Streptomyces emeiensis sp. nov., a novel streptomycete from soil in China

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An actinomycete, strain 4776^T, was isolated from soil collected from Emei Mountain in Sichuan Province, China. The taxonomic status of this strain was established using a polyphasic approach. The organism was found to have morphological and chemotaxonomic characteristics typical of streptomycetes. Phylogenetic analysis based on the almost complete 16S rRNA gene sequence indicated that the novel isolate belongs to the genus *Streptomyces* and consistently falls into a clade together with *Streptomyces prasinopilosus* DSM 40098^T, *Streptomyces prasinus* JCM 4603^T, *Streptomyces bambergiensis* DSM 40590^T, *Streptomyces hirsutus* DSM 40095^T and *Streptomyces cyanoalbus* DSM 40198^T. However, DNA–DNA relatedness and phenotypic data distinguished strain 4776^T from these phylogenetically related type strains. It is therefore concluded that strain 4776^T (= CGMCC 4.3504^T = DSM 41884^T) represents a novel species of the genus *Streptomyces*, for which the name *Streptomyces emeiensis* sp. nov. is proposed.

Streptomycetes continue to be a rich source of novel bioactive, commercially significant compounds (Labeda *et al.*, 1997; Dietera *et al.*, 2003; Bérdy, 2005). Despite the large number of species with validly published names, the genus *Streptomyces* as a whole is underspeciated (Kim & Goodfellow, 2002; Saintpierre *et al.*, 2003; Huang *et al.*, 2004; Xu *et al.*, 2006). In the course of searching for new anti-atherosclerosis drugs targeted on the scavenger receptor BI (SR-BI), an active streptomycete-like strain, strain 4776^T, was isolated from a soil sample collected from Emei Mountain in Sichuan province, China. A polyphasic taxonomic investigation based on a judicious combination of genotypic and phenotypic characteristics revealed that the new isolate represents a novel species of the genus *Streptomyces*.

Strain 4776^T was isolated after two weeks incubation at 28 °C on yeast-malt extract agar (ISP 2; Shirling & Gottlieb, 1966), which had been seeded with a soil sample suspension. The soil sample was collected from Emei Mountain, Sichuan, China. The isolate was maintained on ISP 2 slopes at 4 °C and as glycerol suspensions (20 %, v/v) at –20 °C. Biomass for molecular systematic and most of the chemotaxonomic

studies was obtained after incubation in shake flasks of ISP 2 broth at 28 °C for 4–7 days.

The spore-chain morphology and spore-surface ornamentation of strain 4776^T were recorded by examining gold-coated dehydrated specimens of 10 to 14-day cultures grown on ISP 2 agar by scanning electron microscopy (SEM) (Quanta; FEI). The coverslip technique (Zhou *et al.*, 1998; Kawato & Shinobu, 1959) was used to observe the hyphae and spore-chain characteristics. Aerial spore-mass colour, substrate mycelial pigmentation and the production of diffusible pigments were estimated on a number of agar media (Table 1) following incubation at 28 °C for 14 days.

The isomers of diaminopimelic acid and whole-cell sugar composition were analysed by TLC following procedures described by Hasegawa *et al.* (1983) and Lechevalier & Lechevalier (1980). Menaquinones were extracted and determined using the methods of Collins (1985). The phospholipid analysis was carried out using the technique described by Minnikin *et al.* (1984). The fatty acids were extracted, methylated and estimated by GC using the standard Sherlock MIDI (Microbial Identification) system (Sasser, 1990; Kämpfer & Kroppenstedt, 1996). The G + C content of genomic DNA was determined using the thermal denaturation method of Marmur & Doty (1962) with *Escherichia coli* K12 as a control.

Strain 4776^T was examined for a broad range of biochemical and physiological characteristics according to the

Abbreviation: SEM, Scanning electron microscopy.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain 4776^T is DQ462649.

Light and scanning electron micrographs showing the spore-chain morphology and spore-surface ornamentation of cells of strain 4776^T are available with the online version of this paper.

Table 1. Comparison of cultural characteristics of strain 4776^T and *Streptomyces prasinopilosus* DSM 40098^T

No soluble pigments were produced on the listed agars.

Agar medium	Aerial mycelium		Substrate mycelium	
	Strain 4776 ^T	DSM 40098 ^T	Strain 4776 ^T	DSM 40098 ^T
Czapek Dox	Strong yellowish green; abundant	Yellowish green; moderate	Greyish yellowish brown	Dark yellow
Glycerol-asparagine (ISP 5)	Green; abundant	Green; moderate	Yellow	Greyish yellow
Inorganic salts-starch (ISP 4)	Greyish green; abundant	Pinkish white; abundant	Brown	Strong reddish orange
Oatmeal (ISP 3)	Greyish green; moderate	Deep yellow-green; moderate	Dark brown	Dark yellow
Peptone-yeast extract-iron (ISP 6)	White; abundant	None	Brown	Not distinctive
Yeast extract-malt extract (ISP 2)	Dark green; abundant	Greyish green; moderate	Dark brown	Light yellow
Yeast extract-starch	Dark greyish olive; abundant	Green	Dark brown	Pinkish yellow
Modified Bennett's	Olive green; abundant	Greyish green; moderate	Sudan brown	Dark brown
Santou's	White; abundant	White; moderate	Dark brown	Greyish greenish yellow

established methods of Williams *et al.* (1983) and Kämpfer *et al.* (1991). Tolerance to temperature and pH was tested on ISP 2 agar plates incubated for 7–14 days. Resistance to antibiotics was examined as described by Al-Tai *et al.* (1999). Readings were taken at 1, 3, 7 and 14 days and inhibition zones observed were scored as negative.

Isolation of chromosomal DNA and PCR amplification of the 16S rRNA gene were carried out after Chun & Goodfellow (1995). Sequencing of the PCR product was performed as described by Gu *et al.* (2006). The resultant sequence was aligned manually using CLUSTAL_X version 1.8 (Thompson *et al.*, 1997) with available, almost complete sequences of type strains of the family *Streptomycetaceae* and then with corresponding sequences of representative species of the genus *Streptomyces*. Phylogenetic trees were constructed using the least-squares (Fitch & Margoliash, 1967), maximum-likelihood (Felsenstein, 1981), maximum-parsimony (Fitch, 1971) and neighbour-joining (Saitou & Nei, 1987) algorithms from the PHYLIP package version 3.5c (Felsenstein, 1993) and the TREECON program version 1.3b (Van de Peer & De Wachter, 1994). Evolutionary distance matrices were generated according to the method of Kimura (1980). Tree topologies were evaluated by performing bootstrap analysis based on 1000 resamplings of the neighbour-joining dataset using the SEQBOOT and CONSENSE programs provided in the PHYLIP package (Felsenstein, 1993).

Levels of DNA–DNA relatedness between strain 4776^T and related type strains were determined using the fluorometric micro-well method (Ezaki *et al.*, 1989), with the modifications described by He *et al.*, (2005).

The chemical and morphological properties of strain 4776^T were consistent with its assignment to the genus *Streptomyces* (Williams *et al.*, 1989; Manfio *et al.*, 1995). The organism formed an extensively branched substrate mycelium, aerial hyphae which carried spiny-surfaced spores in

rectiflexibiles and hooked spore chains (Fig. 1) and a greenish aerial spore mass on various standard media (Table 1). The novel strain contained LL-diaminopimelic acid in whole-organism hydrolysates, hexa-, octa- and a minor amount of tetra-hydrogenated menaquinones with nine isoprene units [MK-9 (H₆, H₈ and H₄)] as isoprenologues and phosphatidylethanolamine and phosphatidyl-inositol and phosphatidylinositol mannosides as the major polar lipids (phospholipid type II *sensu* Lechevalier *et al.*, 1977), but lacked characteristic sugars and mycolic acids. The fatty acid profile included mainly saturated iso- and anteiso-branched-chain and straight-chain fatty acids (fatty acid type 2c *sensu* Kroppenstedt, 1985).

The almost complete 16S rRNA gene sequence (1400 nt) was determined for strain 4776^T. The sequence data clearly showed that strain 4776^T is a member of genus *Streptomyces*.

Fig. 1. Scanning electron micrograph showing spore chains and spore-surface ornamentation of cells of *Streptomyces emeiensis* sp. nov. 4776^T grown on yeast-malt extract agar (ISP 2) for 14 days at 28 °C. Bar, 2.5 µm.

Fig. 2. Unrooted neighbour-joining tree (Saitou & Nei, 1987) based on 16S rRNA gene sequences showing the phylogenetic relationship between strain 4776^T and related species of the genus *Streptomyces*. Asterisks refer to branches that were recovered using all four tree-making algorithms. f, m and p, respectively indicate branches that were also formed using the Fitch–Margoliash (Fitch & Margoliash, 1967), maximum-likelihood (Felsenstein, 1981) and maximum-parsimony (Fitch, 1971) tree-making algorithms. Numbers at nodes indicate levels of bootstrap support (%) based on a neighbour-joining analysis of 1000 resampled datasets; only values above 50 % are given. Bar, 0.01 substitutions per nucleotide position.

It was evident from Fig. 2 that strain 4776^T formed a distinct phyletic line with *Streptomyces prasinopilosus* DSM 40098^T. This line was supported by all four tree-making algorithms and by a high bootstrap value. Three tree-making algorithms and a 100 % bootstrap value supported the position that the strain 4776^T–*S. prasinopilosus* line was consistently in the same clade along with *Streptomyces prasinopilosus* DSM 40098^T, *Streptomyces prasinus* JCM 4603^T, *Streptomyces bambergiensis* DSM 40590^T, *Streptomyces hirsutus* DSM 40095^T and *Streptomyces cyanoalbus* DSM 40198^T. 16S rRNA gene sequence similarities between strain 4776^T and these type strains were between 98.6 and 98.8 % (18–19 nucleotide differences at 1390–1402 sites). The novel isolate showed the shortest phylogenetic distance (0.012) with *S. prasinopilosus* DSM 40098^T and *S. prasinus* JCM 4603^T, although it showed a lower 16S rRNA gene sequence identity with *S. prasinopilosus* DSM 40098^T than with the other four neighbours from the BLAST result. This is

probably because the 16S rRNA gene sequence of *S. prasinopilosus* that has been deposited in the GenBank database is shorter than those of the other species and contains more gaps (4 gaps).

DNA–DNA hybridization tests were carried out between strain 4776^T and the phylogenetically close type strains. The DNA–DNA relatedness between strain 4776^T and *S. prasinopilosus* DSM 40098^T (62.7 %), *S. prasinus* JCM 4603^T (55.5 %), *S. hirsutus* DSM 40095^T (46.4 %), *S. bambergiensis* DSM 40590^T (31.7 %) and *S. cyanoalbus* DSM 40198^T (26.1 %) are all well below the 70 % cut-off point generally recognized for genomic species (Wayne *et al.*, 1987), thus suggesting that the novel strain should be considered as a separate species. Comparison of the phenotypic characteristics of strain 4776^T and its close phylogenetic neighbours also revealed significant differences (Table 2). *S. prasinopilosus* was selected for a detailed cultural characteristic comparison with strain 4776^T on the basis of phylogenetic distance and DNA–DNA relatedness data and its close position to the novel isolate in all four phylogenetic trees. Despite the resemblance borne by the two strains, the two strains could be differentiated by several characteristics (Table 1), especially when using ISP 4, ISP 6 and yeast extract–starch agars.

A combination of genotypic and phenotypic data show that strain 4776^T merits recognition as the type strain of a novel species in the genus *Streptomyces*, for which we propose the name *Streptomyces emeiensis* sp. nov.

Description of *Streptomyces emeiensis* sp. nov.

Streptomyces emeiensis (e.mei.en'sis. N.L. masc. adj. *emei*-*ensis* pertaining to Emei, a famous mountain in Sichuan Province, southern China, where the sample yielding the type strain was collected).

Aerobic, mesophilic, Gram-positive actinomycete that develops well-branched substrate and aerial mycelium. Diffusible pigments are not formed, nor are melanin pigments produced on peptone/yeast extract/iron or tyrosine agars. Additional cultural characteristics on various agar media are shown in Table 1. *Rectiflexibiles* and hooked spore chains of elliptic, spiny-surfaced spores are frequently arranged in a verticillate structure. Growth occurs between 15 and 40 °C and at pH values from 5.5 to 9.5, but not at pH 4.5 or 10.5. Growth occurs in the presence of 0.1 % phenol (w/v), 5 % NaCl (w/v) and 0.01 % NaN₃ (w/v), but not in the presence of 7 % NaCl (w/v). Nitrate is reduced. Amylase and gelatinase are not produced. Shows weak antimicrobial activity against strains of *Bacillus subtilis* and *Mycobacterium smegmatis*, but not against strains of *Staphylococcus epidermidis*, *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* or *Candida albicans*. The organism is sensitive to filter-paper discs soaked in the following (µg ml⁻¹): novobiocin (5), streptomycin (10), oxacillin (1), chloramphenicol (30), ciprofloxacin (5) and erythromycin (15). Additional physiological properties

Table 2. Phenotypic characteristics of strain 4776^T and related species of the genus *Streptomyces*

Strains: 1, strain 4776^T; 2, *S. bambergiensis* DSM 40590^T; 3, *S. cyanoalbus* DSM 40198^T; 4, *S. hirsutus* DSM 40095^T; 5, *S. prasinopilosus* DSM 40098^T; 6, *S. prasinus* DSM 40099^T. All strains degrade Tween 60, Tween 80 and elastin. All are negative for degradation of xanthine, hypoxanthine and guanine and are positive for the assimilation of galactose, glucose, D-sucrose, D-fructose, D-mannose, D-cellobiose, D-trehalose, L-rhamnose, D-xylose and sodium citrate. Melanin production of all strains is negative. +, Positive; −, negative; (+), weakly positive; RA, retinaculiaperti; RF, *rectiflexibiles*; SP, spiral.

Characteristic	1	2	3	4	5	6
Aerial spore mass on oatmeal agar	Greyish green	Green	Green or grey	Green	Green	Green
Spore chain	RF & hooked	SP	SP	RA to SP	RA	RA to SP
Spore surface	Spiny	Hairy	Spiny	Spiny	Hairy	Spiny
Production of diffusible pigments	−	+	−	−	−	−
Growth on sole carbon sources (1.0 %, w/v):						
L-Arabinose	+	(+)	+	+	+	+
L-Phenylalanine	+	−	(+)	+	+	+
L-Cysteine (0.1 %)	−	+	+	+	+	+
D-Sorbose	−	+	+	+	+	+
D-Ribose	+	−	−	−	−	−
Methyl α-D-glucopyranoside	−	−	+	(+)	(+)	+
D-Melezitose	+	−	(+)	+	−	+
myo-Inositol	+	+	+	+	−	+
D-Raffinose	+	+	−	+	−	−
Inulin	−	+	+	+	+	+
L-Valine (0.1 %)	−	+	+	+	+	+
Dextrin	+	+	+	−	+	+
Sodium malonate (0.1 %)	−	−	−	−	+	−
Sodium acetate (0.1 %)	−	−	+	−	−	−
Degradation of:						
Adenine	+	−	+	−	−	−
Aesculin	+	−	+	+	+	−
Tween 20	+	(+)	+	+	+	+
Tween 40	+	−	+	+	+	+

are listed in Table 2. The cell-wall is of type I. Type II phospholipids and menaquinone MK-9 (H₆, H₈ and H₄) are detected. The fatty acid profile is composed of anteiso-C_{15:0} (14.6 %), iso-C_{16:0} (13.3 %), anteiso-C_{17:0} (12.6 %), C_{16:0} (9.4 %), C_{16:1ω7c} (8.2 %), anteiso-C_{17:1ω9c} (7.0 %), C_{18:0} (3.7 %), C_{17:1ω8c} (3.6 %), iso H-C_{16:1} (3.6 %), C_{15:0} (3.1 %), iso-C_{15:0} (3.0 %), iso-C_{17:1ω9c} (3.0 %), iso-C_{15:0} (3.0 %), C_{14:0} (2.8 %), C_{18:1ω9c} (2.4 %), C_{18:1ω7c} (1.6 %), iso-C_{17:0} (1.3 %), C_{17:0} (1.1 %), iso-C_{14:0} (1.1 %) and iso I-C_{15:1} (1.1 %). The G + C content of the DNA is 70.8 mol%.

The type strain, strain 4776^T (=CGMCC 4.3504^T=DSM 41884^T), was isolated from a soil sample collected from Emei Mountain, Sichuan Province, China.

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