The growth and culture characteristics of strain CCNWHX 13-160T on available with the online version of this paper.

CCNWHX 13-160 T (Table S2), growth characteristics of strain different media (Table S1), the fatty acid composition of strain

Pollution of soils with heavy metals is becoming one of the most severe environmental hazards. Elevated levels of heavy metals not only decrease soil microbial activity and crop production, but also threaten human health through the food chain (McLaughlin et al., 1999). Selection pressure in polluted habitats has led to adaptation, resulting in microorganisms possessing special resistance mechanisms as a consequence of their permanent exposure to heavy metals. Increasing numbers of environmental micro-organisms have been studied as part of investigations into methods to remediate heavy metal contamination (Thompson & Watling, 1987; Smith et al., 1994). Some micro-organisms, e.g. members of the genera Citrobacter and Pseudomonas, both Gram-negative, rod-shaped bacteria growing in heavy metal-contaminated sites, have been found with the ability to resist and accumulate the heavy metal lead (Aickin & Dean, 1979; Macaskie & Dean, 1987). There have been previous reports on the effects of heavy metals (except for lead) on a range of Streptomyces species (Abbas & Edwards, 1989). Since actinomycetes are susceptible to heavy metals (Lugauskas et al., 2005), little is known about their presence in soils contaminated with heavy metals, especially lead.

The novel strain, CCNWHX 13-160T, was isolated by the dilution plating method from a sample of lead-polluted soil collected from Huixian (33° 54′ 10.3″ N 106° 07′ 44.3″ E; altitude of 1049 m), Gansu province, north-west China, in July 2006. The medium used was modified Gause’s synthetic agar (16.0 g soluble starch, 4.0 g D-glucose; 1.0 g potassium nitrate, 0.5 g potassium phosphate dibasic trihydrate, 0.5 g sodium chloride, 20 g ferrous sulfate heptahydrate, 0.5 g magnesium sulfate heptahydrate, 0.001 g ferrous sulfate heptahydrate, 0.5 g sodium chloride, 20 g agar powder, 0.5 mg vitamin B compound and 1000 ml distilled water; pH 7.2). The isolate was maintained on modified Gause’s synthetic agar slopes and as glycerol suspensions (20 %, v/v) at −20 °C. Biomass for most of the chemotaxonomic and molecular systematic studies was harvested after incubation in shake flasks of modified Gause’s broth at 28 °C for 4–7 days.

Morphological properties were examined by light microscopy (CX31; Olympus) and scanning electron microscopy (6360LV; JSM) after cultivation for 2 weeks on modified Gause’s synthetic agar medium at 28 °C. Colours were determined using the methods described by Kelly (1964).

Analysis of the diaminopimelic acid isomers and whole-cell sugars in whole-cell hydrolysates was performed according
to Lechevalier & Lechevalier (1980). Fatty acids were extracted as described by Kämpfer & Kroppenstedt (1996) and estimated by GC using the standard Sherlock MIDI (Microbial Identification) system. Menaquinones were examined by the method of Collins (1985) and phospholipids were determined following the procedure of Lechevalier et al. (1981).

Strain CCNWHX 13-160<sup>T</sup> was examined for a range of chemotaxonomic and physiological properties following the methods of Williams et al. (1983). International Streptomyces Project (ISP) media were used to determine the colours of diffusible pigments and the utilization of sole carbon and nitrogen sources (Shirling & Gottlieb, 1966). Temperature and pH tolerances were determined on Bennett’s agar plates after incubation for 2 weeks. Resistance to antibiotics was carried out according to Al-Tai et al. (1999).

Genomic DNA extraction and 16S rRNA gene PCR amplification were carried out according to Chun & Goodfellow (1995). The universal bacterial 16S rRNA gene primers [forward primer P1 (5’-CGGGATCCAGAGTTTGATCCCTGGCTCAGAACGAACGCT-3’) and reverse primer P6 (5’-CGGGATCCAGAGTTTGATCCCTGGCTCAGACACTTACCCCC-3’)] were used. The PCR product was purified and sequenced directly by an automated DNA sequencing system (ABI 3730XL). The 16S rRNA gene sequence of the strain was aligned manually by CLUSTAL_X version 1.8 (Thompson et al., 1997) with the almost complete 16S rRNA gene sequences of type strains of recognized species of the genus Streptomyces obtained from GenBank/EMBL/ DDBJ. A phylogenetic tree was constructed using the neighbour-joining (Saitou & Nei, 1987), minimum-evolution (Rehetsky & Nei, 1993) and maximum-parsimony (Fitch, 1971) methods in the TREECON software package version 1.3b (Van de Peer & De Wachter, 1994) and the MEGA3.1 software package (Kumar et al., 2004). The genetic distance matrices were estimated by the Kimura two-parameter model (Kimura, 1980). The topology of the tree was evaluated in a bootstrap analysis based on 1000 replicates (Felsenstein, 1985). The DNA G+C content was determined using the thermal melting protocol (Marmur & Doty, 1962) with Escherichia coli K-12 as the standard. DNA–DNA relatedness was determined by the initial renaturation rate method in triplicate (De Ley et al., 1970).

The methods of Amoroso et al. (1998) were used to determine the lead resistance of strain CCNWHX 13-160<sup>T</sup>. Spore suspensions (1 x 10<sup>9</sup> c.f.u. ml<sup>-1</sup>) of the strain were prepared as described by Kieser et al. (2000). Samples of liquid medium (16.0 g soluble starch, 4.0 g D-glucose, 1.0 g potassium nitrate, 0.5 g potassium phosphate dibasic trihydrate, 0.5 g magnesium sulfate heptahydrate and 1000 ml distilled water; pH 6.0) containing different concentrations of Pb(NO<sub>3</sub>]<sub>2</sub> (0.5–5.0 mM) and each inoculated with 100 µl spore suspension were incubated with shaking (150 r.p.m.) at 28 °C for 4 days. After being centrifuged (5000 g, 10 min), the cell pellets were washed three times with 25 mM Tris-EDTA buffer (pH 8.0). To analyse the weight changes of the culture, the pellets were dried to constant weight at 105 °C. Residual lead in the supernatants was determined by atomic absorption spectrophotometry (180–80; Hitachi). All samples were analysed in triplicate and mean values were determined.

The chemotaxonomic and morphological properties of strain CCNWHX 13-160<sup>T</sup> were consistent with those of members of the genus Streptomyces (Williams et al., 1989). The strain formed a highly branched substrate mycelium and aerial hyphae which differentiated into Rectiflexibles spore chains with smooth, greenish white spores (Fig. 1). The growth of the organism was moderate on ISP3, ISP4, ISP5 and ISP6 agars, but poor on nutrient agar. The colour of the aerial hyphal mass was white to greyish white and the substrate mycelium was light yellow to brownish red on ISP6, Bennett’s agar and ISP3. A brown diffusible pigment was produced on ISP4, ISP5, Bennett’s agar and Gause’s synthetic agar (Table 1 and Supplementary Table S1, available in IJSEM Online).

The whole cell hydrolysates contained LL-diaminopimelic acid, but no diagnostic sugars (cell wall type I) (Lechevalier & Lechevalier, 1980). The major menaquinones of the novel strain were hexahydrogenated, octahydrogenated and tetrahydrogenated with nine isoprene units [MK-9(H6, H8 and H4)]. The major polar lipids were phosphatidylethanolamine, phosphatidylglycerol and phosphatidylglycerol mannosides (phospholipid type II) (Lechevalier et al., 1981). Analysis of the major fatty acid components showed that the organism contained mainly iso- and anteiso-branched-chain fatty acids and a small proportion of unsaturated fatty acids (Supplementary Table S2, available in IJSEM Online).

The almost complete 16S rRNA gene sequence (1429 nt) of strain CCNWHX 13-160<sup>T</sup> was aligned with 16S rRNA gene sequences of other Streptomyces species and a distinct phylogenetic line was formed with Streptomyces pseudovelezuelae NBRC 12904<sup>T</sup>. The strain was closely related to S. plumbiresistens sp. nov.

![Fig. 1. Scanning electron micrograph of the Rectiflexibles spore chains and smooth-surfaced spores of strain CCNWHX 13-160<sup>T</sup> after cultivation for 2 weeks at 28 °C on modified Gause’s synthetic agar medium. Bar, 2 µm.](image-url)
pseudovenezuelae NBRC 12904T and Streptomyces resistomyricicus NBRC 12814T with sequence similarities of 98.9 and 98.8%, respectively (Fig. 2).

DNA–DNA relatedness studies were carried out between strain CCNWHX 13-160T and the most closely related type strains (S. pseudovenezuelae NBRC 12904T and S. resistomyricicus NBRC 12814T); DNA–DNA relatedness values were 49.7 ± 0.8 and 43.2 ± 1.1%, respectively, and both values were significantly lower than the 70% cut-off point recommended for the delineation of genomic species (Wayne et al., 1987).

It is clear that strain CCNWHX 13-160T differs from its most closely related phylogenetic neighbours S. pseudovenezuelae NBRC 12904T and S. resistomyricicus NBRC 12814T (Table 1). Physiological characteristics, degradation of organic compounds and production of diffusible pigments enabled strain CCNWHX 13-160T to be distinguished from closely related type strains.

Strain CCNWHX13-160T grew well in liquid medium supplemented with 0.5 mM Pb²⁺ and visible growth was observed in the presence of 2.0 mM Pb²⁺. S. pseudovenezuelae NBRC 12904T and S. resistomyricicus NBRC 12814T could not grow in the presence of 2.0 mM Pb²⁺ (see Supplementary Table S3, available in IJSEM Online). The MIC of Pb²⁺ for strain CCNWHX 13-160T was 4.0 mM. The MIC was determined by the intersection of the relative survival curve with the horizontal axis. The relative survival curve was produced using weight changes of cultures that were supplemented with different concentrations of lead compared with non-lead-supplemented controls under the same conditions (see Supplementary Fig. S1, available in IJSEM Online). Several strains of the genus Frankia are known to be resistant to Pb²⁺ (MIC 5–8 mM) (Richards et al., 2002). However, Escherichia coli W3110 (MIC 2.0 mM), Bacillus subtilis 168 (MIC 3.0 mM) and Micromonospora echinospora ATCC 15836T (MIC 3.0 mM) are less resistant to lead (Richards et al., 2002).

Based on a combination of phenotypic and genotypic studies, strain CCNWHX 13-160T represents a novel species of the genus Streptomyces, for which the name Streptomyces plumbiresistens sp. nov. is proposed.

**Description of Streptomyces plumbiresistens sp. nov.**

Streptomyces plumbiresistens (plum.bi.re.sis.tens. L. n. plumbum lead; L. part adj. resistens resisting; N.L. part
The type strain, CCNWHX 13-160\(^T\) (=ACCC 41207\(^T\) = HAMBI 2991\(^T\)), was isolated from a lead-contaminated soil sample collected from Gansu Province, north-west China. The genomic DNA G+C content of the type strain is 70.9 mol%.

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**References**


