Haloechinothrix alba gen. nov., sp. nov., a halophilic, filamentous actinomycete of the suborder *Pseudonocardineae*

Shu-Kun Tang,^{1†} Yun Wang,^{2†} Hua Zhang,³ Jae-Chan Lee,⁴ Kai Lou,² Chang-Jin Kim⁴ and Wen-Jun Li¹

Correspondence

Wen-Jun Li
wjli@ynu.edu.cn
Chang-Jin Kim
changjin@kribb.re.kr

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

²Xinjiang Institute of Microbiology, Xinjiang Academy of Agricultural Science, Urumqi, Xinjiang, 830091, PR China

³The National Engineering Center for Research of Microbial Pharmaceuticals and New Drug Research and Development Center, North China Pharmaceutical Group Corporation, Shijiazhuang 050015, PR China

⁴Functional Metabolite Research Center KRIBB, 52 Eoeun-dong, Yuseong gu, Daejeon 305-806, Republic of Korea

A novel halophilic, filamentous actinomycete strain, designated YIM 93221^T, was isolated from a salt lake in Xinjiang province, north-west China, and subjected to a polyphasic taxonomic characterization. The isolate grew with 9–23 % (w/v) NaCl and did not grow without NaCl. The isolate formed spiny aerial mycelium and did not form spores at maturity. The isolate contained *meso*-diaminopimelic acid as the diagnostic diamino acid and glucose, glucosamine, mannose and an unknown sugar as the major whole-cell sugars. The phospholipids were diphosphatidylglycerol, phosphatidylglycerol, phosphatidylethanolamine, phosphatidylinositol, phosphatidylinositol mannosides and an unknown phospholipid. MK-8(H₄) was the predominant menaquinone. The major fatty acid was iso-C_{16:0}. The DNA G+C content was 68.1 mol%. Phylogenetic analysis based on 16S rRNA gene sequences indicated that strain YIM 93221^T formed a distinct lineage within the suborder *Pseudonocardineae* and showed 91.9–94.8 % 16S rRNA gene sequence similarity with members of the suborder *Pseudonocardineae*. On the basis of the evidence from this polyphasic study, a novel genus and species, *Haloechinothrix alba* gen. nov., sp. nov., are proposed. The type strain of *Haloechinothrix alba* is YIM 93221^T (=DSM 45207^T =CCTCC AB 208140^T).

Since the first halophilic, filamentous actinomycete, *Actinopolyspora halophila*, was reported (Gochner *et al.*, 1975), it has been known that some filamentous actinomycetes can grow with and tolerate high salt concentrations. However, in recent decades, only a few halophilic actinomycetes have been discovered and cultured, such as the genera *Actinopolyspora* and *Streptomonospora* (Cui *et al.*, 2001) and some species belonging to the genera *Nocardiopsis*, *Saccharomonospora* and *Prauserella*. Recently,

on the basis of extensive studies on the biological characteristics of halophilic filamentous actinomycetes, an efficient isolation medium, cellulose-casein-multisalts (CCMS) medium (Tang *et al.*, 2008), was designed and used for the isolation of filamentous halophilic actinomycetes from hypersaline environments. By using this method, over 2000 halophilic actinomycete strains, which cannot grow without NaCl and have optimal growth with 10–15 % NaCl, have been isolated from hypersaline soil in Xinjiang province in China. Phylogenetic analysis based on 16S rRNA gene sequences has revealed, in addition to the above-mentioned genera, two new genera, *Haloactinospora* (Tang *et al.*, 2008) and *Haloglycomyces* (Guan *et al.*, 2009), and three novel species, *Amycolatopsis halophila* (Tang *et al.*, 2010), *Saccharopolyspora halophila* (Tang *et al.*, 2009a) and *Saccharopolyspora qijiaojiangensis* (Tang *et al.*,

†These authors contributed equally to this work.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain YIM 93221^T is GQ366705.

A micrograph of spiny aerial mycelium and a chromatogram of polar lipids of strain YIM 93221^T are available as supplementary material with the online version of this paper.

2009c). Here, we report the characterization of another strain, designated YIM 93221^T.

Strain YIM 93221^T was isolated from a soil sample collected from Qijiaoing Lake, which is a salt lake in Xinjiang Province, north-west China (43° 27' N 91° 29' E), after 3 weeks of incubation at 37 °C on CCMS medium (Tang *et al.*, 2008). Strain YIM 93221^T was maintained on modified International *Streptomyces* Project (ISP) 4 agar containing 15 % (w/v) NaCl at 4 °C and as a glycerol suspension (20 %, v/v) at –20 °C. Biomass for chemical and molecular studies was obtained by cultivation in ISP 4 without agar (15 %, w/v, NaCl; pH 7.0) at 37 °C and 150 r.p.m. for 1 week.

Cultural characteristics were determined after incubation for 3–4 weeks by methods given by the ISP (Shirling & Gottlieb, 1966). All media were supplemented with 15 % (w/v) NaCl for growth. The colours of substrate and aerial mycelia and any soluble pigments produced were determined by comparison with chips from the ISCC-NBS colour charts (Kelly, 1964). Growth was good on inorganic salts-starch agar (ISP 4) and oatmeal agar, moderate on Czapek's agar and nutrient agar and weak on glycerol/asparagine agar; there was no growth on yeast extract-malt extract agar or potato agar. The aerial mycelium was white and the substrate mycelium was yellow-white (Supplementary Table S1, available in IJSEM Online). No soluble pigments were produced. Morphological characteristics of strain YIM 93221^T were observed by light microscopy (model BH2; Olympus) and scanning electron microscopy (JSM 5600LV; JEOL) after incubation on ISP 4 agar and oatmeal agar containing 15 % (w/v) NaCl at 37 °C for 4 weeks. The substrate mycelium was well developed and fragmented into rod-like elements, while the aerial mycelium was 'hedgehog-like' or spiny. No spores were formed at maturity (Fig. 1 and Supplementary Fig. S1).

Fig. 1. Scanning electron micrograph of fragmented substrate mycelium and spiny or 'hedgehog-like' aerial mycelium of strain YIM 93221^T grown on ISP 4 (15 % NaCl, w/v) at 37 °C for 4 weeks. Bar, 2 μm.

Growth was tested at 5–55 °C (at intervals of 5 °C) on ISP 4 containing 15 % (w/v) NaCl and at 0–30 % (w/v) NaCl (at intervals of 1 %) using ISP 4 as the basal medium. Growth was investigated at pH 4.0–10.0 (at intervals of 1 pH unit) using the following buffer systems: 0.1 M citric acid/0.1 M sodium citrate (pH 4.0–5.0), 0.1 M KH₂PO₄/0.1 M NaOH (pH 6.0–8.0) and 0.1 M NaHCO₃/0.1 M Na₂CO₃ (pH 9.0–10.0). Media and procedures used for determination of physiological features and carbon source utilization were those described by Williams *et al.* (1989). Enzyme activity and acid production from carbohydrates were determined by using the API ZYM and API 50CH systems (bioMérieux) according to the manufacturer's instructions. Anaerobic growth was determined using the GasPak anaerobic system (BBL) according to the manufacturer's instructions. Strain YIM 93221^T could grow at 20–45 °C, at pH 4.0–8.0 and with 9–23 % NaCl, but could not grow in the absence of NaCl, showing that strain YIM 93221^T was a moderately halophilic actinomycete. The phenotypic and chemotaxonomic characteristics of strain YIM 93221^T are distinctly different from those of other genera of the suborder *Pseudonocardineae* (Table 1). The detailed physiological and biochemical characteristics of strain YIM 93221^T are given in the species description.

Isomers of diaminopimelic acid were analysed according to the procedures developed by Hasegawa *et al.* (1983). The whole-cell sugars were detected by HPLC after pre-column derivatization with 1-phenyl-3-methyl-5-pyrazolone (Tang *et al.*, 2009b). Polar lipids were extracted and examined by two-dimensional TLC and identified using described procedures (Minnikin *et al.*, 1984). Menaquinones were isolated according to Minnikin *et al.* (1984) and separated by atmospheric-pressure photoionization LC-MS (Tang *et al.*, 2008). For fatty acid analysis, strain YIM 93221^T was cultured on tryptic soy agar (Difco) containing 15 % NaCl at 37 °C for 7 days. Cellular fatty acid analysis was performed as described by Sasser (1990) using the Microbial Identification System (MIDI). Genomic DNA of strain YIM 93221^T for the determination of G+C content was prepared according to the method of Marmur (1961). The G+C content of the DNA was determined by reversed-phase HPLC of nucleosides according to Mesbah *et al.* (1989). Strain YIM 93221^T contained *meso*-diaminopimelic acid as the cell-wall diamino acid, with glucose (47.2 %), glucosamine (18.7 %), mannose (11.3 %) and an unknown sugar (11.3 %) as the major whole-cell sugars; minor amounts of ribose (6.9 %) and galactose (4.6 %) were also detected. The phospholipids were diphosphatidylglycerol, phosphatidylglycerol, phosphatidylethanolamine, phosphatidylinositol, phosphatidylinositol mannosides and one unknown phospholipid (Supplementary Fig. S2). The predominant menaquinone was MK-8(H₄) (95.4 %), and a minor amount of MK-8(H₆) (4.6 %) was also detected. The cellular fatty acid profile contained major amounts of branched fatty acids and minor straight-chain and methyl fatty acids: iso-C_{14:0} (1.2 %), C_{14:0} (1.7 %), iso-C_{15:0} (1.0 %), C_{15:1}ω6c (0.8 %), C_{15:0} (2.7 %), iso-C_{15:1}

Table 1. Differential phenotypic characteristics of strain YIM 93221^T and the most closely related genera of the suborder *Pseudonocardineae*

Data for reference genera were obtained from Goodfellow *et al.* (1989), Korn-Wendisch *et al.* (1989), Korn-Wendisch *et al.* (1995), Tang *et al.* (2008) and Tian *et al.* (2009). +, Positive; –, negative; +/–, some species are positive and some are negative.

Characteristic	Strain YIM 93221 ^T	<i>Sciscionella</i>	<i>Thermocrisum</i>	<i>Saccharopolyspora</i>
Aerial mycelium	Abundant	Sparse	Abundant	Abundant
Spiny aerial mycelium	+	–	–	–
Spores	–	–	+	+
Growth in:				
0 % NaCl	–	+	+	+/–
20 % NaCl	+	–	–	+/–
Temperature range (°C)	20–45	10–37	20–62.5	10–63
Whole-cell sugar type	C	A	A	A
Major whole-cell sugars*	Glc, Man, GlcN, UK	Ara, Gal, Glc	Ara, Man, Glc	Ara, Gal
Predominant menaquinone	MK-8(H ₄)	MK-9(H ₄)	MK-9(H ₄)	MK-9(H ₄)
Phospholipids†	DPG, PG, PE, PI, PIM, PL	DPG, PC, PE, PME, PI, PL	PE, OH-PE, PI	DPG, PC, PE, PI, PIM
Major fatty acid(s) (>10 %)‡	i-C _{16:0}	i-C _{16:0} , i-C _{16:0} 2-OH	i-C _{16:0}	i-C _{15:0} , i-C _{16:0} , i-C _{17:0}
DNA G + C content (mol%)	68.1	69	69–73	66.3–74

*Ara, Arabinose; Gal, galactose; Glc, glucose; GlcN, glucosamine; Man, mannose; UK, unknown sugar.

†DPG, Diphosphatidylglycerol; OH-PE, hydroxy-phosphatidylethanolamine; PC, phosphatidylcholine; PE, phosphatidylethanolamine; PG, phosphatidylglycerol; PI, phosphatidylinositol; PIM, phosphatidylinositol mannoside; PL, phospholipid; PME, phosphatidylethanolamine.

‡i, Iso-branched.

(2.3 %), iso-C_{16:0} (43.5 %), C_{16:0} (8.6 %), 10-methyl C_{16:0} (5.6 %), iso-C_{17:0} (0.8 %), anteiso-C_{17:0} (1.6 %), C_{17:1ω8c} (6.1 %), C_{17:1ω6c} (2.6 %), C_{17:0} (3.5 %), 10-methyl C_{17:0} (3.1 %), iso-C_{18:0} (0.8 %), C_{18:1ω9c} (2.7 %), C_{18:0} (1.8 %), 10-methyl C_{18:0} (tuberculostearic acid; 0.6 %) and C_{16:1ω7c} and/or iso-C_{15:0} 2-OH (8.1 %). The G + C content of the DNA was 68.1 mol%.

Extraction of genomic DNA and PCR amplification of the 16S rRNA gene were performed as described by Li *et al.* (2007). Multiple alignments with sequences from the most closely related members of the suborder *Pseudonocardineae* and calculations of sequence similarity were carried out using the EzTaxon server 2.1 (Chun *et al.*, 2007). Phylogenetic analyses were performed using three tree-making algorithms: neighbour-joining (Saitou & Nei, 1987), maximum-likelihood (Felsenstein, 1981) and maximum-parsimony (Fitch, 1971). A phylogenetic tree was constructed using the neighbour-joining method from *K*_{nuc} values (Kimura, 1980) using MEGA version 4.0 (Tamura *et al.*, 2007). The topology of the phylogenetic tree was evaluated by the bootstrap resampling method of Felsenstein (1985) with 1000 replicates.

The phylogenetic analysis based on 16S rRNA gene sequences revealed that strain YIM 93221^T falls within the radius of the suborder *Pseudonocardineae* and has the highest sequence similarity to *Saccharopolyspora rosea* IMMIB L-1070^T (GenBank accession no. AM992060; 94.8 %). The sequence similarity between strain YIM 93221^T and members of other genera of the suborder *Pseudonocardineae* was 91.9–94.8 %. In the phylogenetic tree based on the neighbour-joining algorithm, strain YIM 93221^T and *Sciscionella marina* SCSIO

00231^T (GenBank accession no. EU503139) formed a distinct clade supported by a high bootstrap value (66 %). This relationship was supported by the other tree-making methods used in this study (Fig. 2). All of the above data confirmed that strain YIM 93221^T should be assigned to the suborder *Pseudonocardineae*.

Strain YIM 93221^T was different from members of other genera of the suborder *Pseudonocardineae* in some morphological and physiological properties (Table 1): strain YIM 93221^T was a halophilic actinobacterium that could grow with 23 % NaCl but not without NaCl, whereas members of the genera *Sciscionella*, *Thermocrisum* and *Saccharopolyspora* (except *Saccharopolyspora halophila* and *Saccharopolyspora qijiaojiangensis*) are non-halophilic actinomycetes that can grow without NaCl but not with 15 % NaCl. Moreover, strain YIM 93221^T exhibited some chemotaxonomic differences from the genera *Sciscionella*, *Thermocrisum* and *Saccharopolyspora*: strain YIM 93221^T had type C as the whole-cell sugar type (no diagnostic sugar), MK-8(H₄) as the predominant menaquinone and phospholipids containing phosphatidylglycerol (no phosphatidylcholine), whereas members of the genera *Sciscionella*, *Thermocrisum* and *Saccharopolyspora* have type A as the whole-cell sugar type (arabinose and/or galactose as the diagnostic sugars), MK-9(H₄) as the predominant menaquinone and phospholipids containing phosphatidylcholine (no phosphatidylglycerol).

Therefore, on the basis of phenotypic and phylogenetic differentiation of the new isolate, we propose that strain YIM 93221^T represents a novel species of a new genus, *Haloechinothrix alba* gen. nov., sp. nov.

Fig. 2. Phylogenetic dendrogram obtained by distance-matrix analysis of 16S rRNA gene sequences, showing the position of strain YIM 93221^T in the suborder *Pseudonocardineae*. Asterisks indicate that the corresponding node was also found in trees generated with the maximum-likelihood (Felsenstein, 1981) and maximum-parsimony (Fitch, 1971) algorithms. Bootstrap values (>50%) based on 1000 replications are shown at branch nodes. *Bifidobacterium gallicum* JCM 8224^T was used as an outgroup. Bar, 2% sequence divergence. Details of other sequences used to generate the tree are available in Supplementary Table S2.

Description of *Haloechinothrix* gen. nov.

Haloechinothrix (Ha.lo.e.chi.no'thrix. Gr. n. *hals*, *halos* salt; Gr. n. *echinos* hedgehog; Gr. fem. n. *thrix* hair; N.L. fem. n. *Haloechinothrix* halophilic, hedgehog-like filament, referring to halophilic filamentous actinomycetes with spiny aerial mycelium).

Gram-staining-positive, strictly aerobic, moderately halophilic, filamentous actinomycetes. Substrate mycelium fragments into rod-like elements and does not form chains of spores at maturity. Spiny aerial mycelium. The whole-cell hydrolysates contain *meso*-diaminopimelic acid as the cell-wall diamino acid. Glucose, glucosamine, mannose and an unknown sugar are the major whole-cell sugars. The phospholipids are diphosphatidylglycerol, phosphatidylglycerol, phosphatidylethanolamine, phosphatidylinositol, phosphatidylinositol mannosides and an unknown phospholipid. The predominant menaquinone is MK-8(H₄). The major fatty acid is iso-C_{16:0}. The G + C content of the genomic DNA is about 68 mol%. The type species is *Haloechinothrix alba*.

Description of *Haloechinothrix alba* sp. nov.

Haloechinothrix alba (al'ba. L. fem. adj. *alba* white).

Exhibits the following properties in addition to those given in the genus description. Aerial mycelium is white and substrate mycelium is yellow–white on most tested media. No diffusible pigments are produced. Grows at 20–45 °C (optimum 37 °C), at pH 4.0–8.0 (optimum pH 7.0) and with 9–23 % (w/v) NaCl (optimum 15 % NaCl). Starch and Tweens 20, 40, 60 and 80 are degraded, but aesculin, casein, cellulose, chitin and urea are not. Negative for gelatin liquefaction, nitrate reduction, milk peptonization and coagulation and H₂S and melanin production. With API

ZYM, positive for esterase (C4), esterase lipase (C8), leucine arylamidase, valine arylamidase, cystine arylamidase and naphthol-AS-BI-phosphohydrolase, but negative for alkaline phosphatase, lipase (C14), α -fucosidase, α -galactosidase, β -galactosidase, β -glucuronidase, α -glucosidase, β -glucosidase, α -mannosidase, *N*-acetyl- β -glucosaminidase, trypsin and α -chymotrypsin. Utilizes D-mannose, rhamnose, trehalose, erythritol, dulcitol, xylitol, starch, trisodium citrate, L-lysine, alanine, L-arginine, L-asparagine, glycine, L-histidine, L-proline, L-serine, L-threonine, L-tyrosine and hypoxanthine as sole carbon or nitrogen sources, but not D-arabinose, cellobiose, D-fructose, galactose, D-glucose, lactose, maltose, raffinose, D-ribose, sucrose, D-xylose, glycerol, inositol, mannitol, sorbitol, sodium acetate, sodium propionate, adenine, methionine, L-phenylalanine or xanthine. With API 50CH, does not produce acid. The DNA G + C content of the type strain is 68.1 mol%.

The type strain is YIM 93221^T (=DSM 45207^T =CCTCC AB 208140^T), isolated from a salt lake in Xinjiang province, north-west China.

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References

Chun, J., Lee, J.-H., Jung, Y., Kim, M., Kim, S., Kim, B. K. & Lim, Y.-W. (2007). EzTaxon: a web-based tool for the identification of

prokaryotes based on 16S ribosomal RNA gene sequences. *Int J Syst Evol Microbiol* 57, 2259–2261.

Cui, X. L., Mao, P. H., Zeng, M., Li, W. J., Zhang, L. P., Xu, L. H. & Jiang, C. L. (2001). *Streptomonospora salina* gen. nov., sp. nov., a new member of the family *Nocardiopsaceae*. *Int J Syst Evol Microbiol* 51, 357–363.

Felsenstein, J. (1981). Evolutionary trees from DNA sequences: a maximum likelihood approach. *J Mol Evol* 17, 368–376.

Felsenstein, J. (1985). Confidence limits on phylogenies: an approach using the bootstrap. *Evolution* 39, 783–791.

Fitch, W. M. (1971). Toward defining the course of evolution: minimum change for a specific tree topology. *Syst Zool* 20, 406–416.

Gochbauer, M. B., Leppard, G. G., Komaratat, M. K., Novitsky, T. & Kushner, D. (1975). Isolation and characterization of *Actinopolyspora halophila*, gen. et sp. nov., an extremely halophilic actinomycete. *Can J Microbiol* 21, 1500–1511.

Goodfellow, M., Lacey, J., Athalye, M., Embley, T. M. & Bowen, T. (1989). *Saccharopolyspora gregorii* and *Saccharopolyspora hordei*: two new actinomycete species from fodder. *J Gen Microbiol* 135, 2125–2139.

Guan, T.-W., Tang, S.-K., Wu, J.-Y., Zhi, X.-Y., Xu, L.-H., Zhang, L.-L. & Li, W.-J. (2009). *Haloglycomyces albus* gen. nov., sp. nov., a halophilic, filamentous actinomycete of the family *Glycomycetaceae*. *Int J Syst Evol Microbiol* 59, 1297–1301.

Hasegawa, T., Takizawa, M. & Tanida, S. (1983). A rapid analysis for chemical grouping of aerobic actinomycetes. *J Gen Appl Microbiol* 29, 319–322.

Kelly, K. L. (1964). *Inter-Society Color Council – National Bureau of Standards Color Name Charts Illustrated with Centroid Colors*. Washington, DC: US Government Printing Office.

Kimura, M. (1980). A simple method for estimating evolutionary rates of base substitutions through comparative studies of nucleotide sequences. *J Mol Evol* 16, 111–120.

Korn-Wendisch, F., Kempf, A., Grund, E., Kroppenstedt, R. M. & Kutzner, H. J. (1989). Transfer of *Faenia rectivirgula* Kurup and Agre 1983 to the genus *Saccharopolyspora* Lacey and Goodfellow 1975, elevation of *Saccharopolyspora hirsuta* subsp. *taberi* Labeda 1987 to species level, and emended description of the genus *Saccharopolyspora*. *Int J Syst Bacteriol* 39, 430–441.

Korn-Wendisch, F., Rainey, F., Kroppenstedt, R. M., Kempf, A., Majazza, A., Kutzner, H. J. & Stackebrandt, E. (1995). *Thermocrisium* gen. nov., a new genus of the order *Actinomycetales*, and description of *Thermocrisium municipale* sp. nov. and *Thermocrisium agreste* sp. nov. *Int J Syst Bacteriol* 45, 67–77.

Li, W.-J., Xu, P., Schumann, P., Zhang, Y.-Q., Pukall, R., Xu, L.-H., Stackebrandt, E. & Jiang, C.-L. (2007). *Georgenia ruanii* sp. nov., a novel actinobacterium isolated from forest soil in Yunnan (China), and emended description of the genus *Georgenia*. *Int J Syst Evol Microbiol* 57, 1424–1428.

Marmur, J. (1961). A procedure for the isolation of deoxyribonucleic acid from microorganisms. *J Mol Biol* 3, 208–218.

Mesbah, M., Premachandran, U. & Whitman, W. B. (1989). Precise measurement of the G + C content of deoxyribonucleic acid by high-performance liquid chromatography. *Int J Syst Bacteriol* 39, 159–167.

Minnikin, D. E., O'Donnell, A. G., Goodfellow, M., Alderson, G., Athalye, M., Schaal, A. & Parlett, J. H. (1984). An integrated procedure for the extraction of bacterial isoprenoid quinones and polar lipids. *J Microbiol Methods* 2, 233–241.

Saitou, N. & Nei, M. (1987). The neighbor-joining method: a new method for reconstructing phylogenetic trees. *Mol Biol Evol* 4, 406–425.

Sasser, M. (1990). Identification of bacteria by gas chromatography of cellular fatty acids. *USFCC Newsl* 20, 16.

Shirling, E. B. & Gottlieb, D. (1966). Methods for characterization of *Streptomyces* species. *Int J Syst Bacteriol* 16, 313–340.

Tamura, K., Dudley, J., Nei, M. & Kumar, S. (2007). MEGA4: molecular evolutionary genetics analysis (MEGA) software version 4.0. *Mol Biol Evol* 24, 1596–1599.

Tang, S.-K., Tian, X.-P., Zhi, X.-Y., Cai, M., Wu, J.-Y., Yang, L.-L., Xu, L.-H. & Li, W.-J. (2008). *Haloactinospora alba* gen. nov., sp. nov., a halophilic filamentous actinomycete of the family *Nocardiopsaceae*. *Int J Syst Evol Microbiol* 58, 2075–2080.

Tang, S.-K., Wang, Y., Cai, M., Zhi, X.-Y., Lou, K., Xu, L.-H., Jiang, C.-L. & Li, W.-J. (2009a). *Saccharopolyspora halophila* sp. nov., a novel halophilic actinomycete isolated from a saline lake in China. *Int J Syst Evol Microbiol* 59, 555–558.

Tang, S.-K., Wang, Y., Chen, Y., Lou, K., Cao, L.-L., Xu, L.-H. & Li, W.-J. (2009b). *Zhihengliuella alba* sp. nov., and emended description of the genus *Zhihengliuella*. *Int J Syst Evol Microbiol* 59, 2025–2032.

Tang, S.-K., Wang, Y., Wu, J.-Y., Cao, L.-L., Lou, K., Xu, L.-H., Jiang, C.-L. & Li, W.-J. (2009c). *Saccharopolyspora qijiaojiangensis* sp. nov., a novel halophilic actinomycete isolated from a salt lake. *Int J Syst Evol Microbiol* 59, 2166–2170.

Tang, S.-K., Wang, Y., Guan, T.-W., Lee, J.-C., Kim, C.-J. & Li, W.-J. (2010). *Amycolatopsis halophila* sp. nov., a halophilic actinomycete isolated from a salt lake. *Int J Syst Evol Microbiol* 60, 1073–1078.

Tian, X.-P., Zhi, X.-Z., Qiu, Y.-Q., Zhang, Y.-Q., Tang, S.-K., Xu, L.-H., Zhang, S. & Li, W.-J. (2009). *Sciscionella marina* gen. nov., sp. nov., a marine actinomycete isolated from a sediment in the northern South China Sea. *Int J Syst Evol Microbiol* 59, 222–228.

Williams, S. T., Goodfellow, M. & Alderson, G. (1989). Genus *Streptomyces* Waksman and Henrici 1943, 339^{AL}. In *Bergey's Manual of Systematic Bacteriology*, vol. 4, pp. 2452–2492. Edited by S. T. Williams, M. E. Sharpe & J. G. Holt. Baltimore: Williams & Wilkins.