Streptomonospora algeriensis sp. nov., a halophilic actinomycete isolated from soil in Algeria

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Abstract A halophilic actinomycete strain, designated H27^T, was isolated from a soil sample collected from a hypersaline habitat in Djelfa Province (North-Central Algeria), and then investigated using a polyphasic taxonomic approach. The strain was observed to produce poor aerial mycelium, which formed short chains of oval to cylindrical-shaped spores at maturity, and non fragmented substrate mycelium. The optimum NaCl concentration for growth was found to be 10–15 % (w/v) and the optimum growth temperature and pH were found to be 28–37 °C and 6–7, respectively. The diagnostic diamino acid in the cell-wall peptidoglycan was identified as *meso*-diaminopimelic acid. The predominant menaquinones of strain H27^T were identified as MK-11 (H_4) and MK-10 (H_6). The major fatty acids were found to be iso-$C_{16:0}$, anteiso-$C_{17:0}$, 10 methyl $C_{17:0}$ and 10 methyl $C_{16:0}$. The diagnostic phospholipids detected were phosphatidylethanolamine, diphosphatidylglycerol, phosphatidylglycerol, phosphatidylcholine and phosphatidylinositol. The chemotaxonomic properties of strain H27^T are consistent with those shared by members of the genus *Streptomonospora*. 16S rRNA gene sequence analysis indicated that strain H27^T is most closely related to *Streptomonospora alba* DSM 44588^T (98.8 %) and *Streptomonospora flavalba* DSM 45155^T (98.7 %) whereas the DNA–DNA relatedness values between strain H27^T and the two type strains were 17.1 and 57.9 %, respectively. Based on the combined

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genotypic and phenotypic evidence, it is proposed that strain H27^T should be classified as representative of a novel species, for which the name *Streptomonospora algeriensis* sp. nov. is proposed. The type strain is H27^T (=DSM 45604^T =CCUG 63369^T =MTCC 11563^T).

Keywords *Streptomonospora* · *Streptomonospora algeriensis* sp. nov · Halophilic actinomycete · Algerian soil · Polyphasic taxonomy

Introduction

The genus *Streptomonospora* was described by Cui et al. (2001) and was affiliated with the family *Nocardiopsaceae* of the order *Streptosporangiales* (Zhi et al. 2009). Currently, the genus contains eight recognized species, *Streptomonospora salina* (Cui et al. 2001), *Streptomonospora alba* (Li et al. 2003), *Streptomonospora halophila* (Cai et al. 2008), *Streptomonospora amylolytica* and *Streptomonospora flavalba* (Cai et al. 2009), *Streptomonospora sediminis*, *Streptomonospora nanhaiensis* and *Streptomonospora arabica* (Zhang et al. 2013). The genus is characterized by cell walls of type IIIC (*meso*-diaminopimelic acid without diagnostic sugar); a type PII phospholipid pattern (phosphatidylethanolamine); the presence of menaquinones with nine or ten isoprenoid chains and a varying degree of hydrogenation as predominant menaquinone; and the presence of $C_{16:0}$, $C_{17:0}$, iso-$C_{15:0}$ and iso-$C_{16:0}$ as the major fatty acids. The G + C content of the genomic DNA of members of the genus is 70.7–74.4 mol%.

During our study of the taxonomy of halophilic actinomycetes (Meklat et al. 2011), an isolate H27^T, was isolated from Djelfa region in Algeria. Based on data from the present polyphasic taxonomic research, it is proposed that strain H27^T represents a novel species of the genus *Streptomonospora*, named *Streptomonospora algeriensis* sp. nov. The type strain is H27^T (=DSM 45604^T =CCUG 63369^T =MTCC 11563^T).

Materials and methods

Isolation and maintenance of strain

Strain H27^T was isolated from a soil sample collected from Djelfa Province (Algeria). Isolation was carried out by a dilution-plate method using complex medium (CM) agar (Chun et al. 2000) supplemented with actidione (50 μg ml^{-1}) and 20 % (w/v) NaCl and incubated for 5 weeks. The strain was purified and maintained at 4 °C on CM slants agar containing 20 % (w/v) NaCl and at −20 °C as 20 % (v/v) glycerol suspensions.

Strain H27^T was deposited in the German Collection of Microorganisms and Cell Cultures (DSMZ), Germany, as strain DSM 45604^T; in the Culture Collection, University of Göteborg (CCUG), Sweden, as strain CCUG 63369^T and in the Microbial Type Culture Collection (MTCC), India, as strain MTCC 11563^T.

Phenotypic characterization

Cultural characteristics were investigated after 7, 14 and 21 days of incubation at 30 °C on media of the International *Streptomyces* Project, ISP 2 and ISP 4 (Shirling and Gottlieb 1966), and also on CM agar (Chun et al. 2000) and nutrient agar (NA) (Waksman 1961). The degree of growth was determined and the colours of the substrate and aerial mycelia and any soluble pigments produced were determined by comparison with ISCC-NBS colour charts (Kelly and Judd 1976). All media used for morphological characteristics contained 15 % (w/v) NaCl. The morphological characteristics of strain H27^T, including spore-chain morphology, spore size and surface ornamentation, were assessed by light microscopy (B1, Motic) and scanning electron microscopy (Hitachi, S450).

Several physiological tests were used to characterize strain H27^T. Growth and production of acid from carbohydrates, and decarboxylation of organic acids were evaluated using the method of Gordon et al. (1974). Degradation of different other organic compounds was studied as described by Goodfellow (1971). Lysozyme sensitivity and production of nitrate reductase were determined according to the methods of Gordon and Barnett (1977) and Marchal et al. (1987), respectively. Growth at different temperatures, pH and NaCl concentrations, and in the presence of antibiotics was determined on NA medium.

Chemotaxonomy

Amino acid and sugar analyses of whole-cell hydrolysates were performed according to the procedures described by Becker et al. (1964) and Lechevalier and

Lechevalier (1970). Phospholipids were analyzed according to the method developed by Minnikin et al. (1977). The fatty acid profile was determined by the method of Sasser (1990), using the Microbial Identification System (MIDI). Menaquinones were isolated according to Minnikin and O'Donnell (1984) and were analyzed by HPLC (Kroppenstedt 1982, 1985).

Phylogenetic analyses

Strain H27^T was grown in CM broth supplemented with 15 % (w/v) NaCl and genomic DNA was extracted with a DNA extraction kit (MasterPure Gram Positive DNA Purification kit; Epicentre Biotechnologies). PCR amplification of the 16S rRNA gene was performed as described by Rainey et al. (1996). PCR products were purified with a PCR product purification kit (Qiagen). The primers used for sequencing were as listed in Coenye et al. (1999). The sequences obtained were compared with sequences present in the public sequence databases as well as with the EzTaxon-e server (http://eztaxon-e.ezbiocloud.net/; Kim et al. 2012). Phylogenetic analyses were conducted using MEGA version 5 (Tamura et al. 2011). The 16S rRNA gene sequence of strain H27^T was aligned against neighbouring nucleotide sequences using CLUSTAL W (with default parameters) (Larkin et al. 2007). Phylogenetic trees were reconstructed by using the neighbour-joining method (Saitou and Nei 1987) with the model of Jukes and Cantor (1969), the maximum-likelihood method (Felsenstein 1985) with Kimura's 2-parameter (Kimura 1980) model and maximum-parsimony (Fitch 1977) methods. The topology of the trees was evaluated by bootstrap analysis based on 1,000 replicates (Felsenstein 1985).

DNA–DNA hybridization

DNA–DNA hybridization was carried out as described by De Ley et al. (1970) incorporating the modifications described by Huss et al. (1983). The experiments were done as duplicates in 2× SSC buffer in the presence of 10 % formamide at 71 °C.

Results and discussion

Morphological observation of a 3 weeks old culture of strain H27^T revealed that the substrate mycelium was abundant, well developed and non-fragmented but the aerial mycelium was poor. Strain H27^T was found to show good growth on CM agar and NA media but to exhibit poor growth on ISP 2 and ISP 4 media. Yellow–white aerial mycelium was found to be produced on CM agar and NA media but no aerial mycelium was formed on ISP 2 and ISP 4 media. The substrate mycelium was pale observed to be yellow on all tested media. No diffusible pigment was detected on any tested media. The aerial mycelium was found to form short chains of spores at maturity, which were straight to flexuous; spores were observed to be oval to cylindrical-shaped with smooth surfaces and to be non-motile (Fig. 1). The substrate mycelium was found to produce, very rarely, non-motile isolated ovoid spores (Fig. S1), which were observed only on CM agar medium.

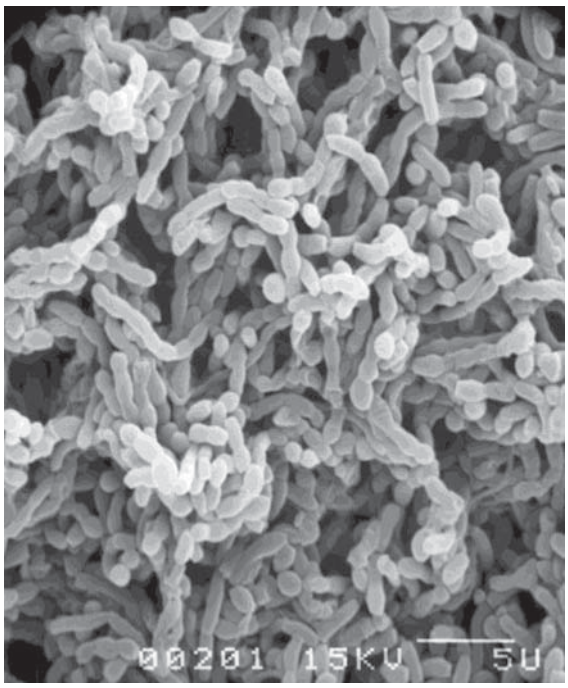

Fig. 1 Scanning electron micrograph of aerial mycelium of strain H27^T grown on CM agar medium containing 15 % (w/v) NaCl for 28 days at 30 °C. *Bar* 5 μm

Strain H27^T was determined to contain *meso*-diaminopimelic acid (but not glycine) in its cell wall. Whole-cell hydrolysates were found to contain galactose (in addition to glucose), which is typical of cell-wall type III and whole-cell sugar pattern type C (Lechevalier and Lechevalier 1970). Strain H27^T was found to possess phosphatidylethanolamine, diphosphatidylglycerol, phosphatidylglycerol, phosphatidylcholine, phosphatidylinositol and two

Table 1 Differential physiologic and chemotaxonomic characteristics of strain H27^T (*Streptomonospora algeriensis* sp. nov.) compared with its closest relative recognized species of the genus *Streptomonospora*

Characteristics	Type strains		
	1	2	3
Utilization of			
Arabinose	−	−	+
Cellobiose	+	−	−
Maltose	+	−	+
Rhamnose	−	−	+
Alanine	−	−	+
Proline	−	−	+
Serine	−	−	+
Hydrolysis of			
Starch	−	−	+
Tyrosine	−	−	+
Production of melanoid pigments	−	−	+
Production of nitrate reductase	−	+	−
NaCl range of growth (%, w/v)	7–20	5–25	5–25
pH range of growth	5–8	5–9	5–9
Temperature optimum (°C)	30	28	37
Menaquinone composition			
MK-9 (H_4)	−	+	−
MK-9 (H_8)	−	+	+
MK-10 (H_2)	−	+	−
MK-10 (H_4)	+	+	−
MK-10 (H_6)	+	−	+
MK-10 (H_8)	−	−	+
MK-11 (H_4)	+	−	−
Phospholipid composition			
PE	+	+	−
MPE	−	+	−
PS	−	+	−
PIM	−	−	+
Sugar in whole-cell hydrolysates (with galactose)	Glucose	Arabinose	Glucose

All data presented in this table were realized under the same conditions

Strains *1 S. algeriensis* H27^T; *2 S. alba* DSM 44588^T; *3 S. flavalba* DSM 45155^T ; + Positive; − negative; *PE* phosphatidylethanolamine; *MPE* methylphosphatidylethanolamine; *PS* phosphatidylserine; *PIM* phosphatidylinositol mannosides

glycolipids (Fig. S2). The predominant menaquinones were determined to be MK-11 (H_4) (41.0 %) and MK-10 (H_6) (23.9 %); MK-10 (H_4) (2.0 %) was also detected. The fatty acids profile was composed as follows: iso-$C_{16:0}$ (39.2 %), anteiso-$C_{17:0}$ (28.9 %), 10 methyl $C_{17:0}$ (6.7 %), 10 methyl $C_{16:0}$ (6.2 %) and anteiso-$C_{15:0}$ (4.1 %). The morphological and chemical characteristics described above clearly support the placement of strain H27^T within the genus *Streptomonospora*.

Good growth was found to occur at 28–37 °C, pH 6.0–7.0 and in the presence of 10–15 % of NaCl. The organism was found to be resistant to kanamycin (5 μg ml^{-1}), erythromycin (10 μg ml^{-1}), streptomycin (10 μg ml^{-1}) and penicillin (25 μg ml^{-1}), but sensitive to chloramphenicol (25 μg ml^{-1}) and lysozyme (0.005 % w/v). Detailed results of the physiological and biochemical analyses are given in Table 1 and in the species description. It is evident from Table 1 that there are several phenotypic characteristics that clearly separate strain H27^T from the nearest recognized species *S. alba* and *S. flavalba*.

Phylogenetic analysis of an almost complete 16S rRNA gene sequence (GenBank accession number HQ918204) showed that strain H27^T is related to members of the genus *Streptomonospora* and exhibits highest 16S rRNA gene sequence similarity to *S. alba* (98.8 %) and *S. flavalba* (98.7 %). The phylogenetic relationship between strain H27^T and the other *Streptomonospora* species is seen in the neighbour–joining dendrogram (Fig. 2). DNA–DNA relatedness between strain H27^T and the type strains *S. alba* DSM 44588^T and *S. flavalba* DSM 45155^T were respectively mean values of 17.1 % (14.7 and 19.6 %) and 57.9 % (58.3 and 57.5 %). These hybridization values are significantly less than 70 %, the threshold value for the delineation of genomic species (Wayne et al. 1987). Thus, on the basis of polyphasic taxonomic evidence, it is suggested that strain H27^T represents a novel species of the genus *Streptomonospora*, for which the name *Streptomonospora algeriensis* sp. nov. is proposed.

Description of *Streptomonospora algeriensis* sp. nov

Streptomonospora algeriensis (al.ger.i.en'sis. N.L. fem. adj. *algeriensis*, pertaining to Algeria, the source of the soil from which the type strain was isolated).

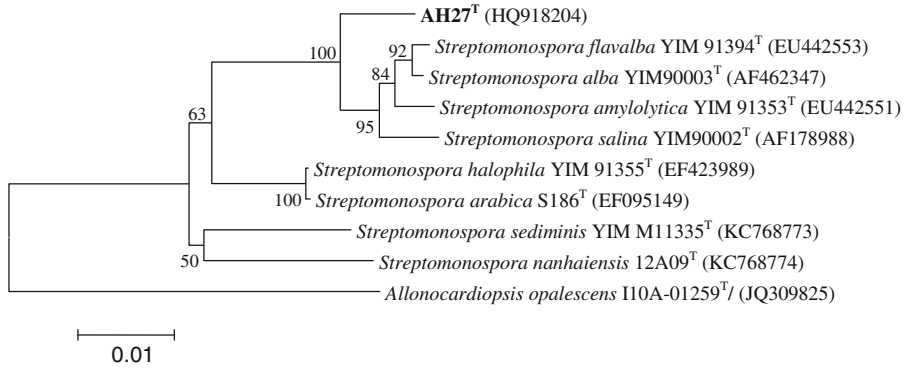

Fig. 2 Phylogenetic tree for species of the genus *Streptomonospra* calculated from almost complete 16S rRNA gene sequences using Jukes and Cantor (1969) evolutionary distance methods and the neighbour–joining method of Saitou and Nei (1987). This illustrates the taxonomic position of strain H27^T relative to the other species of the genus. Numbers at the nodes are bootstrap values, expressed as a percentage of 1,000 resamplings (only values >50 % are shown). *Allonocardiopsis opalescens* DSM 45601^T was used as the outgroup. *Bar* 0.01 nucleotide substitution per site

Halophilic filamentous actinomycete that forms well-developed and non-fragmented substrate mycelium. Aerial mycelium is not abundant and shows a yellow–white colour on CM agar and NA media. Produces short chains of non-motile spores, which are straight to flexuous. Substrate mycelium produces, very rarely, non-motile isolated spores, which are ovoid.

Diffusible pigments are not produced on CM agar, NA media, ISP2 and ISP 4 media. Temperature and pH ranges for growth are 20–45 °C and pH 5.0–8.0, with optima at 28–37 °C and pH 6.0–7.0. The NaCl concentration range for growth is 7–20 %, with optimal growth occurring at 10–15 %. Utilizes cellobiose, erythritol, fructose, galactose, glucose, maltose and mannose, but not adonitol, arabinose, glycerol, inositol, lactose, mannitol, melezitose, melibiose, raffinose, rhamnose, salicin, sorbitol, sucrose, trehalose and xylose. Positive for casein and Tween 80 hydrolysis, but negative for adenine, gelatin, guanine, hypoxanthine, starch, testosterone, tyrosine and xanthine hydrolysis. Acetate, citrate and pyruvate are decarboxylated, but not benzoate, butyrate, oxalate, propionate, succinate and tartrate. L-alanine, L-proline and L-serine are not used as a source of nitrogen. Nitrate reductase is not produced. Whole-cell hydrolysates contain *meso*-diaminopimelic acid, galactose and glucose. Polar lipids consist of phosphatidylethanolamine, diphosphatidylglycerol, phosphatidylglycerol, phosphatidylcholine, phosphatidylinositol and two glycolipids. The predominant menaquinones are MK-11 (H_4) and MK-10 (H_6). Major fatty acids are iso-$C_{16:0}$, anteiso-$C_{17:0}$, 10 methyl $C_{17:0}$ and 10 methyl $C_{16:0}$.

The type strain, H27^T (=DSM 45604^T =CCUG 63369^T =MTCC 11563^T), was isolated from an Algerian soil sample collected from Djelfa Province. The GenBank accession number for the 16S rRNA gene sequence of strain H27^T is HQ918204.

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References

Becker B, Lechevalier MP, Gordon RE, Lechevalier HA (1964) Rapid differentiation between *Nocardia* and *Streptomyces* by paper chromatography of whole-cell hydrolysates. J Appl Microbiol 12:421–423

Cai M, Zhi XY, Tang SK, Zhang YQ, Xu LH, Li WJ (2008) *Streptomonospora halophila* sp. nov., a halophilic actinomycete isolated from a hypersaline soil. Int J Syst Evol Microbiol 58:1556–1560

Cai M, Tang SK, Chen YG, Li Y, Zhang YQ, Li WJ (2009) *Streptomonospora amylolytica* sp. nov. and *Streptomonospora flavalba* sp. nov., two novel halophilic actinomycetes isolated from a salt lake. Int J Syst Evol Microbiol 59:2471–2475

Chun J, Bae KS, Moon EY, Jung SO, Lee HK, Kim SJ (2000) *Nocardiopsis kunsanensis* sp. nov., a moderately halophilic actinomycete isolated from a saltern. Int J Syst Evol Microbiol 50:1909–1913

Coenye T, Falsen E, Vancanneyt M, Hoste B, Govan JR, Kersters K, Vandamme P (1999) Classification of *Alcaligenes*

faecalis-like isolates from the environment and human clinical samples as *Ralstonia gilardii* sp. nov. Int J Syst Bacteriol 49:405–413

Cui XL, Mao PH, Zeng M, Li WJ, Zhang LP, Xu LH, Jiang CL (2001) *Streptimonospora salina* gen. nov., sp. nov., a new member of the family *Nocardiopsaceae*. Int J Syst Evol Microbiol 51:357–363

De Ley J, Cattoir H, Reynaerts A (1970) The quantitative measurement of DNA hybridization from renaturation rates. Eur J Biochem 12:133–142

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

Fitch WM (1977) On the problem of discovering the most parsimonious tree. Am Nat 111:223–257

Goodfellow M (1971) Numerical taxonomy of some nocardioform bacteria. J Gen Microbiol 69:33–90

Gordon RE, Barnett DA (1977) Resistance to rifampicin and lysozyme of strains of some species of *Mycobacterium* and *Nocardia* as a taxonomic tool. Int J Syst Bacteriol 27:176–178

Gordon RE, Barnett DA, Handerhan JE, Pang CHN (1974) *Nocardia coeliaca*, *Nocardia autotrophica*, and the nocardin strain. Int J Syst Bacteriol 24:54–63

Huss VAR, Festl H, Schleifer KH (1983) Studies on the spectrophotometric determination of DNA hybridization from renaturation rates. Syst Appl Microbiol 4:184–192

Jukes TH, Cantor CR (1969) Evolution of protein molecules. In: Munro HN (ed) Mammalian protein metabolism, vol 3. Academic Press, New York, pp 21–132

Kelly KL, Judd DB (1976) Color. Universal language and dictionary of names (National Bureau of Standards special publication 440). Washington, DC: US Department of Commerce

Kim OS, Cho YJ, Lee K, Yoon SH, Kim M, Na H, Park SC, Jeon YS, Lee JH, Yi H, Won S, Chun J (2012) Introducing EzTaxon-e: a prokaryotic 16S rRNA gene sequence database with phylotypes that represent uncultured species. Int J Syst Evol Microbiol 62:716–721

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

Kroppenstedt RM (1982) Separation of bacterial menaquinones by HPLC using reverse phase (RP18) and a silver loaded ion exchanger as stationary phases. J Liq Chromatogr 5:2359–2367

Kroppenstedt RM (1985) Fatty acid and menaquinone analysis of actinomycetes and related organisms. In: Goodfellow M, Minnikin DE (eds) Chemical methods in bacterial systematics. Academic Press, London, pp 173–179

Larkin MA, Blackshields G, Brown NP, Chenna R, McGettigan PA, McWilliam H, Valentin F, Wallace IM, Wilm A, Lopez R, Thompson JD, Gibson TJ, Higgins DG (2007) CLUSTALW and CLUSTALX version 2. Bioinformatics 23:2947–2948

Lechevalier MP, Lechevalier HA (1970) Chemical composition as a criterion in the classification of aerobic actinomycetes. Int J Syst Bacteriol 34:435–444

Li WJ, Xu P, Zhang LP, Tang SK, Cui XL, Mao PH, Xu LH, Schumann P, Stackebrandt E, Jiang CL (2003) Streptomonospora alba sp. nov., a novel halophilic actinomycete, and emended description of the genus *Streptomonospora* Cui et al. 2001. Int J Syst Evol Microbiol 53:1421–1425

Marchal N, Bourdon JL, Richard CL (1987) Les milieux de culture pour l'isolement et l'identification biochimique des bactéries. Doin Press, Paris

Meklat A, Sabaou N, Zitouni A, Mathieu F, Lebrihi A (2011) Halophilic actinomycetes in Saharan soils of Algeria: isolation, taxonomy and antagonistic properties. Appl Environ Microbiol 77:6710–6714

Minnikin DE, O'Donnell AG (1984) Actinomycete envelope lipid and peptidoglycan composition. In: Goodfellow M, Mordarski M, Williams ST (eds) The biology of the actinomycetes. Academic Press, London, pp 337–388

Minnikin DE, Patel PV, Alshamaony L, Goodfellow M (1977) Polar lipid composition in the classification of *Nocardia* and related bacteria. Int J Syst Bacteriol 27:104–117

Rainey FA, Ward-Rainey N, Kroppenstedt RM, Stackebrandt E (1996) The genus *Nocardiopsis* represents a phylogenetically coherent taxon and a distinct actinomycete lineage: proposal of *Nocardiopsaceae* fam. nov. Int J Syst Bacteriol 46:1088–1092

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. Technical note 101. Microbial ID, Newark

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

Tamura K, Peterson D, Peterson N, Stecher G, Nei M, Kumar S (2011) MEGA5: molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods. Mol Biol Evol 28:2731–2739

Waksman SA (1961) Classification, identification, and descriptions of genera and species. In: The actinomycetes, vol. 2. Baltimore, Williams & Wilkins, pp 331–332

Wayne LG, Brenner DJ, Colwell RR, Grimont PAD, Kandler O, Krichevsky MI, Moore LH, Moore WEC, Murray RGE, Stackebrandt E, Starr MP, Trüper HG (1987) International committee on systematic bacteriology. Report of the ad hoc committee on the reconciliation of approaches to bacterial systematic. Int J Syst Bacteriol 37:463–464

Zhang DF, Pan HQ, He J, Zhang XM, Zhang YG, Klenk HP, Hu JC, Li WJ (2013) Description of *Streptomonospora sediminis* sp. nov. and *Streptomonospora nanhaiensis* sp. nov., and reclassification of *Nocardiopsis arabia* (Hozzein and Goodfellow, 2008) as *Streptomonospora arabica* comb. nov. and emended description of the genus *Streptomonospora*. Int J Syst Bacteriol 63:4447–4455

Zhi XY, Li WJ, Stackebrandt E (2009) An update of the structure and 16S rRNA gene sequence-based definition of higher ranks of the class *Actinobacteria*, with the proposal of two new suborders and four new families and emended descriptions of the existing higher taxa. Int J Syst Evol Microbiol 59:589–608