A novel actinomycete strain, designated TRM 46012\(^T\), was isolated from sediment of Aiding Lake in Tulufan Basin (42\(^\circ\) 64\' N 89\(^\circ\) 26\' E), north-west China. The strain was aerobic and Gram-staining-positive with an optimum NaCl concentration for growth of 0–5 % (w/v). The isolate had sparse aerial mycelium and produced bud-shaped spores at the end of the aerial mycelium on ISP medium 4. The isolate contained l-l-diaminopimelic acid as the diagnostic diamino acid and ribose as the major whole-cell sugar. The polar lipids were diphosphatidylglycerol, phosphatidylglycerol, phosphatidylethanolamine, phosphatidylcholine, phosphatidylinositol, phosphatidylinositol mannoside, one unidentified phospholipid and three unidentified glycolipids. The predominant menaquinones were MK-9(H\(_6\)), MK-9(H\(_8\)) and MK-9(H\(_4\)). The major fatty acids were iso-C\(_{16:0}\), anteiso-C\(_{17:0}\) and anteiso-C\(_{15:0}\). The G+C content of the DNA was 74.4 mol%. Phylogenetic analysis showed that strain TRM 46012\(^T\) had 16S rRNA gene sequence similarity of 95.7 % with the most closely related species with a validly published name, *Streptomyces cheonanensis*, and it could be distinguished from all species in the genus *Streptomyces* by using the data from this polyphasic taxonomic study. On the basis of these data, strain TRM 46012\(^T\) should be designated as a representative of a novel species of the genus *Streptomyces*, for which the name *Streptomyces aidingensis* sp. nov. is proposed. The type strain is TRM 46012\(^T\) (=CGMCC 4.5739\(^T\)=NBRC 108211\(^T\)).

The genus *Streptomyces* was initially introduced by Waksman & Henrici (1943) and encompasses more than 600 species with validly published names at the time of writing. Species of the genus *Streptomyces* are aerobic, Gram-positive actinomycetes and have a high DNA G+C content (69–73 mol%); most of them are able to form an extensively branched substrate mycelium and also to produce aerial hyphae that typically differentiate into chains of spores (Kämpfer et al., 2008). Streptomyces are used extensively in the medical industry because of their ability to generate a number of chemical compounds including antibiotics, enzymes, enzyme inhibitors and antitumour agents (Chun et al., 1997; Kim et al., 2006). Strain TRM 46012\(^T\) was isolated from a sediment sample collected from Aiding Lake, which is a salt lake in Xinjiang Province, north-west China. Here, we report on the classification and characterization of strain TRM 46012\(^T\) and propose a novel species of the genus *Streptomyces*.

Strain TRM 46012\(^T\) was isolated from sediment samples collected from Aiding Lake, which is a salt lake surrounded by the Gobi desert in Xinjiang province and the lowest land point (−154.3 m) in China (42\(^\circ\) 64\' N 89\(^\circ\) 26\' E). The strain was isolated using the standard dilution plate method and grown on chitin–asparagine medium (Xia et al., 2011) after 7 days of aerobic incubation at 28 °C. Strain TRM 46012\(^T\) was maintained on ISP medium 4 (Shirling & Gottlieb, 1966) 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 tryptic soy broth without agar at 28 °C, 180 r.p.m., for 7 days.

Cultural characteristics were determined after incubation by methods given by the International Streptomyces Project (ISP) (Shirling & Gottlieb, 1966). The colours of substrate and aerial mycelia and any soluble pigments produced were determined by comparison with chips from the Inter-Society Colour Council-National Bureau
of Standards (ISCC–NBS) colour charts (Kelly, 1964). Cultural characteristics on seven standard media were recorded after incubation at 28 °C for 10 days. The organism did not grow on ISP medium 2, ISP medium 3 or ISP medium 5; poor growth was observed on Czapek’s agar and Bennett’s agar; moderate growth was observed on ISP medium 4 and ISP medium 6; only sparse aerial mycelium was formed. Brown soluble pigments were produced on Czapek’s agar and ISP medium 6. Morphological characteristics of strain TRM 46012T were observed by light microscopy (Axioskop 20; Zeiss) and scanning electron microscopy (Quanta; FEI) after incubation on ISP medium 4 at 28 °C for 10 days. The aerial mycelia were sparse, with irregular branches; bud-shaped spores formed at the ends of the aerial mycelium (Fig. 1).

For NaCl tolerance test, growth was studied at 28 °C on ISP medium 4 containing 0, 1, 3, 5, 8, 10, 13, 15, 18, 20, 25 and 30 % (w/v) NaCl. Growth was investigated on ISP medium 4 containing 1 % (w/v) NaCl at 5–55 °C (at intervals of 5 °C) and at pH 4–12 (at 1 pH-unit intervals). 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 the method of Collins (1985) and analysed by HPLC (Groth et al., 1997). Cellular fatty acid composition was determined using the Microbial Identification System (MIDI Sherlock version 6.0). DNA G+C content was determined by HPLC as described by Tamaoka & Komagata (1984). The cell wall of strain TRM 46012T contained 11-diaminopimelic acid. Whole-cell hydrolysates contained mainly ribose. The menaquinones were MK-9(H₈), MK-9(H₆) and MK-9(H₄). The polar lipids were diphosphatidylglycerol, phosphatidylglycerol, phosphatidylethanolamine, phosphatidylcholine, phosphatidylinositol, phosphatidylinositol mannoside, one unidentified phospholipid and three unidentified glycolipids (Fig. S1, available in IJSEM Online). Major cellular fatty acids were iso-C₁₅:₀ (41.6 %), anteiso-C₁₇:₀ (19.3 %), anteiso-C₁₅:₀ (14.8 %), iso-C₁₆:₁ H (6.0 %) and C₁₆:₀ (5.3 %); fatty acids present in smaller amounts (>1 %) were iso-C₁₅:₀ (2.7 %), iso-C₁₇:₀ (1.7 %), iso-C₁₄:₀ (1.3 %) and anteiso-C₁₇:₁ (9c (1.0 %). The G+C content of the DNA was 74.4 mol%.

Genomic DNA extraction and PCR amplification of the 16S rRNA gene from strain TRM 46012T were performed using an established method (Chun & Goodfellow, 1995). Multiple alignments with sequences from the closely related members of the genus Streptomyces 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, maximum-parsimony and maximum-likelihood using MEGA version 5 (Tamura et al., 2011). 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 TRM 46012T falls within the radius of the genus Streptomyces and has the highest sequence similarity to Streptomyces cheonanensis VC-A46T (GenBank accession no. AY822606; 95.7 %) and Streptomyces iranensis HM 35T (GenBank accession no. FJ472862; 95.4 %). All other species of the genus Streptomyces showed lower sequence similarity to strain TRM 46012T. In the phylogenetic tree based on the neighbour-joining algorithm, strain TRM 46012T clustered clearly with Streptomyces cheonanensis VC-A46T and Streptomyces specialis GW41-1564T (Fig. 2). This relationship was supported by other tree-making methods used in this study (Figs S2 and S3). All of the above data confirmed that strain TRM 46012T should be assigned to the genus Streptomyces.

Strain TRM 46012T was different from members of other species of the genus Streptomyces in some morphological

Fig. 1. Scanning electron micrograph of aerial mycelium and spores of strain TRM 46012T grown on ISP medium 4 at 28 °C for 10 days. Bar, 5 μm.
and physiological properties (Table 1). Scanning electron microscopic observations of strain TRM 46012T showed that the aerial mycelia were sparse, with irregular branches; bud-shaped spores formed at the ends of the aerial mycelium but no spore-chains were formed. These features enable strain TRM 46012T to be differentiated from Streptomyces cheonanensis NBRC 100940T, the nearest neighbouring species, and other phylogenetically closely related species. Moreover, strain TRM 46012T exhibited some chemotaxonomic differences from Streptomyces cheonanensis NBRC 100940T, Streptomyces iranensis JCM 17327T, Streptomyces sodiiphilus JCM 13581T and Streptomyces specialis JCM 16611T. Strain TRM 46012T contained ribose in whole-cell hydrolysates; MK-9(H₆), MK-9(H₈) and MK-9(H₁₂) were the predominant menaquinones; the polar lipids included diphosphatidylglycerol, phosphatidylglycerol, phosphatidylethanolamine, phosphatidylcholine, phosphatidylinositol and phospha
dilinositol mannoside. In contrast, the phylogenetically closely related species have no ribose as whole-cell sugar and the diagnostic polar lipids and predominant cellular fatty acids are also different from those of strain TRM 46012T.

On the basis of a combination of phylogenetic distinctness and differences in chemotaxonomic and morphological characteristics, strain TRM 46012T represents a novel species in the genus Streptomyces, for which the name Streptomyces aidingensis sp. nov. is proposed.

**Description of Streptomyces aidingensis sp. nov.**

Streptomyces aidingensis (ai.ding.en’sis; N.L. masc. adj. aidingensis of or belonging to Aiding lake, a salt lake in Tulufan city, north-west China, where the strain was isolated).
Aerobic, Gram-stain-positive actinomycete. Sparse aerial mycelium with irregular branches. Bud-shaped spores form at the ends of the aerial mycelium, spore surface is smooth; no spore-chains on aerial mycelium. No growth on ISP medium 2, ISP medium 3 or ISP medium 5; poor growth on Czapek’s agar and Bennett’s agar; moderate growth on ISP medium 4 and ISP medium 6 with only sparse aerial mycelium. Brown soluble pigments are produced on Czapek’s agar and ISP medium 6. Growth occurs at 23–37 °C and pH 5.0–9.0. NaCl tolerance range is up to 5%. Optimum growth at pH 7.0 and 2 % NaCl (w/v) at 28 °C. Starch, riboflavin, fucose, arabinose, glucose, sucrose and mannitol can be used as sole carbon sources for growth, but not inositol, fructose, glycerol, cellobiose, L-rhamnose, maltose, D-xylose, melezitose or mannose. Positive for gelatine liquefaction, catalase production, milk coagulation and milk peptonization, negative for urease, melanin production, starch hydrolysis, H2S production, nitrate reduction and oxidase reaction. Tweens 20, 40, 60 and 80 are hydrolysed, but cellulose, aesculin, adenine, xanthine and hypoxanthine are not. The cell wall contains dL-diaminopimelic acid. The whole-cell sugar pattern mainly consists of ribose. The predominant menaquinones are MK-9(H6), MK-9(H8) and MK-9(H4). The polar lipids are diphasphatidylglycerol, phosphatidylglycerol, phosphatidylethanolamine, phosphatidylcholine, phosphatidylinositol, phosphatidylinositol mannoside, one unidentified phospholipid and three unidentified glycolipids. Major fatty acids are iso-C16:0, anteiso-C17:0 and anteiso-C15:0.

The type strain is TRM 46012T (=CGMCC 4.5739T=NIBRC 108211T), was isolated from sediments collected from Aiding salt lake located in the Tulufan Basin in the north-west of China. The G+C content of the genomic DNA of the type strain is 74.4 mol%.

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