**Streptomonospora halotolerans** sp. nov., an actinomycete isolated from soil

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A novel actinomycete, designated strain NEAU-Jh2-17ᵀ, was isolated from muddy soil collected from a riverbank in Jilin Province, northern China, and characterized using a polyphasic approach. The 16S rRNA gene sequence of strain NEAU-Jh2-17ᵀ showed highest similarity to those of *Streptomonospora nanhaiensis* 12A09ᵀ (99.26 %), *Nocardiopsis rosea* YIM 90094ᵀ (97.31 %), *Streptomonospora halophila* YIM 91355ᵀ (97.24 %) and *Streptomonospora arabica* S186ᵀ (97.02 %). Phylogenetic analysis based on 16S rRNA gene sequences demonstrated that strain NEAU-Jh2-17ᵀ fell within a cluster consisting of the type strains of species of the genus *Streptomonospora* and formed a stable clade with *S. nanhaiensis* 12A09ᵀ in trees generated with two algorithms. Key morphological and chemotaxonomic properties also confirmed the affiliation of strain NEAU-Jh2-17ᵀ to the genus *Streptomonospora*. The cell wall contained meso-diaminopimelic acid as the diagnostic diamino acid and whole-cell hydrolysates contained glucose, ribose and galactose. The polar lipids were diphosphatidylglycerol (DPG), phosphatidylethanolamine (PE), phosphatidylglycerol (PG), phosphatidylcholine (PC), phosphatidylinositol (PI), phosphatidylinositol mannoside (PIM), two unknown phospholipids (PLs) and two unknown glycolipids (GLs). The predominant menaquinones were MK-10(H₂), MK-10(H₁₀), MK-10(H₆) and MK-10(H₄). Major fatty acids were C₁₈:₀ 10-methyl, anteiso-C₁₇:₁₀, C₁₆:₁₀ 10-methyl, iso-C₁₇:₁₀, C₁₇:₁₀ 10-methyl and C₁₈:₁₀. The DNA G+C content was 71.82 mol%. However, a combination of DNA–DNA hybridization results and some phenotypic characteristics demonstrated that strain NEAU-Jh2-17ᵀ could be distinguished from its closely related relatives. Therefore, strain NEAU-Jh2-17ᵀ is considered to represent a novel species of the genus *Streptomonospora*, for which the name *Streptomonospora halotolerans* sp. nov. is proposed. The type strain is NEAU-Jh2-17ᵀ (≡CGMCC 4.7218ᵀ=JCM 30347ᵀ).

The genus *Streptomonospora*, belonging to the family *Nocardiopsaceae* (Stackebrandt et al., 1997), was established by Cui et al. (2001) (with *Streptomonospora salina* as the type species) to accommodate a group of strictly halophilic filamentous actinomycetes forming a distinct branch in the 16S rRNA gene phylogenetic tree adjacent to the genera *Nocardiopsis* and *Thermobifida*. Subsequently, the description of the genus *Streptomonospora* was emended by Li et al. (2003) and Zhang et al. (2013) on the basis of whole-cell hydrolysates, polar lipid pattern, menaquinone composition, fatty acids and DNA G+C content. Members of the genus *Streptomonospora* are characterized by several chemical markers: the diagnostic diamino acid of the peptidoglycan is meso-diaminopimelic acid; whole-cell hydrolysates contain galactose; the phospholipid pattern is complex, with diphosphatidylglycerol, phosphatidylglycerol, phosphatidylcholine and phosphatidylinositol present in all recognized species of the genus except *S. salina*. The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain NEAU-Jh2-17ᵀ is KM000838.

Two supplementary figures are available with the online Supplementary Material.
(Cui et al., 2001), phosphatidylinositol mannosides present in most of them, and phosphatidylethanolamine, methyl-phosphatidylethanolamine, glycolipids and phosphatidylserine present in some; the menaquinone compositions may depend on the growth medium and consist mainly of menaquinones with nine or ten isoprenoid chains and a varying degree of hydrogenation, although MK-11(H$_6$) and MK-11(H$_8$) as predominant menaquinones have been reported in *Streptomonospora sediminis* and *Streptomonospora nanhaiensis* (Zhang et al., 2013); and C$_{16:1}$-0, C$_{17:0}$, iso-C$_{15:0}$ and iso-C$_{16:0}$ are major fatty acids. At the time of writing, the genus *Streptomonospora* comprises nine recognized species: *S. salina* (Cui et al., 2001; Li et al., 2003), *S. alba* (Li et al., 2003), *S. halophilica* (Cai et al., 2008), *S. amylolytica* and *S. flavula* (Cai et al., 2009), *S. sediminis*, *S. nanhaiensis* and *S. arabica* (Zhang et al., 2013) and *S. algeriensis* (Meklat et al., 2014). These were all isolated from soil of hypersaline habitats such as saline soil of a salt lake and marine sediment, with the exception of *S. arabica* isolated from a sand-dune soil, which was allocated to the genus *Streptomonospora* with the reclassification of *Nocardiosis arabia* (Hozzein & Goodfellow, 2008) by Zhang et al. (2013). During the course of investigation of novel rare actinomycetes from muddy soil collected from a riverbank in Jilin Province, northern China, a novel actinomycete, strain NEAU-Jh2-17$^{	op}$, was obtained and subjected to a polyphasic taxonomic study. It is proposed that strain NEAU-Jh2-17$^{	op}$ represents a novel species of the genus *Streptomonospora*. Strain NEAU-Jh2-17$^{	op}$ was isolated using the standard dilution plate method and was grown on humic acid-vitamin agar (Hayakawa & Nonomura, 1987) supplemented with cycloheximide (50 mg L$^{-1}$) and nalidixic acid (20 mg ml$^{-1}$). After 28 days of aerobic incubation at 28°C, a colony was transferred and purified on International Streptomyces Project (ISP) medium 3 (Shirling & Gottlieb, 1966), and maintained as glycerol suspensions (20%, v/v) at −80°C. Morphological characteristics were observed by light microscopy (Nikon ECLIPSE E200) and scanning electron microscopy (Hitachi S-3400N) using cultures grown on ISP 3 agar at 28°C for 4 weeks. Cultural characteristics were determined on ISP media 2–7 (Shirling & Gottlieb, 1966), Czapek’s agar (Waksman, 1967) and nutrient agar (Waksman, 1961) after 14 days at 28°C. Colour determination was done with colour chips from the ISCC-NBS colour charts (Kelly, 1964). Growth at different temperatures (4, 10, 15, 20, 28, 30, 32, 35, 37, 40, 45, 50, 55 and 60°C) was determined on ISP 2 medium after incubation for 14 days. Growth tests for pH range (pH 4.0–10.0, at intervals of 1.0 pH unit) and NaCl tolerance (0, 3, 5, 7, 10, 11, 13, 15, 18, 20, 23 and 25%, w/v) were done in SY broth (per 100 millilitre distilled water: starch, 1 g; yeast extract, 1 g; K$_2$HPO$_4$, 0.05 g; MgSO$_4$, 0.05 g; pH 7.2) at 28°C for 14 days on a rotary shaker. Hydrolysis of Tweens 20, 40 and 80 and production of catalase and urease were tested as described by Smibert & Krieg (1994). Decomposition of cellulose was tested as described by Williams et al. (1989). The utilization of sole carbon and nitrogen sources, hydrolysis of starch and aesculin, reduction of nitrate, peptidase activity of milk, liquefaction of gelatin and production of H$_2$S were examined as described previously (Gordon et al., 1974; Yokota et al., 1993).

Biomass for chemical studies was prepared by growing the organism in SY broth in shake flasks at 28°C for 14 days. Cells were harvested by centrifugation, washed with distilled water and freeze-dried. The isomer of diaminopimelic acid in the cell-wall hydrolysates was derivatized and analysed by HPLC (McKerrow et al., 2000) using an Agilent TC-C$_{18}$ column (250×4.6 mm, i.d. 5 μm) with a mobile phase consisting of acetonitrile/0.05 mol phosphate buffer (pH 7.2) 1−1 (15:85, v/v) at a flow rate of 0.5 ml min$^{-1}$. Peak detection used an Agilent G1321A fluorescence detector with 365 nm excitation and 455 nm longpass emission filters. Whole-cell sugars were analysed according to the procedures developed by Lechevalier & Lechevalier (1980). Polar lipids were examined by two-dimensional TLC and identified using the method of Minnikin et al. (1984). Menaquinones were extracted from freeze-dried biomass and purified according to Collins (1985). Extracts were analysed by an HPLC-UV method (Wu et al., 1989) using an Agilent Extend-C$_{18}$ column (150×4.6 mm, i.d. 5 μm) at 270 nm. The mobile phase was acetonitrile/isopropyl alcohol (60:40, v/v). To determine cellular fatty acid compositions, strain NEAU-Jh2-17$^{	op}$ was cultivated in SY broth in shake flasks at 28°C for 14 days. Fatty acid methyl esters were extracted from the biomass as described by Gao et al. (2014) and analysed by GC-MS using the method of Xiang et al. (2011). Extraction of chromosomal DNA and PCR amplification of the 16S rRNA gene sequence was carried out using a standard procedure (Kim et al., 2000). The PCR product was purified and cloned into the vector pMD19-T (Takara) and sequenced using an Applied Biosystems DNA sequencing model (3730XL). The almost full-length 16S rRNA gene sequence of strain NEAU-Jh2-17$^{	op}$ (1527 bp) was obtained and aligned with multiple sequences obtained from the GenBank/EMBL/DDBJ databases using CLUSTAL X 1.83 software. The alignment was manually verified and adjusted before reconstruction of phylogenetic trees. The phylogenetic trees reconstructed by the neighbour-joining (Saitou & Nei, 1987) and maximum-likelihood (Felsenstein, 1981) algorithms using MEGA software version 5.05 (Tamura et al., 2011) were based on a comparison of 1366 nt present in all of the strains, omitting unaligned regions. The stability of the topology of the phylogenetic tree was assessed using the bootstrap method with 1000 replications (Felsenstein, 1985). A distance matrix was generated using Kimura’s two-parameter model (Kimura, 1980). All positions containing gaps and missing data were eliminated from the dataset (complete deletion option). 16S rRNA gene sequence similarities between strains were calculated on the basis of pairwise alignment using the EzTaxon-e server (Kim et al., 2012).
The G+C contents of the genomic DNA were determined using the thermal denaturation (T_m) method (Mandel & Marmur, 1968) with *Escherichia coli* JM109 DNA used as the control. DNA–DNA relatedness tests between strain NEAU-Jh2-17^T^ and *S. nanhaiensis* 12A09^T^, *Nocardiopsis rosea* YIM 90094^T^, *S. halophila* YIM 91355^T^ and *S. arabica* DSM 45083^T^ were 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 multicell changer and a temperature controller with *in-situ* temperature probe (Varian). The concentration and purity of DNA samples were determined by measuring the optical density at 260, 280 and 230 nm. The DNA samples used for hybridization were diluted to an OD260 of about 1.0 using 0.1× saline sodium citrate (SSC) buffer, then sheared using a JY92-II ultrasonic cell disruptor (ultrasonic time 3 s, interval time 4 s, 90 times). DNA renaturation rates were determined in 2× SSC buffer at 70 °C. The experiments were performed with three replications and the DNA–DNA relatedness values were expressed as the mean of the three values.

Morphological observation of a 4-week culture of strain NEAU-Jh2-17^T^ grown on ISP 3 medium revealed that it shared the same morphological characteristics as members of the genus *Streptomonospora*. The aerial mycelium was well developed but not fragmented; at maturity, it formed short chains of oval to cylindrical spores with smooth surfaces (0.4–0.5× 0.9–1.0 μm), which were straight to flexuous (Fig. 1a). The substrate mycelium was abundant and non-fragmented. Single, oval spores with wrinkled surfaces were borne on sporophores of substrate mycelium (Fig. 1b). Both types of spores were non-motile. Strain NEAU-Jh2-17^T^ exhibited good growth on ISP 2, 3, 5 and 7, Czapek’s agar and nutrient agar, moderate growth on ISP 6 agar, but no growth on ISP 4 agar. White aerial mycelium was produced on ISP 3 and 5 agar, but no aerial mycelium was formed on ISP 2, 4, 6 and 7, Czapek’s agar or nutrient agar. The substrate mycelium colour was yellowish white on ISP 3, 4, 5, 6 and 7 media, pale greenish yellow on ISP 2 medium, brilliant orange yellow on nutrient agar and brilliant yellow on Czapek’s agar. No diffusible pigment was observed on any of the media tested. The isolate grew well between pH 7.0 and 9.0, with an optimum pH of 8.0. The range of temperature for growth was 20–37 °C, with the optimum growth temperature being 28 °C. Strain NEAU-Jh2-17^T^ grew in the presence of 0–10 % (w/v) NaCl. Detailed physiological characteristics are presented in the species description.

The cell-wall hydrolysates of strain NEAU-Jh2-17^T^ contained meso-diaminopimelic acid as the diagnostic diamino acid. Whole-cell hydrolysates contained glucose, ribose and galactose. The polar lipids consisted of diphostatidyglycerol (DPG), phosphatidylethanolamine (PE), phosphatidyglycerol (PG), phosphatidylcholine (PC), phosphatidylinositol (PI), phosphatidylinositol mannoside (PIM), two unknown phospholipids (PLs) and two unknown glycolipids (GLs) (Fig. S1, available in the online Supplementary Material). The menaquinones were MK-10(H2) (20.2 %), MK-10(H4) (19.7 %), MK-10(H6) (19.4 %), MK-10(H8) (15.9 %) and small amounts of MK-11(H2) (4.8 %), MK-11(H4) (4.6 %), MK-10(H6) (4.2 %), MK-9(H4) (4.2 %), MK-9(H6) (3.9 %) and MK-11(H4) (3.1 %). The cellular fatty acid profile was composed of C18:0 10-methyl (20.9 %), anteiso-C17:0 (16.2 %), C16:0 10-methyl (11.7 %), iso-C15:0 (11.3 %), C17:0 10-methyl (10.3 %), C18:0 (10.0 %), C18:1ω7c (4.5 %), iso-C17:0 (4.5 %), C17:0 (2.7 %), iso-C14:0 (2.0 %), C15:0 (1.8 %), C16:1ω7c (1.7 %), C17:1ω7c (0.9 %), C14:0 (0.9 %) and C16:0 (0.7 %). The chemotaxonomic data are consistent with the assignment of strain NEAU-Jh2-17^T^ to the genus *Streptomonospora*.

EZTaxon-e analysis of the 16S rRNA gene sequence indicated that strain NEAU-Jh2-17^T^ should be assigned to the genus
Streptomonospora. Its closest relatives were *S. nanhaiensis* 12A09T (99.26 % 16S rRNA gene sequence similarity), *N. rosea* YIM 90094T (97.31 %), *S. halophila* YIM 91355T (97.24 %) and *S. arabica* S186T (97.02 %). The phylogenetic tree based on 16S rRNA gene sequences showed that strain NEAU-Jh2-17T formed a stable clade with *S. nanhaiensis* 12A09T (supported by a high bootstrap value of 100 %; Fig. 2) and the clade adjacent to this group consisted of the type strains of species of the genus *Streptomonospora* in the neighbour-joining tree, while *N. rosea* YIM 90094T together with the two other members of the genus *Nocardiopsis* were separate from strain NEAU-Jh2-17T, although the second highest 16S rRNA gene sequence similarity was found to *N. rosea* YIM 90094T. This relationship was also supported by the maximum-likelihood algorithm (Fig. S2).

DNA–DNA hybridizations were employed to further clarify the relatedness between the novel strain and *S. nanhaiensis* 12A09T, *N. rosea* YIM 90094T, *S. halophila* YIM 91355T and *S. arabica* DSM 45083T. Strain NEAU-Jh2-17T shared mean DNA–DNA relatedness of 30.91 ± 0.70 % with *S. nanhaiensis* 12A09T, 33.35 ± 1.50 % with *N. rosea* YIM 90094T, 33.77 ± 2.73 % with *S. halophila* YIM 91355T and 48.39 ± 1.91 % with *S. arabica* DSM 45083T. These values are below the threshold value of 70 % recommended by Wayne et al. (1987) for assigning strains to the same genomic species.

Comparative studies between strain NEAU-Jh2-17T and *S. nanhaiensis* 12A09T, *N. rosea* YIM 90094T, *S. halophila* YIM 91355T and *S. arabica* DSM 45083T revealed that they were significantly different in terms of phenotypic and chemotaxonomic characteristics as summarized in Table 1. For example, strain NEAU-Jh2-17T was unable to grow above 37 °C, in contrast to its closely related species (*S. nanhaiensis* 12A09T and *N. rosea* YIM 90094T were even able to grow at 50 and 60 °C, respectively). Strain NEAU-Jh2-17T was able to tolerate up to 10 % NaCl, a value distinctly lower than those of the four reference strains (18–25 %). In addition, the novel strain was able to utilize L-tyrosine and L-serine but could not hydrolyse aesculin, characteristics that readily distinguish it from its closely related species. Strain NEAU-Jh2-17T could be differentiated from *N. rosea* YIM 90094T based on the

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**Fig. 2.** Neighbour-joining tree based on 16S rRNA gene sequences (1366 bp, omitting unaligned regions) showing the relationship between strain NEAU-Jh2-17T and its closest relatives (including all type strains of species of the genus *Streptomonospora*). The out-group used was *Streptosporangium album* DSM 43023T. Only bootstrap values above 50 % (percentages of 1000 replications) are indicated. Asterisks indicate branches also recovered in the maximum-likelihood tree. Bar, 0.01 nt substitutions per site.
Table 1. Differential phenotypic and chemotaxonomic characteristics between strain NEAU-Jh2-17\textsuperscript{T} and closely related species of the genus *Streptomonospora*

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
<th>2*</th>
<th>3*</th>
<th>4*</th>
<th>5*</th>
</tr>
</thead>
<tbody>
<tr>
<td>Formation of single spores on substrate mycelium</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Single spore surface</td>
<td>Wrinkled</td>
<td>Smooth\textsuperscript{a}</td>
<td>None\textsuperscript{b}</td>
<td>Smooth\textsuperscript{a}</td>
<td>Wrinkled\textsuperscript{a}</td>
</tr>
<tr>
<td>NaCl concentration for growth (% w/v)</td>
<td>0–10</td>
<td>0–20</td>
<td>0–18</td>
<td>0–25</td>
<td>0–20</td>
</tr>
<tr>
<td>Growth temperature (°C) (optimum)</td>
<td>20–37 (28)</td>
<td>10–50 (37)</td>
<td>20–60 (37–40)</td>
<td>15–45 (37)</td>
<td>10–40 (28)</td>
</tr>
<tr>
<td>Reduction of nitrate</td>
<td>−</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>Hydrolysis of aesculin</td>
<td>−</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Coagulation of milk</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>+</td>
</tr>
<tr>
<td>Peptonization of milk</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>+</td>
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<tr>
<td>Utilization of:</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>L-Tyrosine</td>
<td>+</td>
<td>−</td>
<td>( + )\textsuperscript{a}</td>
<td>−</td>
<td>−</td>
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<tr>
<td>L-Serine</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
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<tr>
<td>L-Alanine</td>
<td>+</td>
<td>+</td>
<td>−</td>
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<td>−</td>
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<tr>
<td>L-Aspartic acid</td>
<td>+</td>
<td>+</td>
<td>−</td>
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<td>L-Glutamic acid</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>−</td>
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<tr>
<td>L-Threonine</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
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<tr>
<td>Glycine</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>Whole-cell sugars†</td>
<td>Glu, Gal, Rib</td>
<td>Glu, Gal\textsuperscript{a}</td>
<td>ND\textsuperscript{b}</td>
<td>Glu, Gal\textsuperscript{a}</td>
<td>Glu, Gal, Rib\textsuperscript{a}</td>
</tr>
<tr>
<td>Polar lipids‡</td>
<td>DPG, PG, PC, PE, PI, PIM, PL, GL</td>
<td>DPG, PG, PC, PI, PIM, PL, GL</td>
<td>DPG, PG, PC, PE, PI, PIM, PL, GL</td>
<td>DPG, PG, PC, PI, PIM, PL, GL</td>
<td>DPG, PG, PC, PE, PI, PIM, PL, GL</td>
</tr>
<tr>
<td>Predominant menaquinones (&gt;10%)</td>
<td>MK-10(H\textsubscript{2,4,6,8})</td>
<td>MK-10(H\textsubscript{4,6}), MK-11(H\textsubscript{4,6})\textsuperscript{a}</td>
<td>MK-11(0,2,4)\textsuperscript{b}</td>
<td>MK-9(H\textsubscript{4}), MK-10(H\textsubscript{6,8})\textsuperscript{a}</td>
<td>MK-10(H\textsubscript{6,8})\textsuperscript{b}</td>
</tr>
<tr>
<td>DNA G + C content (mol%)</td>
<td>71.8</td>
<td>74.4\textsuperscript{a}</td>
<td>67.9\textsuperscript{b}</td>
<td>72.1\textsuperscript{a}</td>
<td>72.3\textsuperscript{a}</td>
</tr>
</tbody>
</table>


†Glu, Glucose; Gal, galactose; Rib, ribose.

‡DPG, Diphosphatidylglycerol; PG, phosphatidylglycerol; PC, phosphatidylcholine; PI, phosphatidylinositol; PIM, phosphatidylinositol mannoside; PE, phosphatidylethanolamine; PME, phosphatidylmethylthanolamine; PGL, phosphoglycolipid; PL, phospholipid; GL, glycolipid.
formation of single spores on substrate mycelium. Other phenotypic characteristics such as the surface of single spores, reduction of nitrate, coagulation and peptonization of milk, and chemotaxonomic characteristics could also be used to differentiate the new isolate from its closest relatives. Therefore, it is evident from the genotypic and phenotypic data that strain NEAU-Jh2-17T represents relatives. Therefore, it is evident from the genotypic and phenotypic data that strain NEAU-Jh2-17T represents relatives. Therefore, it is evident from the genotypic and phenotypic data that strain NEAU-Jh2-17T represents relatives. Therefore, it is evident from the genotypic and phenotypic data that strain NEAU-Jh2-17T represents relatives.

**Description of Streptomonospora halotolerans sp. nov.**

*Streptomonospora halotolerans* (ha.lo.to’le.rans. Gr. n. hals salt; L. part. tolerans tolerating; N.L. part. adj. halotolerans referring to the ability to tolerate high salt concentrations).

Gram-positive, aerobic. Good growth on ISP 2, 3, 5 and 7, Czapek’s agar and nutrient agar, moderate growth on ISP 6 agar, but no growth on ISP 4 agar. The aerial mycelium colour is white on ISP 3 and 5 agar. The substrate mycelium colour is in the yellow colour-series. Diffusible pigments are not produced on any of the media tested. At maturity, the aerial mycelium forms spore chains (smooth surfaces) and single spores (wrinkled surfaces) are borne on short sporophores of the substrate mycelium on ISP 3 medium. Aerial and substrate mycelia are not fragmented. Growth occurs at pH 7.0–9.0, the optimum being pH 8.0. Tolerates up to 10.0 % NaCl and grows at temperatures between 20 and 37 °C, with an optimum temperature of 28 °C. Positive for production of H2S and negative for reduction of nitrate, production of catalase, cellulase and urease, liquefaction of gelatin, hydrolysis of aesculin, starch and Tween 20, 40 and 80, and peptonization of milk. L-arabinose, D-fructose, D-galactose, D-glucose, inositol, lactose, maltose, D-mannose, raffinose, D-mannitol, L-rhamnose, D-ribose, D-sorbitol, sucrose and D-xylene are utilized as sole carbon sources. L-Alanine, L-arginine, L-asparagine, L-aspartic acid, L-glutamic acid, L-glutamine, L-serine, L-threonine and L-tyrosine are utilized as sole nitrogen sources but creatine and glycine are not. Cell wall contains meso-diaminopimelic acid and the whole-cell hydrolysates are glucose, ribose and galactose. The polar lipids contain diphosphatidylglycerol (DPG), phosphatidylethanolamine (PE), phosphatidylglycerol (PG), phosphatidylcholine (PC), phosphatidylinositol (PI), phosphatidylinositol mannoside (PIM), two unknown phospholipids (PLs) and two unknown glycolipids (GLs). The predominant menaquinones are MK-10(H2), MK-10(H4), MK-10(H6) and MK-10(H8). Major fatty acids (> 10 %) are C18:0 10-methyl, anteiso-C17:0 C16:0 10-methyl, iso-C15:0 C17:0 10-methyl and C18:0.

The type strain is NEAU-Jh2-17T ( = CGMCC 4.7218= JCM 30347T), isolated from muddy soil collected from a riverbank in Jilin Province, northern China. The DNA G+C content of the type strain is 71.82 mol%.

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