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### Paper:

Zhang, B., Tang, S., Yang, R., Chen, X., Zhang, D., Zhang, W., Li, S., Chen, T., Liu, G. et. al. (2019). *Streptomyces dangxiongensis* sp. nov., isolated from soil of Qinghai-Tibet Plateau. *International Journal of Systematic and Evolutionary Microbiology*  
<http://dx.doi.org/10.1099/ijsem.0.003550>

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*Streptomyces dangxiongensis* sp. nov., isolated from soil of Qinghai-Tibet  
Plateau

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Running title: *Streptomyces dangxiongensis* sp. nov.

Key words: *Streptomyces dangxiongensis* sp. nov., actinobacterium, taxonomy

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Category: New Taxa (Actinobacteria)

A footnote:

The GenBank/EMBL/DDBJ accession number for the genome and 16S rRNA gene sequence of strain Z022<sup>T</sup> are SAMN10237529 and KF729589, respectively.

1 **Abstract**

2 A novel actinobacterial strain, designated Z022<sup>T</sup>, isolated from a soil sample collected  
3 from Dangxiong in Tibet Autonomous Region (China), was determined by polyphasic  
4 taxonomic approach. The organism had chemotaxonomic and morphological properties  
5 consistent with its classification in the genus *Streptomyces*. Strain Z022<sup>T</sup> showed high similarity  
6 value to *Streptomyces lucensis* NBRC 13056<sup>T</sup> (98.87 %) and *S. achromogenes* subsp.  
7 *achromogenes* NBRC 12735<sup>T</sup> (98.68 %) based on the 16S rRNA gene phylogenetic tree. The  
8 genomic DNA G+C content of strain Z022<sup>T</sup> based on the genome sequence was 72.16 mol%.  
9 DNA–DNA relatedness values between strain Z022<sup>T</sup> and strain *Streptomyces lucensis* NBRC  
10 13056<sup>T</sup> was 23.7±1.3 % and significantly lower than 70 %. Chemotaxonomic data revealed that  
11 strain Z022<sup>T</sup> possessed MK-9(H<sub>8</sub>) and MK-9(H<sub>6</sub>) as the predominant menaquinone, LL-  
12 diaminopimelic acid as the diagnostic diamino acid, and galactose, glucose, xylose and ribose  
13 as whole cell sugars. Diphosphatidylglycerol (DPG) and phosphatidylethanolamine (PE) were  
14 the predominant polar lipids; anteiso-C<sub>15:0</sub>, iso-C<sub>16:0</sub>, and anteiso-C<sub>17:0</sub> were the major fatty acids.  
15 On the basis of these genotypic and phenotypic data, it is proposed that isolate Z022<sup>T</sup> (=JCM  
16 31053<sup>T</sup> =CGMCC 4.7273<sup>T</sup>) should be classified in the genus *Streptomyces* as *Streptomyces*  
17 *dangxiongensis* sp. nov.

18

19 The genus *Streptomyces* first described by Waksman and Henrici [1]. Members of the genus  
20 *Streptomyces* have LL-diaminopimelic acid with no characteristic sugars in the cell wall (wall  
21 chemotype I) [2] and have high genomic DNA G+C contents [3, 4]. Species of the genus *Streptomyces*  
22 typically have a wide range of metabolic pathways and produce many bioactive secondary  
23 metabolites, especially the majority of antibiotics used in medicine [5, 6]. The genus comprises  
24 more than 700 species with validly published names at the time of writing the manuscript  
25 (www.bacterio.net). There are many *Streptomyces* resource in the minimal human influence  
26 area of Qinghai-Tibet Plateau [7-9]. When we investigated the diversity of actinobacteria in  
27 the west of China, a novel actinobacteria was isolated from grassland soil collected from the  
28 Dangxiong aera on the Qinghai-Tibet Plateau, China.

29 Strain Z022<sup>T</sup> was isolated from grass soil sample collected in the Dangxiong, Lhasa city,  
30 Tibet Autonomous Region, China on March, 2014. Dangxiong is located in the center of Tibet  
31 Autonomous Region. The geographic coordinates of sampling site is 30.33N 91.52 E and the  
32 elevation is 4488 m. Strain Z022<sup>T</sup> was isolated by Gause's synthetic agar medium (20.0 g  
33 soluble starch, 1.0 g KNO<sub>3</sub>, 0.5 g K<sub>2</sub>HPO<sub>4</sub>·3H<sub>2</sub>O, 0.5 g MgSO<sub>4</sub>·7H<sub>2</sub>O, 0.001 g FeSO<sub>4</sub>, 0.5 g  
34 NaCl and 20.0 agar in 1.0 liter tap water, pH 7.2), supplemented with nalidixic acid (25 µg ml<sup>-1</sup>)  
35 incubated for 7 days at 28°C. The strain was stored at -86 °C in the presence of 20 % (v/v)  
36 glycerol. The reference strains were *Streptomyces lucensis* JCM 4490<sup>T</sup> and *Streptomyces*  
37 *achromogenes* subsp. *achromogenes* JCM 4121<sup>T</sup>. They all came from the Japan Collection of  
38 Microorganisms.

39 Morphological observation of spores and mycelia were conducted by light microscopy  
40 (BH-2; Olympus) and scanning electron microscopy (JSM-5600LV; JEOL) using cultures  
41 grown on Gause's synthetic agar medium for 20 days. Cultural characteristics was examined  
42 by using standard media ISP 2-7 [10], Czapek's agar [11] and nutrient agar after incubation at  
43 30°C for 14 days. Colours were determined according to colour chips from the ISCC-NBS  
44 Colour Charts standard samples no.2106 [12]. The utilization of sole carbon and nitrogen,  
45 decomposition of starch, cellulose, were examined as described previously [13, 14]. Growth at  
46 various temperatures (4, 10, 20, 30, 37, 40, 45 and 50) and NaCl concentrations (0-10 %) were

47 examined on yeast extract-malt extract (ISP 2). The pH range and the optimum pH were  
48 determined by incubating at 30 °C in ISP 2 broth, of which pH was adjusted to 4-12 by addition  
49 of KH<sub>2</sub>PO<sub>4</sub>/HCl, KH<sub>2</sub>PO<sub>4</sub>/K<sub>2</sub>HPO<sub>4</sub> and K<sub>2</sub>HPO<sub>4</sub>/NaOH (at intervals of 1.0 pH unit).

50 The morphological features of isolate Z022<sup>T</sup> were consistent with its classification in the  
51 genus *Streptomyces* [15]. The cultural characteristics of strain Z022<sup>T</sup> on different kinds of media  
52 were presented in Table 1 and microscopic morphology were showed in Fig. 1. Strain Z022<sup>T</sup>  
53 was an aerobic, Gram-stain-positive and non-motile actinobacterium, which formed branch  
54 substrate hyphae and aerial mycelium that differentiates into straight chains with spiny and/or  
55 hairy spores. It grew well on ISP medium 2-7, Czapek's agar and nutrient agar. Sporulation  
56 was poor on ISP5-6 and Czapek's agar, and can't form on nutrient agar. Aerial mycelia were  
57 white on ISP2, ISP4, ISP5, ISP7 and Czapek's agar, grey on ISP3 and light yellow on ISP6 and  
58 nutrient agar. Brown diffusible pigments were observed on ISP3. The temperature range for  
59 growth of strain Z022<sup>T</sup> was 20-40 °C (optimum, 30 °C). The pH range for growth was 5-9  
60 (optimum, pH 7-8). The maximum NaCl concentration for growth was 7 % (w/v) (optimum, 0-  
61 2 %). Strain Z022<sup>T</sup> could well utilize L-arabinose, D-fructose, D-glucose, D-galactose, weak  
62 utilize D-lactose, D-mannitol and D-xylose as sole carbon sources, but not myo-inositol, D-  
63 raffinose, L-rhamnose or sucrose. It also utilized L-alanine, L-asparagine, L-histidine and L-  
64 cysteine as sole nitrogen sources, but not leucine (Table 2). The strain Z022<sup>T</sup> could degrade  
65 starch, cellulose, gelatin, tween 20, tween 80 and urea [16-18].

66 Biomass for chemical studies was prepared by growing the strain in TSB medium in flasks  
67 on a rotary shaker at 200 r.p.m for 10 days at 30 °C. Biomass was harvested by centrifugation,  
68 washed twice in distilled water, recentrifuged and freeze-dried. Analysis of the diaminopimelic  
69 acid isomers in the cell wall and whole-cell sugars were performed as described previously [2,  
70 19, 20], respectively. The menaquinones were extracted and purified using the method of  
71 Collins *et al.* [21] and analysed by HPLC [22]. Polar lipids were extracted, separated by two-  
72 dimensional TLC and identified according to procedures outlined by Minnikin *et al.* [23].  
73 Cellular fatty acids were extracted, methylated and separated according to the standard protocol

74 of the Sherlock Microbial identification (MIDI) system [24, 25] and the fatty acid methyl ester  
75 peaks were quantified using the TSBA 5.0 database.

76 The chemotaxonomic features of strain Z022<sup>T</sup> were consistent with the genus  
77 *Streptomyces*. The cell wall contained LL-diaminopimelic acid as the diagnostic diamino acid.  
78 The galactose, glucose, xylose and ribose present in whole-organism hydrolysates. The  
79 predominant isoprenoid quinone compound was MK-9(H<sub>8</sub>) (76.3 %) and MK-9(H<sub>6</sub>) (23.7 %).  
80 The polar lipids were diphosphatidylglycerol (DPG), phosphatidylethanolamine (PE), two  
81 unidentified phospholipids (UPL1-2), two unidentified aminolipids (UAL1-2), and one  
82 unidentified phosphoglycolipid (UPGL) (Fig. S1). The major fatty acid found were anteiso-  
83 C<sub>15:0</sub> (25.7 %), iso-C<sub>16:0</sub> (14.3 %), anteiso-C<sub>17:0</sub> (11.9 %), anteiso-C<sub>17:1</sub> ω9c (8.4 %), iso-C<sub>15:0</sub>  
84 (7.3 %), iso-C<sub>16:1</sub> H (6.5 %) and anteiso-C<sub>16:1</sub> ω9c (5.0 %).

85 The genomic DNA of strain Z022<sup>T</sup> was extracted and the 16S rRNA was amplified as  
86 described by Mingma *et al.* [26]. Phylogenetic trees were generated using the neighbour-joining  
87 [27], maximum-likelihood [28] and maximum-parsimony [29] algorithms in MEGA 5.0 [30].  
88 Evolutionary distances were calculated using the model of Jukes and Cantor [31]. Topologies  
89 of the resultant tree were evaluated by bootstrap analyses [32] based on 1000 resamplings. The  
90 almost full-length 16S rRNA gene sequence of strain Z022<sup>T</sup> (1491 nt) was compared with the  
91 corresponding sequences available on the EzTaxon-e server [33]. The result showed that it  
92 closely related to *Streptomyces lucensis* NBRC 13056<sup>T</sup> (98.88 %), *Streptomyces achromogenes*  
93 subsp. *achromogenes* NBRC 12735<sup>T</sup> (98.70 %), *Streptomyces cellostaticus* NBRC 12849<sup>T</sup>  
94 (98.70 %) and *Streptomyces griseochromogenes* NBRC 13413<sup>T</sup> (98.70 %). Strains Z022<sup>T</sup> and  
95 *Streptomyces lucensis* NBRC 13056<sup>T</sup> formed an independent clade by using three treeing  
96 methods (Fig. 2).

97 The genome of strain Z022<sup>T</sup> was sequenced with Illumina MiSeq platform and PacBio RS  
98 II platform. The reads were *de novo* assembled using Newbler (version 2.8) and Hierarchical  
99 Genome Assembly Process (HGAP) version 3.0 [34]. The quality of microbial genomes was  
100 examined using MUMmer version 3.0 and Pilon software [35, 36]. DNA-DNA hybridization

101 was performed by Ezaki *et al.* [37]. The average nucleotide identity (ANI) was calculated using  
102 the ChunLab's online Average Nucleotide Identity (ANI) calculator [38].

103 The whole genome of strain Z022<sup>T</sup> possessed a chromosome DNA with a size of 8,085,191  
104 bp and a plasmid with a size of 72,694 bp (Table S1). The DNA-DNA relatedness value of  
105 strain Z022<sup>T</sup> with *Streptomyces lucensis* JCM 4490<sup>T</sup> and *Streptomyces achromogenes* subsp.  
106 *achromogenes* JCM 4121<sup>T</sup> were 23.7±1.3 % and 16.1±1.6 %, respectively, and both values were  
107 significantly lower than 70 %, the level considered to be the threshold value for the delineation  
108 of genomic species [39]. The whole-genome average nucleotide identity (ANI) value between  
109 strain Z022<sup>T</sup> and *Streptomyces achromogenes* subsp. *achromogenes* NBRC 12735<sup>T</sup>,  
110 *Streptomyces cellostaticus* NBRC 12849<sup>T</sup>, *Streptomyces griseochromogenes* NBRC 13413<sup>T</sup>,  
111 *Streptomyces canus* DSM 40017<sup>T</sup>, *Streptomyces corchorusii* DSM 40340<sup>T</sup> were 87.07 %,   
112 86.02 %, 85.67 %, 82.11 % and 87.87 %, respectively. The DNA G+C content of strain Z022<sup>T</sup>  
113 was 72.16 mol%.

114 Generally, there are many differences between the strain Z022<sup>T</sup> and the reference strains.  
115 For example: the clone colour (Table S1), temperature/pH/NaCl ranges for growth, ability for  
116 utilized different sole carbon and nitrogen (Table 1), the relative abundance of major fatty acid  
117 (Table 2), the length of genome DNA sequence , genome DNA G+C content (Table S2). Based  
118 on the phenotypic, phylogenetic, and chemotaxonomic evidence, strain Z022<sup>T</sup> is clearly  
119 different from all other species of the genus *Streptomyces*, which supports its classification as  
120 a novel species within the genus *Streptomyces*, for which the name *Streptomyces*  
121 *dangxiongensis* sp. nov. is proposed.

## 122 **Description of *Streptomyces dangxiongensis* sp. nov.**

123 *Streptomyces dangxiongensis* (dang.xiong.en'sis. N.L. masc. adj. *dangxiongensis* pertaining to  
124 Dangxiong, Tibet, China, where the type strain was isolated).

125 Aerobic, Gram-stain-positive, non-motile, actinobacterium, which forms branch substrate  
126 hyphae and aerial mycelium that differentiates into straight chains with spiny and/or hairy spores.  
127 Grows well on ISP medium 2-7, Czapek's agar and nutrient agar. Sporulation is poor on ISP5-6 and



128 Czapek's agar, and can't form on nutrient agar. Aerial mycelia are whitish on ISP2, ISP4, ISP5,  
129 ISP7 and Czapek's agar, grey on ISP3 and light yellow on ISP6 and nutrient agar. Brown diffusible  
130 pigments are formed on ISP3. Grows at 20-40°C (optimum, 30 °C), at pH 5-9 (optimum, pH 7-8)  
131 and with 0-7 % (w/v) NaCl (optimum, 0-2 %). Well utilizes L-arabinose, D-fructose, D-glucose,  
132 D-galactose, weak utilize D-lactose, D-mannitol and D-xylose as sole carbon sources, but not  
133 myo-inositol, D-raffinose, L-rhamnose or sucrose. Utilizes L-alanine, L-asparagine, L-histidine and  
134 L-cysteine as sole nitrogen sources, but not leucine. The strain Z022<sup>T</sup> degrades starch, cellulose,  
135 gelatin, tween 20, tween 80 and urea. The cell wall contain LL-diaminopimelic acid. The whole-  
136 cell sugar pattern mainly consists of galactose, glucose, xylose and ribose. The predominant  
137 menaquinones are MK-9(H<sub>8</sub>) and MK-9(H<sub>6</sub>). The polar lipid profile contained  
138 diphosphatidylglycerol (DPG), phosphatidylethanolamine (PE), two unidentified phospholipids  
139 (UPL1-2), two unidentified aminolipids (UAL1-2), and one unidentified phosphatidylglycolipid  
140 (UPGL). The major cellular fatty acids are anteiso-C<sub>15:0</sub>, iso-C<sub>16:0</sub>, and anteiso-C<sub>17:0</sub>.

141 The type strain, Z022<sup>T</sup> (=JCM 31053<sup>T</sup> =CGMCC 4.7273<sup>T</sup>) was isolated from a soil sample  
142 collected from Dangxiong, Tibet, China. The DNA G + C content of the type strain is 72.16 mol%.  
143

144 **Funding information**

145 This work was funded by the National Science Foundation of China (No. 41801045,  
146 31570498), CAS "Light of West China" Program and State Key Laboratory of Cryospheric  
147 Science, Northwest Institute of Eco-Environment and Resources, Chinese Academy Sciences  
148 (SKLCS-OP-2018-10).

149 **Conflicts of interest**

150 The authors declare that there are no conflicts of interest.

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242

243

244 Table 1. Phenotypic properties of strain Z022<sup>T</sup> and closely related type species

245 Strains: 1, Z022<sup>T</sup>; 2, *S. lucensis* JCM 4490<sup>T</sup>; 3, *S. achromogenes* subsp. *achromogenes* JCM  
 246 4121<sup>T</sup>; 4, *S. bungoensis* NBRC 15711<sup>T</sup> (data from Eguchi *et al.* 1993) [17]; 5, *S. canus* NRRL  
 247 B-1989 (data from Yan *et al.* 2013) [18]; 6, *S. chartreusis* NBRC 12753<sup>T</sup> (data from Lee *et al.*  
 248 2014 and Zhang *et al.* 2018) [9, 16]. The data of strain 1, 2 and 3 were obtain in this study.

249 Abbreviations: +, positive; w, weakly positive; -, negative; ND, no data available.

Characteristics	1	2	3	4	5	250
Spore chain	straight	spiral	spiral	spiral	spiral	spiral
Temperature for growth	20-40	10-45	20-40	ND	≤45	251
pH range for growth	5-9	6-8	5-10	ND	>5,<9	4.0-5.0
NaCl for growth(% ,w/v)	0-7	0-3	0-5	<10,>=7	=3;=4	0-5
Carbon source utilization (1.0%, w/v)						253
myo-Inositol	-	w	-	-	-	+
L-Arabinose	+	+	+	+	-	254
D-Fructose	+	w	+	+	+	255
D-glucose	+	+	-	+	-	+
D-Lactose	w	-	-	ND	-	256
D-Galactose	+	+	+	+	-	257
D-Mannitol	w	-	+	+	ND	+
D-Raffinose	-	w	+	-	+	258
L-Rhamnose	-	-	+	-	-	+
Sucrose	-	+	-	w	-	259
D-Xylose	w	+	+	+	-	260
Nitrogen source utilization (0.1%, w/v)						
Leucine	-	w	-	ND	-	261
L-Alanine	+	+	+	ND	-	+
L-Asparagine	+	-	+	ND	-	262
L-Histidine	+	+	+	ND	-	263
L-Cysteine	+	-	-	ND	-	+
Degradation						264
Starch	+	+	+	-	ND	+
Cellulose	+	+	+	ND	-	265
Gelatin	+	+	+	+	-	266
Tween 20	+	+	+	ND	-	-
Tween 80	+	+	+	ND	ND	267
Urease test	+	+	+	-	-	+
						268

269

270 Table 2. Cellular fatty acid composition of strain Z022<sup>T</sup> and related type species.

271 Strains: 1, Z022<sup>T</sup>; 2, *S. lucensis* JCM 4490<sup>T</sup>; 3, *S. achromogenes* subsp. *achromogenes* JCM  
 272 4121<sup>T</sup>; 4, *S. chartreusis* NBRC 12753<sup>T</sup>. Data for strain 1, 2 and 3 were obtained in this study,  
 273 for strain 4 was taken from Zhang *et al.* [9]. TR, Trace amount (<1%); -, not detect. Fatty  
 274 acids amounting to <1% of the total fatty acids in all strains were not shown.

Fatty acid	1	2	3	4
iso-C <sub>14:0</sub>	2.1	TR	1.1	6.4
iso-C <sub>15:0</sub>	7.3	16.0	9.0	5.5
anteiso-C <sub>15:0</sub>	25.7	16.5	30.8	12.1
C <sub>16:0</sub>	4.7	6.7	4.8	7.1
iso-C <sub>16:0</sub>	14.3	11.8	11.1	32.1
iso-C <sub>16:1</sub> H	6.5	1.9	1.9	9.6
anteiso-C <sub>16:1</sub> ω9c	5.0	-	-	-
iso-C <sub>17:0</sub>	2.7	7.1	3.7	TR
anteiso-C <sub>17:0</sub>	11.9	15.1	19.5	5.4
cyclo-C <sub>17:0</sub>	TR	TR	TR	1.1
anteiso-C <sub>17:1</sub> ω9c	8.4	4.9	6.3	4.8
iso-C <sub>18:0</sub>	-	TR	1.5	TR
Sum In Feature 3	-	4.6	1.5	6.6
Sum In Feature 8	2.5	1.6	TR	TR
Sum In Feature 9	4.2	6.0	3.2	2.7

275 Summed Feature 3: C<sub>16:1</sub> ω7c/ω6c or C<sub>16:1</sub> ω6c/ω7c; Summed Feature 8: C<sub>18:1</sub> ω7c or C<sub>18:1</sub> ω6c;  
 276 Summed Feature 9: C<sub>16:0</sub> 10-methyl or iso-C<sub>17:1</sub>ω9c.  
 277

278

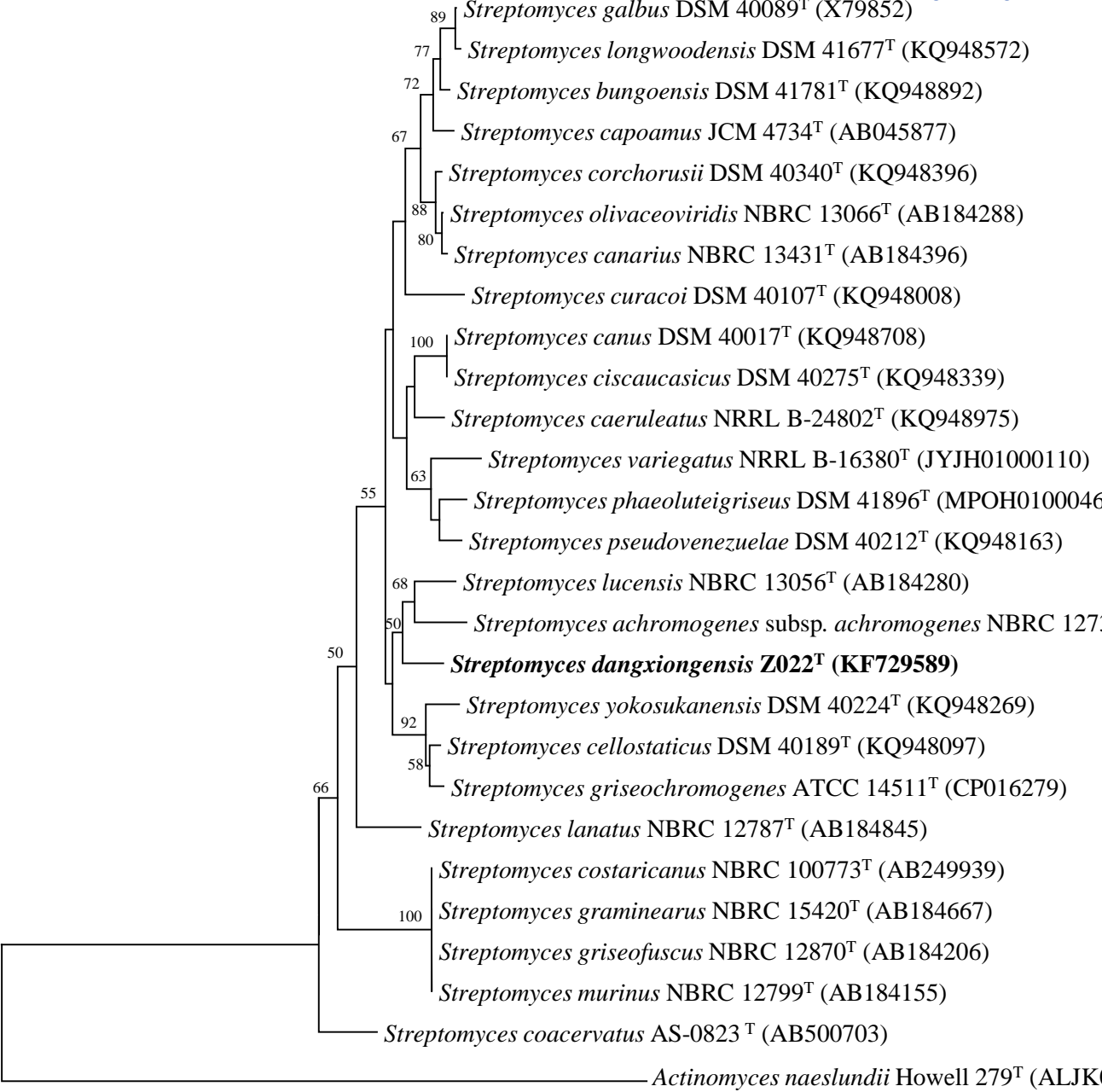
279 Figure 1 Scanning electron micrograph of strain Z022<sup>T</sup> cultivated on Gause's synthetic agar at  
 280 30°C for 4 weeks.

281 Figure 2 Neighbor-joining phylogenetic tree, based on nearly complete 16S rRNA gene  
 282 sequences, showing the relationships between strain Z022<sup>T</sup> and related species of the genus  
 283 *Streptomyces*. *Actinomyces naeslundii* Howell 279<sup>T</sup> was used as an out group. Numbers at  
 284 nodes are bootstrap values based on 1000 resamplings (only values above 50% are shown).

285

Figure

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0.02

## *Streptomyces dangxiongensis* sp. nov., isolated from soil of Qinghai-Tibet

### Plateau

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### **International Journal of Systematic and Evolutionary Microbiology**

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Category: New Taxa (Actinobacteria)

A footnote:

The GenBank/EMBL/DDJB accession number for the genome and 16S rRNA gene sequence of strain Z022<sup>T</sup> are SAMN10237529 and KF729589, respectively.

## Supplementary

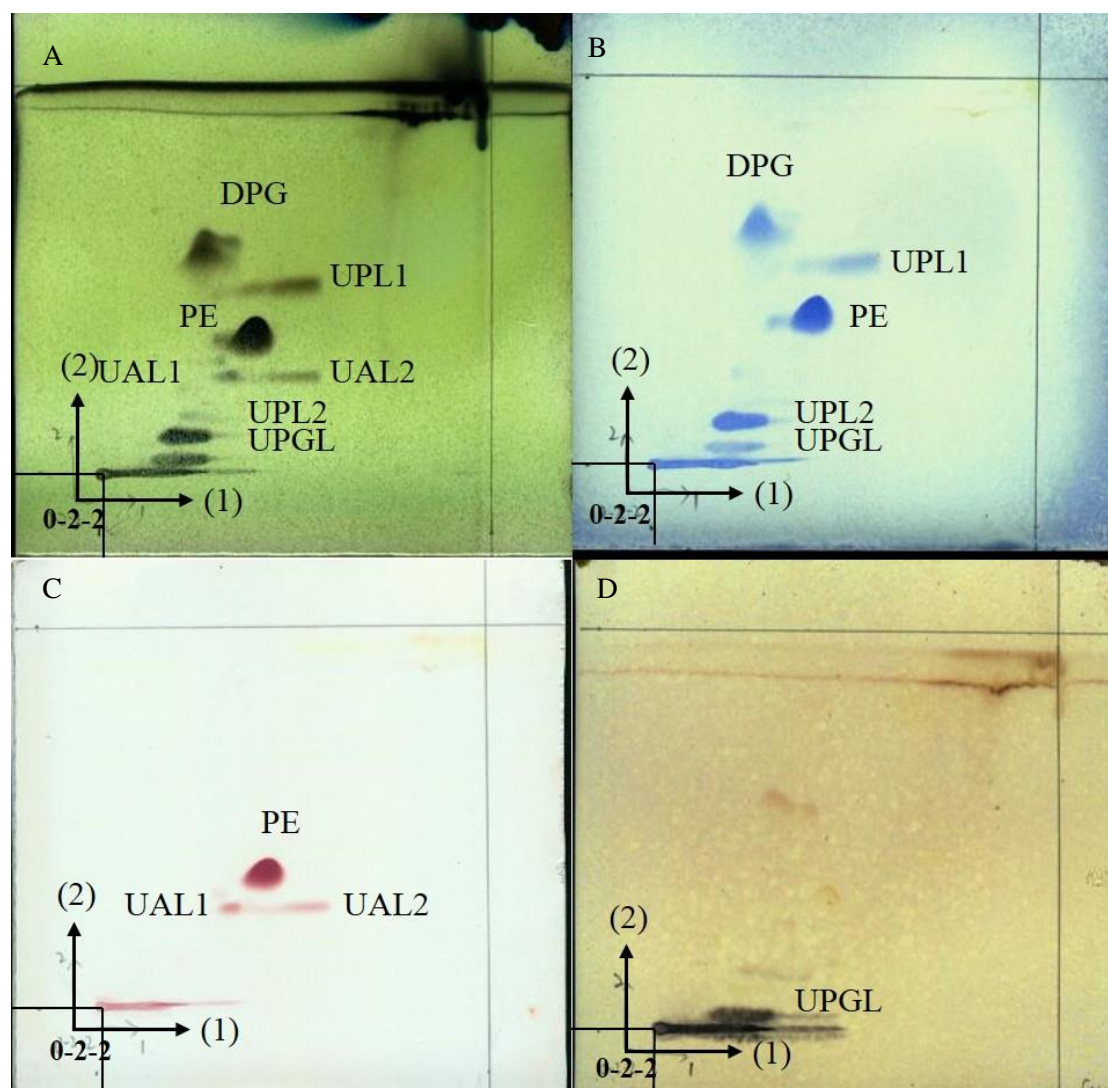


Fig. S1 Polar lipid profiles of strain Z022<sup>T</sup> separated by two-dimensional thin layer chromatography and detected with molybdotophosphoric acid (A), molybdenum blue (B), ninhydrin (C) and alpha-naphthol (D). The solvent systems used were as following: Direction 1 was chloroform/methyl alcohol/H<sub>2</sub>O (65/25/4, by vol.), Direction 2 was chloroform/ acetic acid/methyl alcohol/H<sub>2</sub>O (80/15/12/4, by vol.). Abbreviations: DPG, diphosphatidylglycerol; PE, phosphatidylethanolamine; PG, phosphatidylglycerol; UPL(1-2), unidentified phospholipid 1-2; UAL(1-2), unidentified aminolipid 1-2; UPGL, unidentified phosphoglycerolipid.



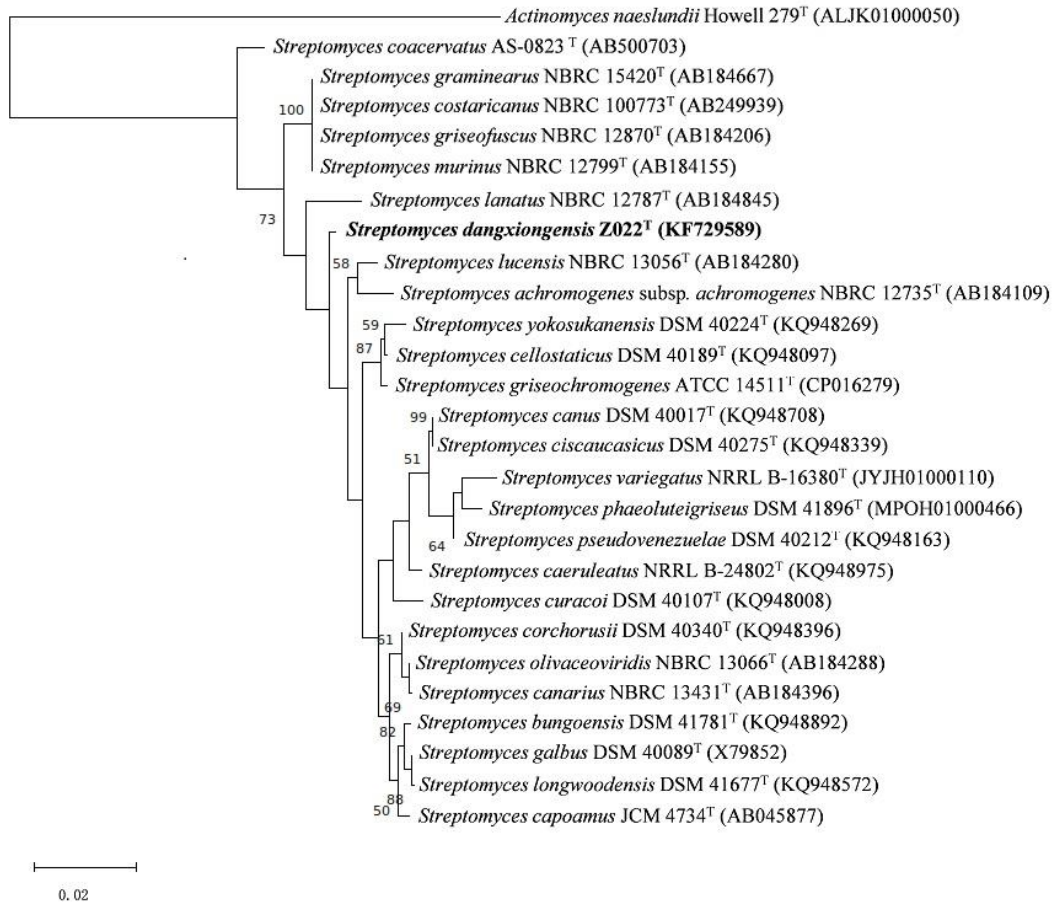


Fig. S2 Maximum-likelihood phylogenetic tree, based on nearly complete 16S rRNA gene sequences, showing the relationships between strain Z022<sup>T</sup> and related species of the genus *Streptomyces*. *Actinomyces naeslundii* Howell 279<sup>T</sup> was used as an out group. Numbers at nodes are bootstrap values based on 1000 resamplings (only values above 50% are shown).

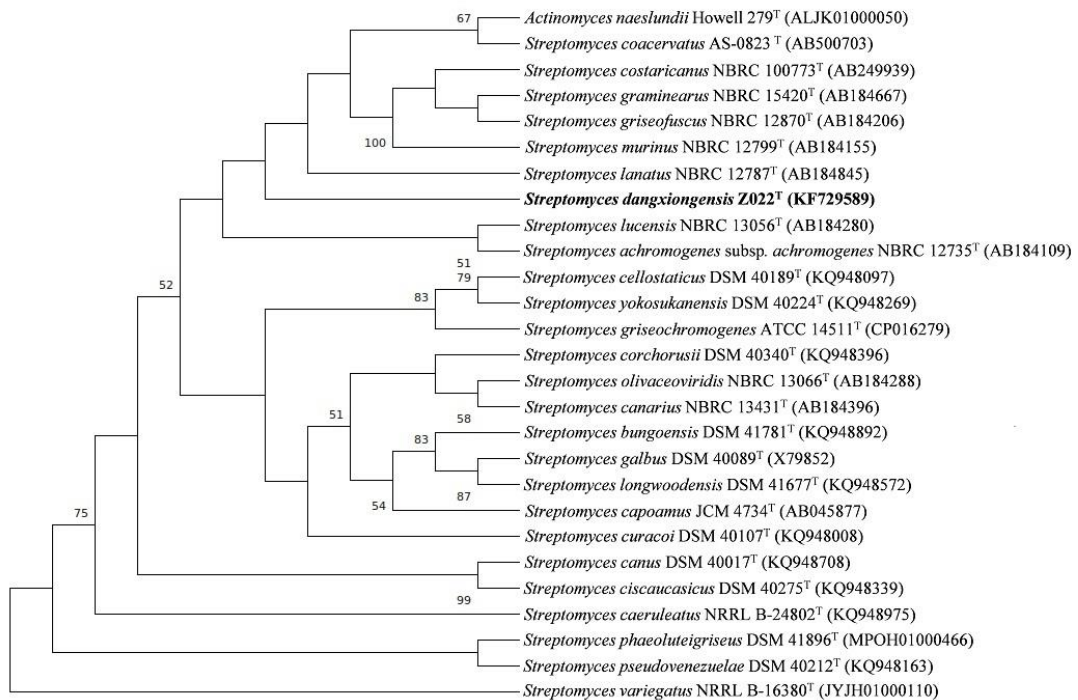


Fig. S3 Maximum-parsimony phylogenetic tree, based on nearly complete 16S rRNA gene sequences, showing the relationships between strain Z022<sup>T</sup> and related species of the genus *Streptomyces*. *Actinomyces naeslundii* Howell 279<sup>T</sup> was used as an out group. Numbers at nodes are bootstrap values based on 1000 resamplings (only values above 50% are shown).

Table S1. Cultural characteristics of strain Z022<sup>T</sup> and closely related type strains on various media at 30°C.

Agar medium	Z022 <sup>T</sup>	<i>S. lucensis</i> JCM 4490 <sup>T</sup>	<i>S. achromogenes</i> subsp. <i>achromogenes</i> JCM 4121 <sup>T</sup>
Yeast extract/extract (ISP2)			
Growth	Good	Good	Good
Sporulation	Good	Poor	Good
Aerial mycelium	White	White	White
Substrate mycelium	Brown	Light yellow	Light brown
Diffusible pigment	None	None	None
Oatmeal (ISP3)			
Growth	Good	Moderate	Good
Sporulation	Good	Moderate	Good
Aerial mycelium	Grey	White	White
Substrate mycelium	Pale grey	Yellow	Light yellow
Diffusible pigment	Brown	None	None
Inorganic salts/starch (ISP4)			
Growth	Good	Good	Good
Sporulation	Good	Moderate	Good
Aerial mycelium	White	Light yellow	White
Substrate mycelium	Light brown	Light yellow	Light yellow
Diffusible pigment	None	None	Black
Glycerol/asparagine (ISP5)			
Growth	Good	Moderate	Moderate
Sporulation	Poor	Moderate	Poor
Aerial mycelium	White	White	White
Substrate mycelium	White	White	White
Diffusible pigment	None	None	None
Peptone/yeast extract/iron (ISP6)			
Growth	Good	Moderate	Moderate
Sporulation	Poor	Poor	Good
Aerial mycelium	Light yellow	White	White
Substrate mycelium	Light yellow	Yellow	Yellow
Diffusible pigment	None	Brown	None
Tyrosine (ISP7)			
Growth	Good	Moderate	Good
Sporulation	Moderate	Moderate	Good
Aerial mycelium	White	White	White
Substrate mycelium	White	White	Light brown
Diffusible pigment	None	None	None
Czapek's agar			
Growth	Good	Moderate	Good
Sporulation	Poor	None	Poor
Aerial mycelium	White	Light Yellow	White
Substrate mycelium	White	Light Yellow	White
Diffusible pigment	None	None	None
Nutrient agar			
Growth	Good	Good	Moderate
Sporulation	None	Moderate	Poor
Aerial mycelium	Light yellow	White	White
Substrate mycelium	Light yellow	White	Light yellow
Diffusible pigment	None	None	None

Table S2. Genome characteristics of strain Z022<sup>T</sup> and five similar strains

Strains: 1, Z022<sup>T</sup>; 2, *S. achromogenes* subsp. *achromogenes* NBRC 12735<sup>T</sup>; 3, *S. cellostaticus* NBRC 12849<sup>T</sup>; 4, *S. griseochromogenes* NBRC 13413<sup>T</sup>; 5, *S. canus* DSM 40017<sup>T</sup>; 6, *S. corchorusii* DSM 40340<sup>T</sup>. \* It is between strain (current line) and Z022<sup>T</sup>.

Strain	G+C content (mol%)	Genome size (bp)	DDBJ/EMBL/GenBank accession number	ANI*
1	72.16	8,085,191	SAMN10237529	100
2	72.54	8,112,410	GCA_000720835.1	87.07
3	70.98	9,835,283	GCA_001513965.1	86.02
4	70.76	10,764,674	GCA_001542625.2	85.67
5	70.24	11,570,753	GCA_001514145.1	82.11
6	72.03	10,309,547	GCA_001514055.1	87.87