ORIGINAL ARTICLE

Streptomyces bohaisensis sp. nov., a novel actinomycete isolated from *Scomberomorus niphonius* in the Bohai Sea

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A novel actinomycete strain, designated 11A07^T, was isolated from young *Scomberomorus niphonius* in the Bohai Sea. Basic local alignment search tool analyses showed that this isolate had the highest 16S rRNA gene sequence similarity of 97.41% with *Streptomyces rimosus* subsp. *paromomycinus* DSM 41429^T. Phylogenetic tree revealed that strain 11A07^T formed a distinct lineage clustered with *Streptomyces panacagri* Gsoil 519^T, *Streptomyces sodiophilus* YIM 80305^T and *Streptomyces albus* subsp. *albus* NRRL B-2365^T having similarities of 97.30%, 97.10% and 96.83%, respectively. Multilocus sequence analysis further demonstrated that the new isolate was different from the selected representatives of *Streptomyces* as a separate phylogenetic line. Strain 11A07^T produced straight or rectiflexible spore chains with smooth surface, white aerial mycelia and brown diffusible pigments on international streptomyces project 2 medium. Maximum tolerated NaCl concentration for growth was 11.0%. Whole-cell sugars were mannose, ribose, glucose, galactose and xylose. The predominant menaquinones were MK-9(H₂), MK-9(H₄) and MK-9(H₆). The fatty-acid profile contained iso-C_{16:0}, C_{18:0} 10-methyl (tuberculostearic acid) and anteiso-C_{17:0} as the major compositions. The polar lipids consisted of diphosphatidylglycerol, phosphatidylethanolamine, phosphatidylinositol, phosphatidylinositol mannoside and an unknown phospholipid. The G+C content of the genomic DNA was 71.4 mol%. These morphological, phenotypic and chemotaxonomic properties showed that strain 11A07^T could be readily distinguished from the most closely related members of the genus *Streptomyces*. Thus, based on the polyphasic taxonomic data, strain 11A07^T (= JCM 19630^T = CCTCC AA 2013020^T = KCTC 29263^T) represents a novel species within the genus *Streptomyces*, for which the name *Streptomyces bohaisensis* sp. nov. is proposed.

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INTRODUCTION

The genus *Streptomyces* was proposed by Waksman and Henrici¹ to encompass an aerobic, spore-forming group of actinomycetes. The *Streptomyces* is widely distributed in nature and encompasses more than 630 species.² Many members of this genus are a source of a broad range of novel bioactive compounds. According to statistics, actinomycete sources account for about 53% of all microbial bioactive secondary metabolites with 7600 of these compounds (75%) being produced by *Streptomyces*.³ However, it is becoming increasingly difficult to find new leading compounds from common actinomycetes and leads to the costly rediscovery of known compounds.⁴ On the other hand, the demand of anticancer and anti-infectious drug discovery is growing. Hence, the investigation for new actinomycete resource is an important element in drug discovery.

Nowadays, marine actinomycetes have been widely explored for potential source of novel compounds as the environmental conditions of the sea are entirely different from the terrestrial conditions.^{5,6} Although new actinomycetes and antibiotics have been discovered from sponges, algae, mangrove plants and other marine animals and plants,^{7,8} the full suite of actinomycete occupying some special ecological niches have not been fully investigated. Therefore our work was focused on the isolation of actinomycetes from a wide variety of marine animals of the Bohai Sea, such as blue mussel, jellyfish, shrimp, fish, crabs, starfish, sea urchins *etc.*, and on screening for their ability to produce antimicrobials. During our continuous screening for new antibiotics, a putatively novel *Streptomyces* strain 11A07^T from a fish in the Bohai Sea had the genetic potential to produce secondary metabolites related to both polyketides and nonribosomal peptides,

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as well as showed potent antimicrobial activities.⁹ In this study, we report the classification and identification of this new isolate based on polyphasic taxonomy. Further, the name *Streptomyces bohaisensis* sp. nov. 11A07^T is proposed as a novel *Streptomyces* species.

MATERIALS AND METHODS

Strain and maintenance condition

The young *Scomberomorus niphonius* (long, slender, laterally flattened, pelagic fish with longitudinal dark spots on the sides and ~15 cm in fork length) was collected from the Bohai Sea, located in eastern Liaoning Peninsula in northern China (39°20' N, 122°17' E). The specimen was rinsed five times with sterile artificial seawater to remove any transient and loosely attached microorganisms from the surface of the *S. niphonius*. 1 cm³ sections of specimen tissue were excised with a sterile scalpel and ground with a sterilized mortar and pestle. Then tissue homogenates were inoculated on oatmeal agar international streptomyces project (ISP 3) plates using a standard dilution plating method, containing nalidixic acid (25 mg l⁻¹) and cycloheximide (50 mg l⁻¹) to inhibit growth of bacteria and fungi. After incubation at 28 °C for 3 weeks, an isolate designated 11A07^T was picked. The strain was maintained on plates of modified Gauze's synthetic medium No.1 (soluble starch 20.0 g; KNO₃ 1.0 g; MgSO₄·7 H₂O 0.5 g; K₂HPO₄ 0.5 g; FeSO₄·7 H₂O 10.0 mg; agar 15.0 g; artificial sea water 1.0 l; adjust pH 7.0) at 4 °C and as suspensions of spores or mycelia fragments in glycerol (20%, v/v) at -80 °C.

Phenotypic characterization

Strain 11A07^T was cultured for 14 days at 28 °C on tryptic soy agar (TSA) using the coverslip technique.¹⁰ Morphological properties were observed by a light microscope (BH-2; Olympus, Tokyo, Japan) and a scanning electron microscope (Quanta200; FEI, Hillsboro, OR, USA).¹¹ Cultural properties were determined using standard ISP media,¹² Czapek's agar, nutrient agar (Difco, Sparks, MD, USA) and potato dextrose agar (Difco) after incubation at 28 °C for 14 days. Colors of the aerial, substrate mycelia and diffusible pigments were determined using color chips from the ISCC-NBS color charts.

Growth at various NaCl concentrations (0, 0.5, 1.0, 2.0, 3.0, 4.0, 5.0, 6.0, 7.0, 10.0, 11.0, 12.0, 15.0%, w/v) and different temperatures (4, 10, 28, 37, 45, 50 °C) was examined by growing the strain on TSA medium as the basal medium. Growth at different pH values (4.0–11.0, at intervals of 1.0 pH unit) was examined on modified TSA medium using the buffer system described by Xu *et al.*¹³ Oxidase activity was determined by the oxidation of tetramethyl-*p*-phenylenediamine. Catalase activity was determined by 3% H₂O₂, and gas production was identified as a positive reaction. Hydrolysis of starch, gelatin, Tweens 20, 40, 60 and 80, milk coagulation and peptonization were carried out according to methods described by Tindall *et al.*¹⁴ Nitrate reduction and H₂S production were determined using conventional procedures.^{14,15} Carbon-source utilization tests were performed according to the methods described by Shirling and Gottlieb¹² and Athalye *et al.*¹⁶ using modified basal medium¹⁷ supplemented with 0.05% yeast extract.

Chemotaxonomic characterization

The biomass used for analyses of cellular fatty acids was obtained from cultures grown in tryptic soy broth for 7 days in flasks shaken at 180 r.p.m. at 28 °C. The cells were harvested by centrifugation at 4500 r.p.m. for 10 min and washed twice with sterile distilled water. Cellular fatty acids were extracted, methylated and analyzed using the Sherlock Microbial Identification System according to the method of Sasser¹⁸ as the manufacturer's instructions. Fatty acids were then analyzed by GC (Agilent Technologies 7890A GC System, Wilmington, DE, USA) using the Microbial Identification software package (Sherlock Version 6.1; Sherlock Microbial Identification System database TSBA6). The diaminopimelic acid isomer was identified by TLC.¹⁹ The whole-cell sugars were separated by HPLC after pre-column derivatization with 1-phenyl-3-methyl-5-pyrazolone.²⁰ Menaquinones were extracted²¹ and determined by HPLC.²² Polar lipids were extracted and examined according to published procedures.^{23,24}

Molecular characterization

Genomic DNA isolation, PCR amplification of 16S rRNA gene, cloning and sequencing were performed with conventional

Table 1 House-keeping gene sequences of the new isolate and those related *Streptomyces* strains used in the present study

Species	Strain	<i>atpD</i>	<i>gyrB</i>	<i>recA</i>	<i>rpoB</i>	<i>trpB</i>
<i>Streptomyces bohaisensis</i>	11A07 ^T	KM349180	KM349181	KM349182	KM349183	KM349184
<i>S. rimosus</i> subsp. <i>paromomycinus</i>	AS 4.1760 ^T = DSM 41429 ^T	FJ406154	FJ406210	FJ406266	FJ406322	FJ406377
<i>S. chrestomyceticus</i>	JCM 4735 ^T = DSM 40545 ^T	FJ406149	FJ406205	FJ406261	FJ406317	FJ406372
<i>S. albobaciens</i>	JCM 4342 ^T	FJ406148	FJ406204	FJ406260	FJ406316	FJ406371
<i>S. albospinus</i>	AS 4.1628 ^T = NBRC 13846 ^T	FJ406146	FJ406202	FJ406258	FJ406314	FJ406369
<i>S. javensis</i>	DSM 41764 ^T = NBRC 100777 ^T	FJ406177	FJ406233	FJ406289	FJ406344	FJ406400
<i>S. yogyakartensis</i>	DSM 41766 ^T = NBRC 100779 ^T	FJ406178	FJ406234	FJ406290	FJ406345	FJ406401
<i>S. violaceusniger</i>	AS 4.1423 ^T = NBRC 13459 ^T	FJ406139	FJ406195	FJ406251	FJ406307	FJ406362
<i>S. albus</i>	AS 4.1845 ^T	EF031314	EF055001	EF055056	EF055111	EF055166
<i>S. lydicus</i>	AS 4.1412 ^T = NBRC 13058 ^T	FJ406136	FJ406192	FJ406248	FJ406304	FJ406359
<i>S. rhizosphaericus</i>	DSM 41760 ^T = NBRC 100778 ^T	FJ406175	FJ406231	FJ406287	FJ406342	FJ406398
<i>S. endus</i>	AS 4.1377 ^T = NRRL 2339 ^T	FJ406134	FJ406190	FJ406246	FJ406302	FJ406357
<i>S. catenulae</i>	AS 4.1701 ^T = ISP 5258 ^T	FJ406152	FJ406208	FJ406264	FJ406320	FJ406375
<i>S. sioyaensis</i>	AS 4.1306 ^T = NRRL B-5408 ^T	FJ406132	FJ406188	FJ406244	FJ406300	FJ406355
<i>S. angustmyceticus</i>	CGMCC 4.1918 ^T = NBRC 3934 ^T	HQ244475	HQ244480	HQ244485	HQ244490	HQ244495
<i>S. hygrosopicus</i> subsp. <i>hygrosopicus</i>	CGMCC 4.1527 ^T = NRRL 2387 ^T	HQ244473	HQ244478	HQ244483	HQ244488	HQ244493
<i>S. sclerotialis</i>	DSM 43032 ^T	FJ406181	FJ406237	FJ406293	FJ406348	FJ406404
<i>S. demainii</i>	DSM 41600 ^T = NRRL B-1478 ^T	FJ406182	FJ406238	FJ406294	FJ406349	FJ406405
<i>S. nigrescens</i>	AS 4.1410 ^T = NBRC 12894 ^T	FJ406135	FJ406191	FJ406247	FJ406303	FJ406358
<i>S. chattanoogaensis</i>	DSM 40002 ^T	FJ406138	FJ406194	FJ406250	FJ406306	FJ406361

methods.²⁵ Sequence analysis of 16S rRNA gene was performed using Basic Local Alignment Search Tool for Nucleotides (BLASTN). The 16S rRNA gene sequence of strain 11A07^T was compared with sequences from EzBioCloud using basic local alignment search tool (<http://eztaxon-e.ezbiocloud.net/>).²⁶ Multilocus sequence analysis was based on five house-keeping genes *atpD* (ATP synthase F1, beta subunit), *gyrB* (DNA gyrase B subunit), *recA* (recombinase A), *rpoB* (RNA polymerase beta subunit) and *trpB* (tryptophan synthetase, beta subunit) using the primers and protocols described previously.²⁷ Sequence data for the five house-keeping loci for each strain were deposited in GenBank with the accession numbers shown in Table 1. All these gene sequences were aligned with corresponding sequences (retrieved from the GenBank/EMBL/DBJ database) using CLUSTAL X1.83.²⁸ The 16S rRNA gene and five house-keeping gene sequence-concatenated phylogenetic trees were constructed by the Neighbor-Joining,²⁹ Maximum Parsimony³⁰ and Maximum-Likelihood³¹ tree-making algorithms by using the software packages MEGA version 5.0.³² Concatenated sequences of all five protein-coding loci were joined head-to-tail in-frame. Evolutionary distance matrices were generated according to the Kimura's two parameter model.³³ The topologies of the resultant trees were evaluated by bootstrap analysis with 1000 replicates.³⁴ The G+C content of genomic DNA prepared by the method of Marmur³⁵ was determined using the HPLC method as described by Mesbah *et al.*³⁶

RESULTS AND DISCUSSION

Strain 11A07^T was Gram staining positive and aerobic growth. The strain produced extensively branched substrate mycelia and aerial hyphae, but not fragmented. Scanning electron microscopy revealed straight or rectiflexible chains of smooth surfaced spores were borne on aerial hyphae. Spore chains were generally straight and very long containing >50 spores (Figure 1). These characteristics supported strain 11A07^T belonging to the genus *Streptomyces*.³⁷ Strain 11A07^T showed abundant growth on ISP 2, ISP 3, ISP 5, TSA, Czapek solution agar and Nutrient agar, but moderate growth on ISP 4 and poor growth on potato dextrose agar. White aerial mycelium was observed on these media, but variety of substrate mycelium color was displayed on different media. Brown diffusible pigments were detected on ISP 2 and Czapek solution agar (Table 2). The growth temperature for strain 11A07^T was 15–40 °C (optimum 28 °C). The strain 11A07^T grew at pH 6–10 (optimum 8–9) and 0–11% (w/v) NaCl (optimum 1). It could utilize glucose, L-rhamnose, D-galactose, inositol, raffinose, D-mannitol, salicin, sorbitol, sucrose and sodium citrate as sole carbon source for

growth, but not L-arabinose, D-fructose and D-xylose. Other physiological characteristics are given in Table 3 and in the species description.

LL-diaminopimelic acid was detected in the peptidoglycan of strain 11A07^T. The cell wall sugars were mannose, ribose, glucose, galactose and xylose. The predominant menaquinones were found with MK-9 (H₂) 12.7%, MK-9 (H₄) 60.3% and MK-9 (H₆) 25.0%. The fatty-acid profile contained iso-C_{16:0} (37.5%), C_{18:0} 10-methyl, tuberculostearic acid (20.0%) and anteiso-C_{17:0} (11.8%) as the major compositions (Supplementary Table S1). The polar lipids identified were diphosphatidylglycerol, phosphatidylethanolamine, phosphatidylinositol, phosphatidylinositol mannoside and an unknown phospholipid (Figure 2). These characteristics were consistent with those of genus *Streptomyces*.

The DNA G+C content of the genomic DNA of this strain was 71.4 mol%. An almost complete 16S rRNA gene sequence (1520 bp) was obtained for isolate 11A07^T. The 16S rRNA gene sequence of strain 11A07^T was submitted in the GenBank Database under the accession number KF682221. Sequence analysis showed that 16S rRNA gene sequence of strain 11A07^T to be most similar to those of *Streptomyces rimosus* subsp. *paromomycinus* DSM 41429^T, *Streptomyces chrestomyceticus* DSM 40545^T, and *Streptomyces panacagri* Gsoil 519^T, with sequence identities of 97.41%, 97.40% and 97.30%, respectively. Further phylogenetic analyses revealed that strain 11A07^T formed a distinct branch separate from other representatives of the genus *Streptomyces* and most closely related with *S. panacagri* Gsoil 519^T (similarity 97.30%), *Streptomyces albus* subsp. *albus* NRRL B-2365^T (similarity 97.10%) and *Streptomyces sodiophilus* YIM 80305^T (similarity 96.83%; Figure 3). Three phylogenetic tree showed that strain 11A07^T forms a cluster with three of the above species, with the exception of *S. sodiophilus* YIM 80305^T by maximum-likelihood algorithm (Supplementary Figures S1 and S2). However, this relationship is not supported by significant bootstrap values nor by the stability. Stackebrandt and Ebers³⁸ demonstrated that strains showing <98.5% 16S rRNA gene sequence similarity presented DNA reassociation values always <70%. And further, Kim *et al.*³⁹ suggested that 98.65% 16S rRNA gene sequence similarity can be used as the threshold for differentiating two species. In view of the lower 16S rRNA gene sequence similarity values of strains *S. panacagri* Gsoil 519^T, *S. sodiophilus* YIM 80305^T, *S. albus* subsp. *albus* NRRL B-2365^T and other close relatives (similarities ≤97.41%), and the distinct phylogenetic positions of these strains, DNA–DNA hybridizations were not investigated in this study.

Figure 1 Scanning electron micrographs of spore chains of strain 11A07^T after incubation at 28 °C for 14 days on TSA medium. (a) Bar 10 μm; (b) Bar 4 μm.

Table 2 Growth and cultural characteristics of strain 11A07^T on different growth media after incubation for 2 weeks at 28 °C

Medium	Growth	Aerial mycelium	Substrate mycelium	Diffusible pigment
Yeast extract-malt extract agar (ISP 2)	Good	White	Vivid yellow pink	Brown
Oatmeal agar (ISP 3)	Good	White	Blackish red	None
Inorganic salts-starch agar (ISP 4)	Moderate	White	Orange	None
Glycerol-asparagine agar (ISP 5)	Good	White	Slight yellow	None
Czapek solution agar (Difco)	Good	White	Vivid yellow pink	Brown
Nutrient agar (Difco)	Good	White	Violet	None
Tryptic soy agar (Difco)	Good	White	Violet	None
Potato dextrose agar (Difco)	Poor	White	Medium gray	None

Table 3 Differential phenotypic and chemotaxonomic characteristics of strain 11A07A^T, and its closest phylogenetic neighbors *Streptomyces panacagri* Gsoil 519^T and *Streptomyces albus* subsp. *albus* KCTC 1082^T (= NRRL B-2365^T), *Streptomyces sodiophilus* YIM 80305^T

Characteristic	11A07 ^T	Gsoil 519 ^T	KCTC 1082 ^T	YIM 80305 ^T
Morphology				
Spore chains	Straight or Rectiflexibiles	Rectiflexibiles	Spirales	Rectiflexibiles
Spore surface	Smooth	Smooth	Smooth	Wrinkled
Spore color	White	Mustard	White/yellow	White/gray
Diffusible pigment on ISP 2	Brown	None	None	None
Physiology				
H ₂ S production	–	+	+	–
Gelatin liquefaction	–	+	+	+
Nitrate reductase	+	–	+	+
Utilization as sole nitrogen source				
D-Galactose	w	+	–	–
D-Fructose	–	+	–	–
D-Xylose	–	–	+	–
D-Mannitol	+	–	+	–
L-Arabinose	–	–	+	–
L-Rhamnose	+	–	+	+
Inositol	+	+	+	–
Raffinose	+	–	–	–
Sucrose	+	+	+	–
Whole-cell sugars	Man, Rib, Glu, Gal, Xyl	Rib, Xyl, Man, Glu	ND	Gal, Glu
Predominant menaquinones (> 10%)	MK-9(H _{2,4,6})	MK-9(H _{6,8})	ND	MK-9(H _{4,6,8})
Diagnostic phospholipids	DPG, PE, PI, PIM, PL	DPG, PE, PIM	ND	PE
Major fatty acids (> 10%)	C _{18:0} , i-C _{16:0} , ai-C _{17:0} , 10-m- C _{18:0}	C _{16:0} , i-C _{15:0} , i-C _{17:0} , ai-C _{15:0} , ai-C _{17:0}	C _{18:0} , C _{20:0} , ai-C _{15:0}	i-C _{16:0} , ai-C _{15:0} , ai-C _{17:0}

Abbreviations: +, Positive; –, negative; ai, anteiso; DPG, diphosphatidylglycerol; Gal, galactose; GL, glycolipids; Glu, glucose; i, iso; m, methyl; Man, mannose; ND, no data available; PC, phosphatidylcholine; PG, phosphatidylglycerol; PI, phosphatidylinositol; PIM, phosphatidylinositol mannoside; PL, phospholipids; PME, phosphatidylmethylethanolamine; PS, phosphatidylserine; Rib, ribose; Xyl, xylose; TBSA, tuberculostearic acid; w, weakly positive.
Data were taken from Cui *et al.*⁴¹ and Li *et al.*⁴²

The strain 11A07^T was further characterized by partial sequencing of *atpD* (981 nt), *gyrB* (891 nt), *recA* (911 nt), *rpoB* (994 nt) and *trpB* (735 nt). The phylogenetic trees based on concatenated sequences (2511 bp) of *atpD* (position 101–595), *gyrB* (position 19–423), *recA* (position 109–612), *rpoB* (position 270–807) and *trpB* (position 45–611) trimmed sequences unambiguously demonstrated that the isolate constituted a separate phylogenetic line within other closely related species of the genus *Streptomyces* (Figure 4, Supplementary Figures S3 and S4). As well as multilocus sequence analysis evolutionary distances were greater than the species-definitive multilocus sequence analysis distance (0.007)⁴⁰ with all of the phylogenetically near species as shown in Supplementary Table S2. These evidences supported the proposal that this strain represents a new species in the genus *Streptomyces*.

Moreover, strain 11A07^T could utilize raffinose as sole carbon source and produce brown diffusible pigments on ISP 2 medium, but

could not hydrolyze gelatin. All of these properties could distinguish the strain 11A07^T from each of the three most closely related species. Other differences in phenotypic characteristics, which were summarized in Table 3, support strain 11A07^T as a novel species. In view of the combination of morphological, physiological and phylogenetic data discussed above, it is evident that strain 11A07^T forms a novel taxon within the genus *Streptomyces*. Therefore, it is proposed that this organism should be recognized as a novel species of the genus *Streptomyces*, for which the name *Streptomyces bohaiensis* sp. nov. is proposed.

Description of *S. bohaiensis* sp. nov.

S. bohaiensis [*bo.hai.en'sis*. N.L. masc. adj. *bohaiensis* of or pertaining to Bohai Sea, where the type strain was isolated]: Gram staining positive and aerobic actinomycete that forms extensively branched substrate

Figure 2 The polar lipid profiles of strains 11A07^T stained with molybdophosphoric acid after separation by two-dimensional TLC. DPG, diphosphatidylglycerol; PE, phosphatidylethanolamine; PI, phosphatidylinositol; PIM, phosphatidylinositol mannoside; PL, unknown phospholipid. A full color version of this figure is available at *The Journal of Antibiotics* journal online.

mycelia and aerial hyphae that carry straight or *rectiflexibile* spore chains containing > 50 smooth spores. Grows well on ISP 2, ISP 3, ISP 5, TSA, Czapek solution agar and nutrient agar. The color of the aerial mycelium is white and the substrate mycelium has different colors on different media. Brown diffusible pigments are produced on ISP 2 and Czapek solution agar. Growth occurs in the presence of 11% NaCl (w/v), temperature 15–40 °C and pH value 6–10, optimum at 1% NaCl, 28 °C, pH 8–9, respectively. Glucose, inositol, raffinose, L-rhamnose, D-galactose, D-mannitol, salicin, sorbitol, sucrose and sodium citrate are utilized as sole carbon source, but not L-arabinose, D-fructose and D-xylose. It can utilize L-valine, L-lysine, L-phenylalanine, L-histidine and L-alanine as sole nitrogen, but not L-methionine and glycine. Test for nitrate reductase is positive. Amylase and catalase activities are produced, but oxidase is not. H₂S production, gelatin liquefaction, milk coagulation and peptonization are negative. Tweens 40, 60 and 80 are hydrolyzed, but Tween 20 is not. Cell wall contains LL-diaminopimelic acid. Mannose, ribose, glucose, galactose and xylose are whole-cell sugars. The predominant menaquinones are MK-9 (H₂), MK-9 (H₄) and MK-9 (H₆). The fatty-acid profile contains iso-C_{16:0}, C_{18:0} 10-methyl, tuberculostearic acid and anteiso-C_{17:0} as the major components. The polar lipids consist of

Figure 3 Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences showing the position of strain 11A07^T in the genus *Streptomyces*. Filled circles indicate branches that were also recovered using the maximum parsimony and maximum-likelihood trees. Bootstrap values (expressed as percentages of 1000 replications) of above 50% are shown at the branch points. Bar, 0.002 sequence divergence.

Figure 4 Maximum-likelihood phylogenetic tree based on five gene (*atpD-gyrB-recA-rpoB-trpB*) concatenated sequences showing the position of strain 11A07^T in the genus *Streptomyces*. Filled circles indicate branches that were also recovered using the maximum parsimony and neighbor-joining trees. Bootstrap values (expressed as percentages of 1000 replications) of above 50% are shown at the branch points. Bar, 0.02 sequence divergence.

diphosphatidylglycerol, phosphatidylethanolamine, phosphatidylinositol, phosphatidylinositol mannoside and an unknown phospholipid. The G+C content of the genomic DNA is 71.4 mol%.

The type strain, 11A07^T (=JCM 19630^T = CCTCC AA 2013020^T = KCTC 29263^T –), was isolated from a young fish (*S. niphonius*) collected from the Bohai Sea of China (39°20' N, 122°17' E).

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