Streptomyces zagrosensis sp. nov., isolated from soil

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The taxonomic position of a novel actinomycete isolated from soil in Fars Province (Iran) was determined using a polyphasic approach. Phenotypic characterization and 16S rRNA gene sequence analysis of the isolate matched those described for members of the genus Streptomyces. On ISP2 medium, strain HM 1154T produced a dark cream, branched substrate mycelium and Retinaculiaperti aerial hyphae that in some images also appeared spiral and that developed into greyish-white spore chains with a smooth surface. The isolate showed optimal growth at 28°C and pH 6–9 with 0–4 % (w/v) NaCl. Whole-cell hydrolysates contained LL-diaminopimelic acid as diagnostic diamino acid, ribose and glucose. The main phospholipids were phosphatidylethanolamine, diphosphatidylglycerol, phosphatidylinositol, three unknown phospholipids and an unknown aminophospholipid; MK-9(H4) and MK-9(H2) were the predominant menaquinones. The major cellular fatty acids were the branched saturated iso-C16 : 0 and anteiso-C15 : 0. Strain HM 1154T exhibited the highest 16S rRNA gene sequence similarities to Streptomyces coerulescens DSM 40146T (99.4 %), Streptomyces varsoviensis DSM 40346T (99.3 %), Streptomyces youssoufiensis DSM 41920T (99.2 %), Streptomyces abikoensis DSM 40831T (99.2 %), Streptomyces rimosus subsp. rimosus DSM 40260T (99.1 %), Streptomyces luteiraeiculi DSM 40508T (99.1 %), Streptomyces thioluteus DSM 40027T (99.1 %), Streptomyces blastmyceticus DSM 40029T (99.0 %) and Streptomyces hiroshimensis DSM 40037T (99.0 %). DNA–DNA hybridization studies showed relatedness values of 11.0–35.8 % with the closest related species. Based on these results, strain HM 1154T is considered to represent a novel species within the genus Streptomyces, for which the name Streptomyces zagrosensis sp. nov. is proposed. The type strain is HM 1154T (=DSM 42018T=UTMC 1154T=CECT 8305T).

The genus Streptomyces was proposed by Waksman & Henrici (1943) (emend. Witt & Stackebrandt, 1990; emend. Wellington et al., 1992) to accommodate aerobic, spore-forming actinomycetes. Members of the genus Streptomyces are Gram-positive bacteria with a DNA rich in G+C content (69–73 mol%) (Williams et al., 1983), contain LL-diaminopimelic acid in the peptidoglycan and lack diagnostic sugars in whole-cell hydrolysates (Lechevalier & Lechevalier, 1970). Species of the genus Streptomyces are common in soil (Zheng et al., 2013; Hamedi et al., 2010; Bouizgarne et al., 2009) and known by their ability to produce biotechnologically useful enzymes (Liu et al., 2013) and most of the biologically active secondary metabolites, such as antibiotics (Kim et al., 2012), anti-tumour agents (Schleissner et al., 2011) and antifungal compounds (Zhao et al., 2010), among others. Peptides, and especially cyclopeptides, have currently received considerable attention.

Abbreviations: DPG, diphosphatidylglycerol; ISP, International Streptomyces Project; PE, phosphatidylethanolamine; PI, phosphatidylinositol.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain HM 1154T is JF917242.

Two supplementary figures are available with the online version of this paper.
because of exhibiting unique structures and interesting pharmacological activities (Laatsch, 2011).

During studies of the taxonomy and antibiotic production of actinomycetes from Iranian soils, the isolate HM 1154<sup>T</sup> was selected by its ability to produce two new cyclopeptides, persipeptide A and B (Mohammadiapanah et al., 2012), and recognized as a potentially novel species in the genus *Streptomyces*. Herein, we describe the taxonomic position of this genomically distinct novel lineage based on a polyphasic approach.

Rhizospheric soil samples were collected at 4–6 cm depth in Fars Province (Iran), and air-dried (Nolan & Cross, 1988), followed by a heat-drying step at 120 °C for 10 min (Nonomura & Ohara, 1971). Strain HM 1154<sup>T</sup> was isolated by using the dilution plating method on glucose-asparagine agar (Nonomura & Ohara, 1969) supplemented with cycloheximide (100 mg ml<sup>-1</sup>) and incubated for 14 days at 28 °C. The strain was maintained on ISP (International Streptomycetes Project) 2 medium agar slants at 4 °C and as 20 % (v/v) glycerol suspensions at −70 °C.

Cultural properties of strain HM 1154<sup>T</sup> were evaluated according to the guidelines of the ISP as described by Shirling & Gottlieb (1966). Aerial and substrate mycelia colours were determined by comparing with chips from the ISCC-CNBS colour charts (Kelly, 1964).

The intact arrangement of the aerial hyphae and spore chains was observed on ISP 2 agar after 14 days at 28 °C using the coverslip technique (Kawato & Shinobu, 1959). Spore chain morphology and spore surface ornamentation were examined with a field-emission scanning electron microscope (FE-SEM Merlin; Zeiss). Growth rates were determined for temperatures 10–50 °C at 5 °C increments and for pH values of 4 to 11 (in increments of 1.0 pH unit) on modified Bennett medium as described by Williams et al. (1989) using the Nα-sesquicarbonate buffer system for preparation of alkaline media. The utilization of carbon sources and acid production were determined using GEN III MicroPlates in an Omnilog device (Biolog). These were inoculated with a cell suspension made in a ‘gelling’ inoculating fluid (IF) C at a cell density of 98 % transmittance, yielding a running time of 3 days in Phenotype Microarray mode at 28 °C. The exported data were further analysed with the opm package for R (Vaas et al., 2012, 2013 version 1.0.6.), using its functionality for merging subsequent measurements of the same plate, statistically estimating parameters from the respiration curves such as the maximum height, and automatically ‘discretizing’ these values into negative and positive reactions. Strain HM 1154<sup>T</sup> in comparison with the reference strains *Streptomyces coelescens* DSM 40146<sup>T</sup>, *Streptomyces varsoviensis* DSM 40346<sup>T</sup>, and *Streptomyces youssoufiensis* DSM 41920<sup>T</sup> were studied in the GEN III MicroPlates in two independent determinations. Reactions that gave contradictory results between the two repetitions were regarded as ambiguous.

Strain HM 1154<sup>T</sup> showed optimal growth on yeast extract-malt extract agar (ISP2 medium), glycerol-asparagine agar (ISP5 medium) and tyrosine agar (ISP7 medium), poor growth on oatmeal agar (ISP3 medium) and peptone yeast-extract-iron agar (ISP6 medium), and no growth on inorganic salts-starch agar (ISP4 medium). Strain HM 1154<sup>T</sup> produced well-developed substrate mycelium and aerial mycelium formed by long spore chains (20–50 spores; spore size 0.4–0.6 μm) (Fig. 1), which is consistent with typical characteristics of members of the genus *Streptomyces* (Kämpfer, 2012). According to the spore chain morphology classification by Pridham et al. (1958), isolate HM 1154<sup>T</sup> showed type *Retinaculapietert* with a smooth surface on ISP2 medium, that in some images also appear spiral. This morphology is common in the genus *Streptomyces* and has been observed in the two related species, *S. coelescens* on ISP2, ISP3, ISP4 and ISP5 media and *S. varsoviensis* on ISP3 and ISP5 media (Kämpfer, 2012). The mycelia pigmentation varied depending on the tested medium. On ISP2 and ISP3 media, both mycelia showed colours between white and dark cream, turning to greyish-white in sporulation phase. Nevertheless, light brownish mycelia were observed on ISP5 and ISP6 and dark orange ones on ISP7. No diffusible pigments were released into the tested media. In addition, a different spore production was displayed, finding the best spore mass on ISP2 medium. Similar observations relating to the different sporulation capacity on various media were already described by Kontro et al. (2005).

Isolate HM 1154<sup>T</sup> grew from 10 to 40 °C, the optimal temperature for growth was at 28 °C; no growth was observed below 10 °C or above 40 °C. Growth occurred in the presence of 0–4 % (w/v) NaCl (optimal range), but not with 5 % NaCl. The pH range for growth was from pH 6 to pH 11 (optimal range was pH 6–9). Results from phenotype microarray analysis shown as a heatmap in Fig. S1 (available in the online Supplementary Material) in comparison to type strains of other species of the genus *Streptomyces* revealed not only significant phenotype differences between strain HM 1154<sup>T</sup> and related species,

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**Fig. 1.** Scanning electron micrograph of strain HM 1154<sup>T</sup> grown on ISP2 medium for 14 days at 28 °C. Bar, 2 μm.
but also confirmed the wide range of organic compounds that species of the genus *Streptomyces* can use as sole sources of carbon for energy and growth (Kämpfer, 2012). A summary of select differential phenotypic characteristics is presented in Table 1.

To carry out studies of cell-wall amino acids and sugars, polar lipids, respiratory lipoquinones, and composition of peptidoglycan, strain HM 1154<sup>T</sup> was cultivated in trypticase soy broth (TSB) for 6 days in shaking cultures at 200 r.m., pH 7.2 and 28 °C. Cell biomass was harvested by centrifugation and washed twice with distilled water. The composition of peptidoglycan hydrolysates was examined by TLC as described by Schleifer & Kandler (1972). Whole-cell sugars were prepared according to Lechevalier & Lechevalier (1970), followed by TLC analysis (Staneck & Roberts, 1974). Polar lipids were extracted, separated by two-dimensional TLC and identified according to procedures outlined by Minnikin *et al.* (1984) with modifications proposed by Kroppenstedt & Goodfellow (2006). Respiratory lipoquinones were extracted from freeze-dried cell material using methanol as described by Collins *et al.* (1977) and analysed by HPLC (Kroppenstedt, 1982). Extraction of cellular fatty acids was carried out from biomass grown in TSB tubes held at 28 °C for 4 days. Analysis was conducted using the Microbial Identification System (MIDI) Sherlock version 6.1 (results evaluated against the TSBA40 peak naming table database) as described by Sasser (1990).

**Table 1.** Differential characteristics of strain HM 1154<sup>T</sup> and the type strains of other closely related species of the genus *Streptomyces*

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
<th>2</th>
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<th>4</th>
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<tbody>
<tr>
<td><strong>Spore chain morphology</strong></td>
<td>Retinaculiaperti</td>
<td>Spiral&lt;sup&gt;c&lt;/sup&gt;</td>
<td>Spiral&lt;sup&gt;b&lt;/sup&gt;</td>
<td>Rectiflexibles*&lt;sup&gt;a&lt;/sup&gt;</td>
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<tr>
<td>Spore surface</td>
<td>Smooth</td>
<td>Spiny&lt;sup&gt;c&lt;/sup&gt;</td>
<td>Smooth&lt;sup&gt;b&lt;/sup&gt;</td>
<td>Smooth&lt;sup&gt;a&lt;/sup&gt;</td>
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<tr>
<td>Diffusible pigment</td>
<td>–</td>
<td>+&lt;sup&gt;c&lt;/sup&gt;</td>
<td>+&lt;sup&gt;a&lt;/sup&gt;</td>
<td>–</td>
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<tr>
<td>Melanoid pigment</td>
<td>–</td>
<td>+&lt;sup&gt;c&lt;/sup&gt;</td>
<td>–&lt;sup&gt;a&lt;/sup&gt;</td>
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<td><strong>Growth with/at:</strong></td>
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<tr>
<td>4% (w/v) NaCl</td>
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<td>–</td>
<td>+&lt;sup&gt;+/–&lt;/sup&gt;</td>
<td>+</td>
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<td>+&lt;sup&gt;+/–&lt;/sup&gt;</td>
<td>+&lt;sup&gt;+/–&lt;/sup&gt;</td>
<td>+</td>
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<tr>
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<td>+&lt;sup&gt;+/–&lt;/sup&gt;</td>
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<td>β-Gentiobiose</td>
<td>+&lt;sup&gt;+/–&lt;/sup&gt;</td>
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<td>Sucrose</td>
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<td>Raffinose</td>
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<td>Melibiose</td>
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<td>Methyl β-D-Glucoside</td>
<td>+&lt;sup&gt;+/–&lt;/sup&gt;</td>
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<td>+&lt;sup&gt;+/–&lt;/sup&gt;</td>
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<tr>
<td>N-Acetyl-D-galactosamine</td>
<td>+&lt;sup&gt;+/–&lt;/sup&gt;</td>
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<td>+&lt;sup&gt;+/–&lt;/sup&gt;</td>
<td>+&lt;sup&gt;+/–&lt;/sup&gt;</td>
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<tr>
<td>N-Acetyl-neuraminic acid</td>
<td>+&lt;sup&gt;+/–&lt;/sup&gt;</td>
<td>–</td>
<td>+&lt;sup&gt;+/–&lt;/sup&gt;</td>
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<tr>
<td>D-Mannose</td>
<td>–</td>
<td>+&lt;sup&gt;+/–&lt;/sup&gt;</td>
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<td>+&lt;sup&gt;+/–&lt;/sup&gt;</td>
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<td>D-Fructose</td>
<td>+&lt;sup&gt;+/–&lt;/sup&gt;</td>
<td>–</td>
<td>+&lt;sup&gt;+/–&lt;/sup&gt;</td>
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<td>+&lt;sup&gt;+/–&lt;/sup&gt;</td>
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<td>+&lt;sup&gt;+/–&lt;/sup&gt;</td>
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<td>Inosine</td>
<td>–</td>
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<td>+&lt;sup&gt;+/–&lt;/sup&gt;</td>
<td>+&lt;sup&gt;+/–&lt;/sup&gt;</td>
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<tr>
<td>D-Sorbitol</td>
<td>+&lt;sup&gt;+/–&lt;/sup&gt;</td>
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<td>+&lt;sup&gt;+/–&lt;/sup&gt;</td>
<td>+&lt;sup&gt;+/–&lt;/sup&gt;</td>
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<tr>
<td>D-Mannitol</td>
<td>–&lt;sup&gt;+/–&lt;/sup&gt;</td>
<td>–</td>
<td>+&lt;sup&gt;+/–&lt;/sup&gt;</td>
<td>+&lt;sup&gt;+/–&lt;/sup&gt;</td>
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<tr>
<td>D-Aspartic acid</td>
<td>+&lt;sup&gt;+/–&lt;/sup&gt;</td>
<td>–</td>
<td>+&lt;sup&gt;+/–&lt;/sup&gt;</td>
<td>+&lt;sup&gt;+/–&lt;/sup&gt;</td>
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<tr>
<td>L-Arginine</td>
<td>–</td>
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<td>D-Galacturonic acid</td>
<td>+&lt;sup&gt;+/–&lt;/sup&gt;</td>
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<td>Citric acid</td>
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<tr>
<td>Adonitol</td>
<td>+&lt;sup&gt;+/–&lt;/sup&gt;</td>
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<td>Cysteine</td>
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<td><strong>Degradation of:</strong></td>
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<tr>
<td>Aesculin</td>
<td>+&lt;sup&gt;+/–&lt;/sup&gt;</td>
<td>–</td>
<td>+&lt;sup&gt;+/–&lt;/sup&gt;</td>
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<tr>
<td>Adenine</td>
<td>–</td>
<td>+&lt;sup&gt;+/–&lt;/sup&gt;</td>
<td>–</td>
<td>+&lt;sup&gt;+/–&lt;/sup&gt;</td>
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<tr>
<td>Allantoin</td>
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<td>–</td>
<td>–</td>
<td>+&lt;sup&gt;+/–&lt;/sup&gt;</td>
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*Data from: a, Hamdali *et al.* (2011); b, Williams *et al.* (1983); c, Li *et al.* (2002).*
Analysis of whole-cell wall revealed the presence of the diaminoc acid l-Diaminopimelic acid, ribose and glucose, indicating wall chemotype I (Lechevalier & Lechevalier, 1970), which is consistent with other species of the genus *Streptomyces* (Williams et al., 1989). The predominant menaquinones were MK-9(H₄) (59.1%) and MK-9(H₂) (25.4%), but also minor amounts of MK-9(H₈) (6.7%), MK-8(H₂) (2.6%) and MK-10(H₂) (2.2%) were displayed. The polar lipids pattern was, as usual in the genus *Streptomyces*, complex and consisted of phosphatidylethanolamine (PE), phosphatidylglycerol (DPG), phosphatidylglycositol (PI), three unknown phospholipids (PL4, PL5 and PL6), an unknown aminophospholipid (APL) and small amounts of three other unknown phospholipids (PL1, PL2 and PL3) (Fig. S2). The main fatty acids were the saturated branched iso-C₁₆:0 (27.9%), and anteiso-C₁₅:0 (22.0%), but C₁₆:0 (9.9%), anteiso-C₁₇:0 (8.5%), C₁₆:1ω7t (8.5%), iso-C₁₅:0 (4.9%), iso-C₁₄:₀ (4.4%), iso-C₁₆:1 H (3.5%) and anteiso-C₁₇:1 C (2.6%) were also found. The qualitative and quantitative combination of straight-chain and iso- and anteiso-branched fatty acids of strain HM 1154T matched with other species of the genus *Streptomyces* and the fatty acid pattern 2c sensu according to the classification established by Kroppenstedt (1985).

Genomic DNA extraction, PCR-mediated amplification of the 16S rRNA gene and purification of the PCR product was carried out as described by Rainey et al. (1996). Phylogenetic analyses based on maximum-likelihood and maximum-parsimony algorithms and the rooting of the resulting trees were conducted as previously described (Montero-Calasanz et al., 2013). Pairwise similarities were calculated as recommended by Meier-Kolthoff et al. (2013). For DNA–DNA hybridization tests, cells were disrupted by using a Constant Systems TS 0.75 kW (UL Instuments). DNA in the crude lysate was purified by chromatography on hydroxyapatite as described by Cashion et al. (1977). DNA–DNA hybridization was carried out as described by De Ley et al. (1970) under consideration of the modifications described by Huss et al. (1983) using a model Cary 100 Bio UV/VIS-spectrophotometer equipped with a Peltier thermostatted 6 × 6 multi-cell changer and a temperature controller with in-situ temperature probe (Varian).

The almost-complete (1508 bp) 16S rRNA gene sequence of strain HM 1154T showed the highest similarity with members of the genus *Streptomyces*, especially with *Streptomyces coeruleoscleros* DSM 40146T (99.4%), *Streptomyces varsoviensis* DSM 40346T (99.3%), *Streptomyces youssoufiensis* DSM 41920T (99.2%), *Streptomyces abikoensis* DSM 40831T (99.2%), *Streptomyces rimosus* subsp. *rimosus* DSM 40260T (99.1%), *Streptomyces luteireticuli* DSM 40509T (99.1%), *Streptomyces thioluteus* DSM 40027T (99.1%), *Streptomyces blastmycetaceus* DSM 40029T (99.0%) and *Streptomyces hiroshimensis* DSM 40037T (99.0%). Similarity values of 98.9–97.0% were determined for another 69 type strains of species of the genus *Streptomyces*. Phylogenetic tree topology inferred from maximum-likelihood and maximum-parsimony algorithms, based on 16S rRNA gene sequences of the strain HM 1154T and the closest related species of the genus *Streptomyces* is shown in Fig. 2. The 16S rRNA gene sequence similarity between strain HM 1154T and closely related type strains indicated the need to prove the genomic distinctness of the type strain representing the novel species by DNA–DNA hybridization (Table 2). DNA–DNA hybridizations between strain HM 1154T and type strains showing similarities of 98.9–97.0% were not conducted based on the observations reported by Meier-Kolthoff et al. (2013), which statistically confirmed that the threshold value, previously established at 97% 16S rRNA gene sequence similarity, was too conservative in microbial species discrimination, and an *Actinobacteria*-specific 16S rRNA gene sequence similarity threshold of 99.0% with a maximum probability of error of 1.00% was determined, to get DNA–DNA hybridization values above the 70% threshold recommended by Wayne et al. (1987) to confirm the species status of novel strains. Genotypic and phenotypic evidences support the distinctiveness of strain HM 1154T from all species of the genus *Streptomyces*. Therefore, we consider strain HM 1154T to represent a novel species of the genus *Streptomyces*, for which the name *Streptomyces zagrosensis* sp. nov. is proposed.

**Description of *Streptomyces zagrosensis* sp. nov.**

*Streptomyces zagrosensis* (za.gros.en’sis N.L. masc. adj. zagrosensis referring to the Zagros mountain range near where type strain was isolated).

Aerobic, Gram-staining-positive actinomycete that forms extensive, branched substrate mycelium and aerial hyphae with long Retinaculapierti spore chains with a smooth surface. On ISP2 medium, colonies are cream, turning to greyish-white in sporulation phase. Optimal growth occurs at 28 °C and at pH 6–9. It grows well in the presence of 0–4% NaCl. Dextrin, sucrose, raffinose, methyl β-D-glucoside, N-acetyl-D-glucosamine, N-acetyl-β-D-mannosamine, N-acetyl-β-D-galactosamine, D-glucose, sodium lactate, D-sorbitol, glycerol, D-aspartic acid, gelatin, glycin-L-proline, L-alanine, L-aspartic acid, L-glutamic acid, L-histidine, L-pyroglutamic acid, L-serine, gelatin, L-galacturonic acid, D-glucuronic acid, D-lactic acid methyl ester, citric acid, α-ketoglutaric acid, L-malic acid, potassium tellurite, Tween 40, γ-amino-n-butyric acid, β-hydroxybutyric acid, α-ketobutyric acid, propionic acid, adonitol and acetic acid can be used as sole carbon sources for growth, but not trehalose, cellobiose, β-gentiobiose, melibiose, N-acetylneuraminic acid, D-mannose, D-galactose, 3-O-methyl-D-glucose, D-fucose, D-fucose, L-rhamnose, inosine, D-serine, D-mannitol, myo-inositol, L-arginine, pectin, L-galactonic, α-L-rhamnose, glucuronamide, mucic acid, cysteine, quinic acid, D-saccharic acid, α-hydroxyphosphoacetic acid, methyl pyruvate, L-lactic acid, D-malic acid, bromosuccinic acid, α-hydroxybutyric acid, acetoclastic acid, sodium formate or butyric acid. N-acetyl-D-glucosamine, N-acetyl-β-D-mannosamine, N-acetyl-D-galactosamine, D-aspartic acid, L-glutamic acid, glycin-L-proline, L-alanine, L-aspartic acid,
L-histidine, L-serine, and γ-amino-n-butyric acid are utilized as sole nitrogen sources, but not N-acetyl-neuraminic acid, inosine, D-serine, cysteine, L-arginine or glucuronamide. Positive for degradation of aesculin and allantoin, but negative for adenine. Whole-cell hydrolysates contain l-l-diaminopimelic acid as the diamino acid, but not diagnostic sugars. The major menaquinones are MK-9(H4) and MK-9(H2). The main phospholipids are PE, DPG, PI, three unknown phospholipids and an unknown aminophospholipid. The fatty acid profile consists mainly

**Table 2.** DNA–DNA hybridizations between strain HM 1154\T\ and type strains of the most closely related species of the genus *Streptomyces*

<table>
<thead>
<tr>
<th>Type strain</th>
<th>DNA–DNA hybridization strain HM 1154\T\ (%)</th>
<th>Pairwise Similarity with strain HM 1154\T\ (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Streptomyces coeruleus</em> DSM 40146\T\</td>
<td>11.0 ± 0.1</td>
<td>99.4</td>
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<tr>
<td><em>Streptomyces varsoviensis</em> DSM 40346\T\</td>
<td>26.1 ± 0.1</td>
<td>99.3</td>
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<tr>
<td><em>Streptomyces youssoufiensis</em> DSM 41920\T\</td>
<td>35.8 ± 1.9</td>
<td>99.2</td>
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<td><em>Streptomyces abikoensis</em> DSM 40831\T\</td>
<td>14.0 ± 1.3</td>
<td>99.2</td>
</tr>
<tr>
<td><em>Streptomyces rimosus</em> subsp. rimosus DSM 40260\T\</td>
<td>20.8 ± 2.5</td>
<td>99.1</td>
</tr>
<tr>
<td><em>Streptomyces hygroscopicus</em> subsp. gleboqus DSM 40823\T\</td>
<td>20.7 ± 1.2</td>
<td>99.1</td>
</tr>
<tr>
<td><em>Streptomyces platensis</em> DSM 41241\T\</td>
<td>13.5 ± 0.9</td>
<td>99.0</td>
</tr>
<tr>
<td><em>Streptomyces ramulosus</em> DSM 40100\T\</td>
<td>31.2 ± 3.1</td>
<td>99.0</td>
</tr>
</tbody>
</table>

*Mean ± SD of two determinations.
of iso-C\textsubscript{16:0} and anteiso-C\textsubscript{15:0} complemented by C\textsubscript{16:0}, anteiso-C\textsubscript{17:0}, and C\textsubscript{16:1} \(\omega7\).

The type strain HM 1154\textsuperscript{T} (=DSM 42018\textsuperscript{T}=UTMC 1154\textsuperscript{T} =CECT 8305\textsuperscript{T}), was isolated from rhizospheric soil taken at a depth of 4–6 cm in Fars Province, Iran.

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References


Antitumor actinopyranones produced by *Streptomyces albus* POR-04


identification of aerobic actinomycetes by thin-layer chromatography.

Vaas, L. A. I., Sikorski, J., Michael, V., Goker, M. & Klenk, H. P.
(2012). Visualization and curve-parameter estimation strategies for
efficient exploration of phenotype microarray kinetics. *PLoS ONE* 7,
e34846.

Vaas, L. A. I., Sikorski, J., Hofner, B., Fiebig, A., Buddruhs, N.,
OmniLog(R) phenotype microarray data. *Bioinformatics* 29, 1823–
1824.

Waksman, S. A. & Henrici, A. T. (1943). The nomenclature and

Wayne, L. G., Brenner, D. J., Colwell, R. R., Grimont, P. A. D., Kandler,
other authors (1987). International Committee on Systematic
Bacteriology. Report of the ad hoc committee on reconciliation of

Wellington, E. M. H., Stackebrandt, E., Sanders, D., Wolstrup, J. &
proposed unification with *Streptomyces* on the basis of phenotypic
and 16S rRNA analysis and emendation of *Streptomyces* Waksman

Williams, S. T., Goodfellow, M., Alderson, G., Wellington, E. M.,

*Streptomyces* Waksman and Henrici 1943, 339AL. 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.

*Streptoverticillum* and *Streptomyces*, and amendation of
*Streptomyces* Waksman and Henrici 1943, 339AL. *Syst Appl Microbiol* 13,
361–371.

Zhao, G. Z., Li, J., Qin, S., Huang, H. Y., Zhu, W. Y., Xu, L. H. & Li, W. J.
(2010). *Streptomyces artemisiae* sp. nov., isolated from surface-
sterilized tissue of *Artemisia annua* L. *Int J Syst Evol Microbiol* 60,
27–32.

*Streptomyces yaanensis* sp. nov., isolated from soil. *Int J Syst Evol
Microbiol* 63, 4719–4723.