

Actinomadura harenae sp. nov., a novel actinomycete isolated from sea sand in Sanya

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Abstract

A novel actinomycete, designated strain NEAU-Ht49^T, was isolated from sea sand sampled in Sanya and characterized by using a polyphasic approach. The 16S rRNA gene sequence analysis showed that strain NEAU-Ht49^T was most closely related to *Actinomadura rhizosphaerae* SDA37^T (98.8%), *Actinomadura logoneensis* NEAU-G17^T (98.6%), *Actinomadura oligospora* ATCC 43269^T (98.6%) and *Actinomadura gamaensis* NEAU-Gz5^T (98.6%). The results of phylogenetic analysis based on the 16S rRNA gene sequences indicated that strain NEAU-Ht49^T formed a cluster with *A. rhizosphaerae* SDA37^T, *A. logoneensis* NEAU-G17^T, *A. oligospora* ATCC 43269^T, *A. gamaensis* NEAU-Gz5^T and *Actinomadura rupiterrae* CS5-AC15^T (96.4%). Meso-diaminopimelic acid was detected in its cell walls and glucose, madurose, mannose and ribose were detected in whole-cell hydrolysate. The polar lipids were found to consist of diphosphatidylglycerol, phosphatidylethanolamine, phosphatidylinositol, phosphatidylinositol-mannoside and two unidentified lipids. The major menaquinone was MK-10(H₈) and the minor menaquinones were MK-9(H₄) and MK-9(H₈). The major fatty acids were C_{16:0}, C_{18:1}ω9c, 10-methyl C_{18:0} and iso-C_{16:0}. Moreover, morphological and chemotaxonomic characteristics of properties of strain NEAU-Ht49^T also confirmed the affiliation of the isolate to the genus *Actinomadura*. However, DNA–DNA relatedness, physiological and biochemical data showed that strain NEAU-Ht49^T could be distinguished from its closest relatives. Therefore, strain NEAU-Ht49^T represents a novel species of the genus *Actinomadura*, for which the name *Actinomadura harenae* sp. nov. is proposed, with strain NEAU-Ht49^T (=CGMCC 4.7499^T=JCM 32659^T) as the type strain.

The genus *Actinomadura*, a member of the family *Thermomonosporaceae*, was first established by Lechevalier and Lechevalier [1] with *Actinomadura madurae* as type species and its description has been emended by Zhang *et al.* [2, 3], Miyadoh and Miyara [4], and Zhao *et al.* [5]. *Actinomadura* strains are mostly distributed in terrestrial soils [6, 7] but many strains are found in other ecosystems such as plant tissues [8, 9] and marine sources [10, 11]. Morphologically, the genus is characterized by the production of well-developed, non-fragmenting vegetative hyphae and aerial mycelium, on the tips of which spore chains of various lengths are arranged in straight, hooked or spiral form. The smooth, spiny or warty-surfaced spores are non-motile, oval or rod-shaped. Single spherical spore vesicles may be produced. The members of

the genus *Actinomadura* are also characterised by a number of chemical properties, including meso-diaminopimelic acid as the diagnostic diamino acid in the cell-wall peptidoglycan and madurose as the characteristic sugar in whole-cell hydrolysates; hexahydrogenated menaquinones with nine isoprene units [MK-9(H₈)] as the predominant isoprenologue; diphosphatidylglycerol, phosphatidylinositol and phosphatidylinositolmannoside as major phospholipids; complex mixtures of fatty acids with major amounts of hexadecanoic (C_{16:0}), 14-methylpentadecanoic (iso-C_{16:0}) and 10-methyloctadecanoic acid (tuberculostearic acid) [12]. The G+C contents of the genomic DNA range from 65.0 to 73.0 mol%. During an investigation of novel rare actinomycetes from sand collected from Wuzhizhou island in Sanya,

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Abbreviations: ANI, average nucleotide identity; BA, Bennett's agar; CA, Czapek's agar; dDDH, digital DNA–DNA hybridization; ISP, International Streptomyces Project; NA, nutrient agar.

The GenBank/EMBL/DBJ accession number for the 16S rRNA gene sequence of strain NEAU-Ht49^T is MK203829. This Whole Genome Shotgun project has been deposited at DDBJ/ENA/GenBank under the accession RFFG00000000. The version described in this paper is version RFFG01000000.1.

Three supplementary figures and three supplementary tables are available with the online version of this article.

an *Actinomadura*-like strain, NEAU-Ht49^T, was isolated. In this study, we performed polyphasic taxonomy on the isolate including morphological, physiological, chemotaxonomic and phylogenetic characteristics and proposed that it should be classified as a new species of the genus *Actinomadura*.

Strain NEAU-Ht49^T was isolated from sea sand collected from Wuzhizhou island in Sanya, Hainan Province, PR China (18° 32' N, 109° 77' E). The sand sample was air-dried at room temperature for 14 days before isolation for actinomycetes. After drying, 5 g sand sample was mixed with 45 ml distilled water and followed shaking on a rotary shaker at 250 r.p.m., 28 °C for 30 min. Then a 200 µl sample of the suspension was spread on a plate of Gause's synthetic agar no. 1 [13] supplemented with cycloheximide (50 mg l⁻¹) and nalidixic acid (20 mg l⁻¹). After 21 days of aerobic incubation at 28 °C, colonies were transferred and purified on oatmeal agar [International *Streptomyces* Project (ISP) medium 3] [14] and maintained as glycerol suspensions (20%, v/v) at –80 °C. The reference strains *Actinomadura rhizosphaerae* SDA37^T was purchased from the Japan NITE Biological Resource Centre (NBRC), *Actinomadura oligospora* ATCC 43269^T was purchased from the Japan Collection of Microorganisms (JCM) and *Actinomadura rupiterrae* CS5-AC15^T was purchased from the Deutsche Sammlung von Mikroorganismen und Zellkulturen (DSMZ). The strains *Actinomadura logoneensis* NEAU-G17^T and *Actinomadura gamaensis* NEAU-Gz5^T were isolated and stored in our laboratory. All strains were cultured under the same conditions for comparative analyses.

Morphological characteristics were observed by light microscopy (ECLIPSE E200, Nikon) and scanning electron microscopy (SU8010, Hitachi) using cultures grown on ISP 3 agar at 28 °C for 7 and 14 days, respectively. Samples for scanning electron microscopy were prepared as described by Jin *et al.* [15]. Cultural characteristics were determined on ISP 1–7 agars [14], Bennett's agar (BA) [16], nutrient agar (NA) [17] and Czapek's agar (CA) [17] after 14 days at 28 °C. Colour determination was done by using colour chips from the ISCC-NBS colour charts standard samples No. 2106 [18]. Growth at different temperatures (4, 10, 15, 20, 28, 35, 37, 40, 45 and 50 °C) was determined on ISP 3 medium after incubation for 14 days. Growth tests for pH range (pH 3.0–12.0, at intervals of 1.0 pH unit) and NaCl tolerance (0, 1, 2, 3, 4, 5, 6, 7, 8, 9 and 10%, w/v) were tested in Glucose-yeast extract powder (GY) broth [19] using the buffer system described by Xu *et al.* [20] at 28 °C for 14 days on a rotary shaker. The utilization of sole carbon and nitrogen sources (0.5 % w/v), decomposition of cellulose, hydrolysis of starch and aesculin, reduction of nitrate, coagulation and peptonization of milk, liquefaction of gelatin, and production of H₂S were examined as described previously [21, 22]. Production of catalase, hydrolysis of Tweens (20, 40 and 80) and production of urease were tested as described by Gordon *et al.* [21] and Williams *et al.* [23].

Biomass for chemotaxonomic studies was prepared by growing these strains in GY broth in shake flasks (250 r.p.m.) at 28 °C for 5 days. Cells were harvested by centrifugation,

washed with distilled water and freeze-dried. The isomer of meso-diaminopimelic acid in the cell-wall peptidoglycan was derivatised and analysed by an HPLC method [24] using an Agilent TC-C18 column (250×4.6 mm i.d. 5 µm) with a mobile phase consisting of acetonitrile: 0.05 mol l⁻¹ phosphate buffer, pH 7.2 (15:85, v/v), at a flow rate of 0.5 ml min⁻¹. The peak detection used an Agilent G1321A fluorescence detector with a 365 nm excitation and 455 nm longpass emission filters. The whole-cell sugars were analysed according to the procedures developed by Lechevalier and Lechevalier [25]. Polar lipids in cells were extracted and identified by the method of Minnikin *et al.* [26]. Menaquinones were extracted from freeze-dried biomass and purified according to Collins [27]. Extracts were analysed by an HPLC-UV method [28] using an Agilent Extend-C18 column (150×4.6 mm, i.d. 5 µm), typically at 270 nm. The mobile phase was acetonitrile–propyl alcohol (60:40, v/v). To determine cellular fatty acid compositions, strain NEAU-Ht49^T and its closely related species were cultivated in GY broth in shake flasks at 28 °C for 5 days. Fatty acid methyl esters were extracted from the biomass as described by Gao *et al.* [29] and analysed by GC-MS using the method of Xiang *et al.* [30].

Extraction of chromosomal DNA and PCR amplification of the 16S rRNA gene sequence were carried out according to the procedure developed by Kim *et al.* [31]. The PCR product was purified and cloned into the vector pMD19-T (Takara) and sequenced using an Applied Biosystems DNA sequencer (model 3730XL). The almost full-length 16S rRNA gene sequence of strain NEAU-Ht49^T (1519 bp) was obtained and multiply aligned in MEGA using the CLUSTAL_W algorithm and trimmed manually where necessary. The phylogenetic dendrograms of the isolate and its closely related strains were reconstructed with the maximum-likelihood [32] and neighbour-joining [33] algorithms using MEGA software version 7.0 [34]. The stability of the topology of each phylogenetic tree was assessed by using the bootstrap method with 1000 repetitions [35]. A distance matrix was generated using Kimura's two-parameter model [36]. All positions containing gaps and missing data were eliminated from the dataset (complete deletion option). The 16S rRNA gene sequence similarities between the strains were calculated on the basis of pairwise alignment using the EzBioCloud server [37].

For draft genome sequencing and assembly, the genomic DNA of strain NEAU-Ht49^T was extracted with the SDS method. The harvested DNA was detected by agarose gel electrophoresis and quantified by Qubit. Whole-genome sequencing was performed on the Illumina HiSeq PE150 platform. A-tailed, ligated to paired-end adaptors and PCR amplified with a 350 bp insert was used for the library construction at the Beijing Novogene Bioinformatics Technology Co., Ltd. Illumina PCR adapter reads and low-quality reads from the paired-end were filtered by the step of quality control using our own compiling pipeline. All good-quality paired reads were assembled by using SOAPdenovo [38, 39] (<https://github.com/aquaskyline>) into a number of scaffolds. Then the filter reads were handled by the next step of the gap-closing. Several genomic metrics are now available to

distinguish between orthologous genes of closely related prokaryotes, including the calculation of average nucleotide identity (ANI) and digital DNA–DNA hybridization (dDDH) values [40, 41]. In the present study, ANI and dDDH values were determined from the genomes of strain NEAU-Ht49^T, *A. logoneensis* NEAU-G17^T (QURH00000000) and *A. oligospora* ATCC 43269^T (JADG00000000) using the ortho-ANu algorithm from Ezbiocloud [37, 40] and the Genome-to-Genome Distance Calculator (GGDC 2.0) at <http://ggdc.dsmz.de>. Because of the lack of whole genome sequences of strains *A. rhizosphaerae* NBRC SDA37^T, *A. gamaensis* NEAU-Gz5^T and *A. rupiterrae* CS5-AC15^T, DNA–DNA relatedness tests between strain NEAU-Ht49^T and these three related type strains were carried out as described by De Ley *et al.* [42], under consideration of the modifications described by Huss *et al.* [43], using a model Cary 100 Bio UV/VIS-spectrophotometer equipped with a Peltier-thermostatted 6×6 multicell changer and a temperature controller with an *in situ* temperature probe (Varian). The concentration and purity of DNA samples were determined by measuring the optical density at 260, 280 and 230 nm. The DNA samples used for hybridization were diluted to OD₂₆₀ around 1.0 using 0.1×SSC (saline sodium citrate buffer), then sheared using a JY92-II ultrasonic cell disruptor (ultrasonic time 3 s, interval time 4 s, 90 times). The DNA renaturation rates were determined in 2×SSC at 70 °C. The experiments were performed with three replications and the DNA–DNA relatedness value was expressed as the mean of the three values.

Morphological observation of a 2 week old culture of strain NEAU-Ht49^T grown on ISP 3 medium revealed that it had the typical characteristics of members of the genus *Actinomadura*. The cells of strain NEAU-Ht49^T were found to be Gram-positive and aerobic. White aerial mycelium was produced abundantly and differentiated into flexuous or straight spore chains consisting of cylindrical spores (0.4–0.6×0.8–1.0 µm); the spore surface was rough (Fig. 1). Strain NEAU-Ht49^T exhibited good growth on ISP 1 agar, ISP 2 agar, ISP 3 agar,

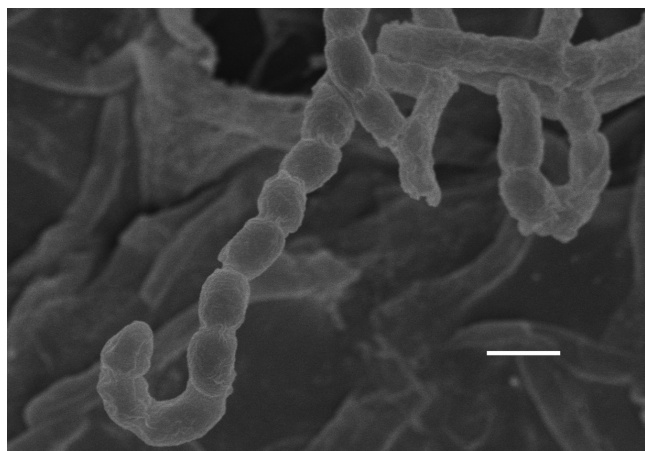


Fig. 1. Scanning electron microscope image of strain NEAU-Ht49^T grown on ISP 3 medium for 2 weeks at 28 °C. Bar 1 µm

ISP 6 agar, ISP 7 agar, NA and BA media; moderate growth on ISP 4; and poor growth on ISP 5 and CA media. The colony colours varied from brilliant yellow to grey-green yellow. Moderate olive brown soluble pigment was observed on ISP 7 medium. A summary of cultural characteristics of the isolate are shown in Tables S1 and Fig. S1 (available in the online version of this article). Strain NEAU-Ht49^T grew at a temperature range of 10–45 °C (optimum, 28 °C), pH 5–10 (pH 7) and NaCl tolerance of 0–3% (0%). The physiological and biochemical properties of strain NEAU-Ht49^T are given in Table 1 and the species description.

Chemotaxonomic analyses revealed that strain NEAU-Ht49^T exhibited characteristics which are typical of members of the genus *Actinomadura*, such as the presence of meso-diaminopimelic acid as the cell-wall diamino acid and glucose, madurose, mannose and ribose as whole-cell sugars. The polar lipids of strain NEAU-Ht49^T consisted of diphosphatidylglycerol, phosphatidylethanolamine, phosphatidylinositol, phosphatidylinositolmannoside and two unidentified lipids (Fig. S2). Menaquinones of strain NEAU-Ht49^T were identified as MK-9(H₆) (61.5%), MK-9(H₄) (21.5%) and MK-9(H₈) (17.0%). The cellular fatty acid profile was found to be composed of C_{16:0} (26.4%), C_{18:1}ω9c (25.3%) and 10-methyl C_{18:0} (22.7%), iso-C_{16:0} (8.5%), C_{16:1}ω7c (5.0%), C_{18:0} (4.8%), C_{14:0} (2.5%), C_{17:1}ω7c (2.4%), C_{17:0} (1.7%), anteiso-C_{17:0} (0.4%) and iso-C_{14:0} (0.3%) (Table S2). The DNA G+C content was 72.1 mol%. All the data of the morphological and chemotaxonomic analyses are consistent with the assignment of strain NEAU-Ht49^T to the genus *Actinomadura*.

The 16S rRNA gene sequence (1519 bp) indicated that strain NEAU-Ht49^T should be assigned to the genus *Actinomadura* using the EzBioCloud analysis and was most closely related to *A. rhizosphaerae* SDA37^T (98.8%), *A. logoneensis* NEAU-G17^T (98.6%), *A. oligospora* ATCC 43269^T (98.6%) and *A. gamaensis* NEAU-Gz5^T (98.6%). The phylogenetic tree based on 16S rRNA gene sequences showed that strain NEAU-Ht49^T formed a stable cluster with *A. rhizosphaerae* SDA37^T, *A. logoneensis* NEAU-G17^T, *A. oligospora* ATCC 43269^T, *A. gamaensis* NEAU-Gz5^T and *A. rupiterrae* CS5-AC15^T (96.4 %) in the neighbour-joining tree (Fig. 2), a relationship also recovered by the maximum-likelihood algorithm (Fig. S3).

The assembled genome sequence of strain NEAU-Ht49^T was found to be 9356375 bp long and composed of 283 contigs with an N50 value of 75833 bp, a DNA G+C content of 72.1 mol% and a coverage of 177×. It was deposited in GenBank under the accession number RFFG00000000. The NCBI Prokaryotic Genome Annotation Pipeline revealed seven copies of the 5S rRNA genes, one copy of the 16S rRNA genes, three copies of the 23S rRNA genes, 65 tRNA genes and three copies of noncoding RNA genes. The 16S rRNA gene sequence from whole genome sequence shared 100% similarity to that from PCR sequencing suggesting that the genome sequence was not contaminated. Other general features of the genome sequence are presented in Table S3.

Table 1. Differential physiological characteristics of strain NEAU-Ht49^T and its closely related type strains

Strains: 1, NEAU-Ht49^T; 2, *Actinomadura rhizosphaerae* SDA37^T; 3, *Actinomadura logoneensis* NEAU-G17^T; 4, *Actinomadura oligospora* ATCC 43269^T; 5, *Actinomadura gamaensis* NEAU-Gz5^T; 6, *Actinomadura rupiterrae* CS5-AC15^T. All data are from this study. +, Positive; –, negative.

Characteristic	1	2	3	4	5	6
Utilization as sole carbon source:						
L-Arabinose	–	+	+	–	+	–
Dulcitol	+	+	–	+	–	–
D-Fructose	+	+	+	–	+	–
D-Galactose	–	–	+	–	+	–
meso-Inositol	+	–	–	–	–	+
Lactose	–	+	+	–	–	+
Maltose	+	+	+	+	+	–
D-Mannitol	+	–	–	–	–	+
Raffinose	–	–	–	–	+	–
L-Rhamnose	+	–	+	–	–	–
D-Ribose	–	+	–	+	–	–
D-Sorbitol	–	+	–	+	–	–
Sucrose	+	–	–	–	+	–
D-Xylose	–	+	–	–	–	–
Utilization as sole nitrogen source:						
L-Asparagine	+	+	–	–	–	–
Creatine	–	+	+	–	–	–
L-Glutamic acid	+	+	–	+	–	+
L-Serine	+	+	+	–	–	–
Growth temperature range (°C)	10–45	20–40	25–42	25–42	15–40	20–42
Growth pH range	5–10	6–8	5–10	6–10	6–8	5–11
NaCl tolerance range (w/v, %)	0–3	0–4	0–4	0–2	0–3	0–2
Aesculin hydrolysis	+	+	–	+	–	+
Cellulose decomposition	+	–	–	–	+	–
Gelatin liquefaction	–	+	–	+	–	+
Nitrate reduction	–	+	–	–	–	–
Production of H ₂ S	–	–	–	–	–	+
Production of urease	+	–	–	–	–	–
Tween hydrolysis:						
40	+	+	–	+	+	+
80	+	+	–	+	+	+

DNA–DNA hybridization was carried out between strain NEAU-Ht49^T and *A. rhizosphaerae* SDA37^T, *A. gamaensis* NEAU-Gz5^T and *A. rupiterrae* CS5-AC15^T to determine whether the isolate represents a novel species. Strain NEAU-Ht49^T displayed a DNA–DNA relatedness of 50.5±3.6%

with *A. rhizosphaerae* SDA37^T, 34.9±3.4% with *A. gamaensis* NEAU-Gz5^T and 25.5±4.1% with *A. rupiterrae* CS5-AC15^T. dDDH and ANI values were employed to further clarify the relatedness between strain NEAU-Ht49^T and *A. logoneensis* NEAU-G17^T and *A. oligospora* ATCC 43269^T. The levels of

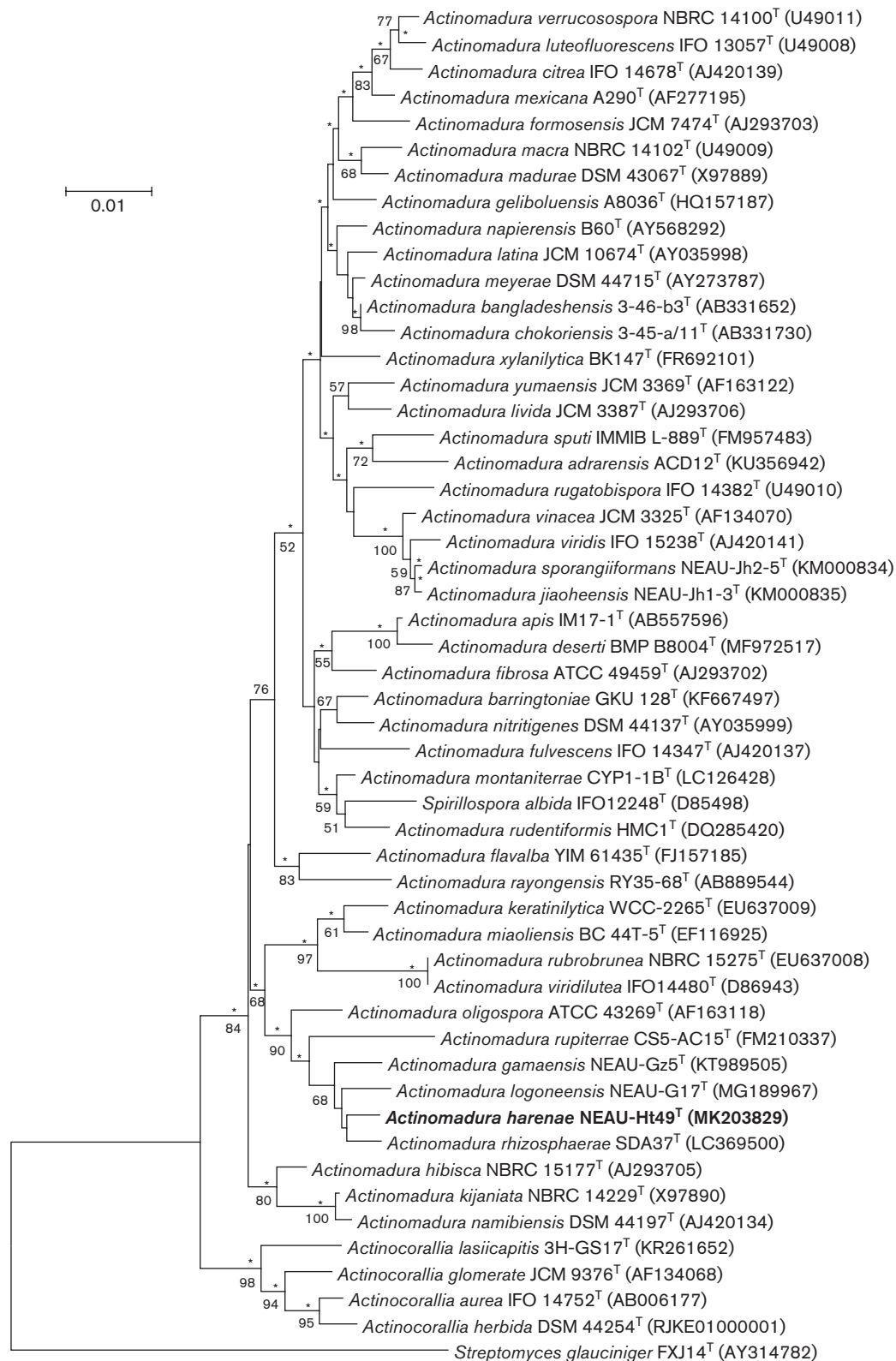


Fig. 2. Neighbour-joining tree based on 16S rRNA gene sequences (1371 bp) showing the relationships between strain NEAU-Ht49^T (in bold) and related species of top 50 16S rRNA gene sequence. Asterisks indicate branches that were also recovered using the maximum-likelihood methods. Bootstrap values (expressed as percentages of 1000 replications) of above 50% are shown at branch points. *Streptomyces glauciniger* FXJ14^T (AY314782) was used as the outgroup. Bar, 0.01 substitutions per nucleotide position.

dDDH between them were 32.9 ± 2.5 and $37.1 \pm 2.5\%$, respectively. These values were below the threshold value of 70% recommended by Wayne *et al.* [44] for assigning strains to the same genomic species. Similarly, low ANI values of 86.8 and 89.0% were found between strain NEAU-Ht49^T and its reference strains respectively for *A. logoneensis* NEAU-G17^T and *A. oligospora* ATCC 43269^T, a result well below the threshold used to delineate prokaryote species [45, 46].

Besides the genotypic evidence above, the novel strain showed remarkable difference to the other closely related type strains by several phenotypic characteristics. For instance, their different colony colours on ISP 2, ISP 3, ISP 7 and Bennett's agar media at 28 °C for 14 days (Fig. S3). Strain NEAU-Ht49^T could grow at 45 °C, while *A. rhizosphaerae* NBRC SDA37^T, *A. logoneensis* NEAU-G17^T, *A. oligospora* ATCC 43269^T, *A. gamaensis* NEAU-Gz5^T and *A. rupiterrae* CS5-AC15^T could not. The novel strain could utilize D-mannitol and meso-inositol as sole carbon source, while its reference strains, *A. rhizosphaerae* NBRC SDA37^T, *A. logoneensis* NEAU-G17^T, *A. oligospora* ATCC 43269^T and *A. gamaensis* NEAU-Gz5^T, could not; L-asparagine was utilized as a sole nitrogen source for strain NEAU-Ht49^T, while in *A. logoneensis* NEAU-G17^T, *A. oligospora* ATCC 43269^T, *A. gamaensis* NEAU-Gz5^T and *A. rupiterrae* CS5-AC15^T it was not. Other phenotypic differences included NaCl tolerance, pH range of growth, decomposition of cellulose, hydrolysis of aesculin and Tweens (40 and 80), liquefaction of gelatin, nitrate reduction, production of H₂S and urease, and utilization of L-arabinose, dulcitol, D-fructose, D-galactose, lactose, maltose, raffinose, L-rhamnose, D-ribose, D-sorbitol, sucrose, D-xylose, creatine, L-glutamic acid and L-serine (Table 1).

In conclusion, it is evident from the genotypic, phenotypic and chemotaxonomic data that strain NEAU-Ht49^T represents a novel species of the genus *Actinomadura*, for which the name *Actinomadura harenae* sp. nov. is proposed.

DESCRIPTION OF *ACTINOMADURA HARENAE* SP. NOV.

Actinomadura harenae (ha.re'nae. L. gen. n. *harenae* of sand).

The cells of the strain are found to be Gram-positive and aerobic. White aerial mycelium is produced abundantly and differentiates into flexuous or straight spore chains consisted of cylindrical spores (0.4–0.6 × 0.8–1.0 μm), the spore surface is rough on ISP 3 medium. Good growth on ISP 1 agar, ISP 2 agar, ISP 3 agar, ISP 6 agar, ISP 7 agar, NA and BA media; moderate growth on ISP 4 agar; and poor growth on ISP 5 agar and CA media. The colony colours vary from brilliant yellow to grey-green yellow on agar media and the strain produces moderate olive brown soluble pigment on ISP 7 medium. Strain NEAU-Ht49^T grows at 10–45 °C (optimum, 28 °C), pH 5–10 (pH 7) and NaCl tolerance of 0–3% (0 %). Positive for decomposition of cellulose, hydrolysis of aesculin and Tweens (40 and 80) and production of urease, but negative for hydrolysis of starch and Tween 20, liquefaction of gelatin, peptonization and coagulation of milk, production of

H₂S, and reduction of nitrate. Dulcitol, D-fructose, D-glucose, meso-inositol, maltose, D-mannitol, D-mannose, L-rhamnose and sucrose are utilized as sole carbon sources, but not L-arabinose, D-galactose, lactose, raffinose, D-ribose, D-sorbitol or D-xylose. L-Alanine, L-arginine, L-asparagine, L-aspartic acid, L-glutamic acid, L-glutamine, glycine, L-proline, L-serine, L-threonine and L-tyrosine are utilized as sole nitrogen sources, but not creatine. The diagnostic diamino acid of the cell wall is meso-diaminopimelic acid. Whole-cell sugars contain glucose, madurose, mannose and ribose. The polar lipid profile consists of diphosphatidylglycerol, phosphatidylethanolamine, phosphatidylinositol, phosphatidylinositolmannoside and two unidentified lipids. The menaquinones are MK-9(H₆), MK-9(H₄) and MK-9(H₈). Major fatty acids are C_{16:0}, C_{18:1} ω9c, 10-methyl C_{18:0} and iso-C_{16:0} (>8%). The G+C content of the DNA of the type strain is 72.1 mol%.

The type strain is NEAU-Ht49^T (=CGMCC 4.7499^T=JCM 32659^T), isolated from sea sand collected from Wuzhizhou island in Sanya, Hainan Province, PR China. The GenBank/EMBL/DDJB accession number for the 16S rRNA gene sequence of strain NEAU-Ht49^T is MK203829. This Whole Genome Shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number RFFG00000000. The version described in this paper is version RFFG01000000.1.

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Conflicts of interest

The authors declare that there are no conflicts of interest.

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