), phosphatidylinositol (PI) and phosphatidylinositol mannosides (PIM). Phosphatidylethanolamine (PE) was detected in strain YIM M 10366^T only (Table 1 and Fig. S2). Moreover, strains YIM M 10366^T and YIM M 10378^T had an unknown

ninhydrin-negative phospholipid that was close to PME on the TLC plates; this phospholipid was not detected in the phospholipid pattern of strain YIM M 10400^T (Fig. S2). The major menaquinones (>5 %) of strain YIM M 10366^T and YIM M 10378^T were MK-9(H_8) and MK-9(H_6), whereas those of strain YIM M 10400^T were MK-9(H_8), MK-9(H_6) and MK-9(H_4). In addition, the amounts of minor menaquinones differed between the strains (Table 1 and Fig. S3). For strain YIM M 10366^T, fatty acids present at >5 % were iso-$C_{16:0}$ (33.8 %), anteiso-$C_{15:0}$ (24.5 %), anteiso-$C_{17:0}$ (17.5 %), iso-$C_{15:0}$ (6.0 %) and iso-$C_{14:0}$ (5.5 %). For strain YIM M 10378^T, fatty acids present at >5 % were anteiso-$C_{15:0}$ (29.0 %), iso-$C_{16:0}$ (27.0 %), anteiso-$C_{17:0}$ (13.7 %) and iso-$C_{14:0}$ (10.2 %). For strain YIM M 10400^T, fatty acids present at >5 % were anteiso-$C_{15:0}$ (32.7 %), iso-$C_{16:0}$ (26.5 %), anteiso-$C_{17:0}$ (13.4 %), iso-$C_{15:0}$ (8.7 %) and iso-$C_{14:0}$ (5.9 %). The fatty acid profile of *S. nanshensis* SCSIO 01066^T was investigated in parallel; fatty acids present at >5 % were iso-$C_{16:0}$ (29.7 %), anteiso-$C_{15:0}$ (29.3 %), anteiso-$C_{17:0}$ (15.1 %), iso-$C_{15:0}$ (7.9 %) and iso-$C_{14:0}$ (5.8 %), which was consistent with the data of Tian *et al.* (2009b). DNA G+C contents of strains YIM M 10366^T, YIM M 10378^T and YIM M 10400^T were 74.5, 71.4 and 71.3 mol%, respectively. The complete chemotaxonomic profiles of these strains are given in the species descriptions and in Tables 1 and S2.

Extraction of genomic DNA and PCR amplification and sequencing of the 16S rRNA gene were performed as described by Li *et al.* (2007). The resultant 16S rRNA gene sequences were aligned with corresponding sequences of representatives of the genus *Streptomyces* (retrieved from EzTaxon 2.1) by using CLUSTAL_X (Thompson *et al.*, 1997). Phylogenetic analysis was carried out by using three tree-making algorithms, the neighbour-joining (Saitou & Nei, 1987), maximum-likelihood (Felsenstein, 1981) and maximum-parsimony (Fitch, 1971) methods. The software MEGA, version 4.0 (Tamura *et al.*, 2007), was used for phylogenetic tree construction with the neighbour-joining and maximum-parsimony tree-making algorithms. The PHYLIP version 3.6 software package was used to reconstruct the maximum-likelihood tree. Genetic distance matrices were estimated by Kimura's two-parameter model (Kimura, 1980). The topology of the phylogenetic tree was evaluated by using the bootstrap resampling method of Felsenstein (1985) with 1000 replicates.

Almost-complete 16S rRNA gene sequences of strains YIM M 10366^T (1532 bp), YIM M 10378^T (1524 bp) and YIM M 10400^T (1527 bp) were determined. These sequences were analysed by preliminary comparison with sequences in the GenBank database and the results indicated that the three isolates were most closely related to members of the genus *Streptomyces*. Strain YIM M 10366^T showed highest 16S rRNA gene sequence similarities to *S. nanshensis* SCSIO 01066^T (97.6 %) and *Streptomyces haliclonae* DSM 41968^T (97.3 %). The highest 16S rRNA gene sequence similarities of strain YIM M 10378^T were to *S. nanshensis* SCSIO 01066^T (97.9 %) and *Streptomyces marinus* DSM 41970^T (97.7 %). Strain YIM M 10400^T showed 98.8 and 97.5 % 16S rRNA gene sequence similarities to *S. nanshensis* SCSIO 01066^T and *S. marinus* DSM 41970^T, respectively. Phylogenetic analysis also showed that the three strains fell into a distinct subclade with *S. nanshensis* SCSIO 01066^T (Figs 1 and S4). Strains YIM M 10378^T and YIM M 10400^T showed 98.6 % sequence similarity, while they both showed 97.4 % similarity to strain YIM M 10366^T. Genomic relatedness between strains YIM M 10366^T, YIM M 10378^T and YIM M 10400^T and *S. nanshensis* SCSIO 01066^T was determined according to the fluorometric microwell method (Ezaki *et al.*, 1989; Christensen *et al.*, 2000; He *et al.*, 2005). Fluorescence intensities were checked using a fluorescence microplate reader (Spectra Max Gemini xp). Hybridizations were performed with six replications. The DNA–DNA hybridization rate was calculated following the method of He *et al.* (2005). DNA–DNA relatedness values between strains YIM M 10366^T, YIM M 10378^T and YIM M 10400^T and *S. nanshensis* SCSIO 01066^T were 45.7, 58.6 and 47.4 %, respectively (SD 5.1, 3.2 and 4.8 %, respectively). Strains YIM M 10378^T and YIM M 10400^T showed 56.7 % hybridization (SD 2.7 %), while they showed 61.8 and 61.0 % hybridization, respectively, with strain YIM M 10366^T (SD 3.1 and 4.6 %, respectively). These values are well below the 70 % cut-off point recommended for recognition of genomic species (Stackebrandt & Goebel, 1994), indicating that strains YIM M 10366^T, YIM M 10378^T and YIM M 10400^T should be considered to represent different genomic species of the genus *Streptomyces*.

In addition to the evidence described above, strains YIM M 10366^T, YIM M 10378^T and YIM M 10400^T can also be distinguished from each other and from their closest relatives by chemotaxonomic characteristics. The differences among them in menaquinone composition were obvious. The DNA G+C contents of strains YIM M 10366^T, YIM M 10378^T and YIM M 10400^T also showed differences. Furthermore, many obvious differences in physiological characteristics among strains YIM M 10366^T, YIM M 10378^T and YIM M 10400^T and *S. nanshensis* SCSIO 01066^T are shown in Tables 1 and S1, including carbon- and nitrogen-source utilization, antibiotic susceptibility tests and several other physiological test results. On the basis of the results obtained in the present study, we consider that strains YIM M 10366^T, YIM M 10378^T and YIM M 10400^T represent three novel species of the genus *Streptomyces*, for which the names *Streptomyces glycovorans* sp. nov., *Streptomyces xishensis* sp. nov. and *Streptomyces abyssalis* sp. nov., respectively, are proposed.

Description of *Streptomyces glycovorans* sp. nov.

Streptomyces glycovorans (gly.co.vo′rans. N.L. pref. *glyco-* from Gr. adj. *glukus* sweet, referring to glucose; L. part. adj. *vorans* eating, devouring; N.L. part. adj. *glycovorans* eating glucose).

Aerobic actinomycete that forms branched substrate mycelium and aerial mycelium that differentiates into

Table 1. Physiological and chemical characteristics of the three novel isolates and their closest relative in the genus *Streptomyces*

Strains: 1, YIM M 10366^T; 2, YIM M 10378^T; 3, YIM M 10400^T; 4, *S. nanshensis* SCSIO 01066^T. Data were obtained in this study under identical conditions. All four strains utilize D-glucose, glycerol and sucrose.

Characteristic	1	2	3	4
Growth at:				
12 °C	+	−	−	+
45 °C	+	−	−	−
Utilization of:				
D-Arabinose	−	−	−	+
Cellobiose	−	+	−	+
D-Galactose	−	−	−	+
Inositol	−	−	−	+
D-Mannose	−	−	−	+
Raffinose	−	−	−	+
L-Rhamnose	−	−	+	+
D-Ribose	+	−	−	+
Trehalose	+	−	−	+
D-Xylose	−	−	−	+
Sodium oxalate	+	−	+	−
Sodium citrate	−	−	−	+
L-Alanine	−	−	+	+
L-Arginine	+	−	−	+
L-Asparagine	+	−	+	+
Glutamic acid	−	−	+	+
Glycine	−	−	+	+
Histidine	−	−	−	+
L-Hydroxyproline	−	−	+	+
Hypoxanthine	+	+	+	−
Lysine	+	−	+	+
Phenylalanine	+	−	+	+
Proline	−	−	+	+
Threonine	−	−	+	+
L-Tyrosine	−	−	+	+
Valine	+	−	+	+
Xanthine	−	−	−	+
Hydrolysis of:				
Urea	−	+	+	+
Tween 20	−	+	+	+
Tween 60	−	−	−	+
Gelatin	+	−	−	−
Milk coagulation	−	+	+	−
Milk peptonization	−	+	+	−
Nitrate reduction	+	+	+	−
Antibiotic resistance				
Ampicillin	−	−	−	+
Ciprofloxacin	+	−	−	+
Clindamycin	+	−	−	−
Erythromycin	+	−	−	+
Norfloxacin	+	−	+	−
Sulfamethoxazole	+	+	−	+
Polar lipids*	DPG, PG, PME, PE, PIM, PI, 6PLs	DPG, PG, PME, PIM, PI, 6PLs	DPG, PG, PME, PIM, PI, 5PLs	PG, DPG, PE, PI, PIM, 4PLs
Menaquinones (%)				
MK-8(H_8)	2.1	−	2.8	2.0
MK-9(H_2)	−	−	0.9	−
MK-9(H_4)	3.4	0.9	9.9	6.8
MK-9(H_6)	9.1	5.1	20.3	12.9

Table 1. cont.

Characteristic	1	2	3	4
MK-9(H_8)	78.6	89.3	64.1	74.3
MK-9(H_{10})	2.1	2.7	1.9	1.8
MK-10(H_6)	4.8	1.2	–	1.9
DNA G+C content (mol%)	74.5	71.4	71.3	73.6

*PL, Unknown polar lipid.

spiral spore chains with smooth-surfaced spores. Soluble pigments are not produced. Optimum growth occurs on Czapek's medium at 28–37 °C, pH 7.0 and 0–3 % (w/v) NaCl. Temperature, pH and NaCl tolerance ranges are 12–45 °C, pH 6.0–9.0 and 0–7 % (w/v) NaCl. Negative for hydrolysis of urea, Tweens 20, 40, 60 and 80, starch and cellulose, milk coagulation and peptonization, oxidase and H_2S production. Positive for nitrate reduction. Catalase is produced. Gelatin is hydrolysed. D-Fructose, glucose, glycerol, maltose, D-mannitol, D-ribose, sucrose, sodium oxalate and trehalose can be utilized as sole carbon sources, but not D-arabinose, cellobiose, D-galactose, inositol, dulcitol, lactose, D-mannose, raffinose, L-rhamnose, D-xylose, sorbitol, sodium citrate or xylitol. L-Arginine, L-asparagine, hypoxanthine, lysine, phenylalanine, serine and valine are used as sole nitrogen sources, but not L-alanine, glutamic acid, glycine, histidine, L-hydroxyproline, proline, threonine, L-tyrosine or xanthine. The diagnostic amino acid in the peptidoglycan is LL-diaminopimelic acid. Glucose, galactose, ribose, mannose, xylose and an unknown sugar are present in whole-cell hydrolysates. Phospholipids are DPG, PG, PME, PE, PI, PIM and six unknown phospholipids. The predominant menaquinone is MK-9(H_8). The major cellular fatty acids are anteiso-$C_{15:0}$, iso-$C_{16:0}$ and anteiso-$C_{17:0}$.

The type strain is YIM M 10366^T (=DSM 42021^T =CCTCC AA 2010005^T), isolated from a marine sediment sample taken at a depth of 778 m from the Xisha Islands sea area of the South China Sea. The genomic DNA G+C content of the type strain is 74.5 mol%.

Description of *Streptomyces xishensis* sp. nov.

Streptomyces xishensis (xi.shen′sis. N.L. masc. adj. *xishensis* of or pertaining to the sea area of the Xisha Islands in the northern part of the South China Sea, from where the type strain was isolated).

Aerobic actinomycete that forms branched substrate hyphae and aerial mycelium that differentiates into spiral spore chains with smooth-surfaced spores. Soluble pigments are not produced. Optimum growth occurs on Czapek's medium at 28–37 °C, pH 7.0 and 0–3 % (w/v) NaCl. Temperature, pH and NaCl tolerance ranges are 28–37 °C, pH 6.0–8.0 and 0–7 % (w/v) NaCl. Negative for hydrolysis of Tweens 20, 40, 60 and 80, starch, cellulose and gelatin, oxidase and H_2S production. Positive for nitrate and catalase reaction, utilization of urea and milk coagulation and peptonization. Cellobiose, fructose, glucose, glycerol, maltose, mannitol and sucrose are used as sole carbon sources, while D-arabinose, inositol, dulcitol, lactose, D-mannose, raffinose, L-rhamnose, D-ribose, trehalose, D-xylose, D-sorbitol, sodium oxalate, sodium citrate and xylitol are not utilized. Serine and hypoxanthine are used as sole nitrogen sources, but not L-alanine, L-arginine, L-asparagine, glutamic acid, glycine, histidine, L-hydroxyproline, lysine, phenylalanine, proline, threonine, L-tyrosine, valine or

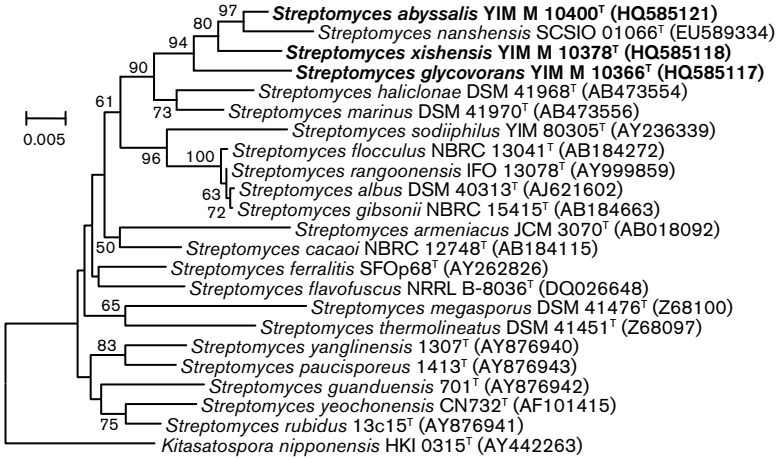

Fig. 1. Neighbour-joining phylogenetic tree reconstructed on the basis of 16S rRNA gene sequences showing the relationships between strains YIM M 10366^T (1532 bp), YIM M 10378^T (1524 bp) and YIM M 10400^T (1527 bp) and related taxa. The sequence of *Kitasatospora nipponensis* HKI 0315^T was used as an outgroup. Numbers represent percentage confidence levels from 1000 replicate bootstrap samplings; values ⩾50 % are shown. Bar, 0.005 substitutions per nucleotide position.

xanthine. The diagnostic amino acid in the peptidoglycan is LL-diaminopimelic acid. Glucose, galactose, ribose, mannose, xylose and an unknown sugar are present in whole-cell hydrolysates. Phospholipids are DPG, PG, PME, PIM, PI and six unknown phospholipids. The predominant menaquinone is MK-9(H_8). The major cellular fatty acids are anteiso-$C_{15:0}$, iso-$C_{16:0}$, anteiso-$C_{17:0}$ and iso-$C_{14:0}$.

The type strain is YIM M 10378^T (=DSM 42022^T =CCTCC AA 2010006^T), isolated from a marine sediment sample collected from a depth of 1198 m in the Xisha Islands sea area of the South China Sea. The genomic DNA G+C content of the type strain is 71.4 mol%.

Description of *Streptomyces abyssalis* sp. nov.

Streptomyces abyssalis (a.bys.sa′lis. L. n. *abyssus* an abyss, the deep sea; L. masc. suff. -*alis* suffix denoting pertaining to; N.L. masc. adj. *abyssalis* pertaining to abyssal depths of the ocean, from which the type strain was isolated).

Aerobic actinomycete that forms branched substrate mycelium and aerial mycelium that differentiates into spiral spore chains with smooth-surfaced spores. Soluble pigments are not produced. Optimum growth occurs on Czapek's medium at 28–37 °C, pH 7.0 and 0–3 % (w/v) NaCl. Temperature, pH and NaCl tolerance ranges are 28–37 °C, pH 6.0–8.0 and 0–6 % (w/v) NaCl. Negative for hydrolysis of Tweens 20, 40, 60 and 80, starch, cellulose and gelatin, oxidase and H_2S production. Positive for nitrate, catalase, utilization of urea and milk coagulation and peptonization. D-Fructose, glucose, glycerol, maltose, mannitol, L-rhamnose, sucrose and sodium oxalate are used as sole carbon sources, but not D-arabinose, cellobiose, D-galactose, inositol, dulcitol, lactose, D-mannose, raffinose, D-ribose, trehalose, D-xylose, D-sorbitol, sodium citrate or xylitol. L-Alanine, L-asparagine, glutamic acid, glycine, L-hydroxyproline, hypoxanthine, lysine, phenylalanine, proline, serine, threonine, L-tyrosine and valine are used as sole nitrogen sources, but not L-arginine, histidine or xanthine. The diagnostic amino acid in the peptidoglycan is LL-diaminopimelic acid. Glucose, galactose, ribose, mannose and two unknown sugars are present in whole-cell hydrolysates. Phospholipids are DPG, PG, PME, PIM, PI and five unknown phospholipids. Predominant menaquinones are MK-9(H_4), MK-9(H_6) and MK-9(H_8). The major cellular fatty acids are anteiso-$C_{15:0}$, iso-$C_{16:0}$ and anteiso-$C_{17:0}$.

The type strain is YIM M 10400^T (=DSM 42024^T =CCTCC AA 2010008^T), isolated from a marine sediment sample taken at a depth of 3587 m from the Xisha Islands sea area of the South China Sea. The genomic DNA G+C content of the type strain is 71.3 mol%.

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