



Actinoplanes solisilvae sp. nov., Isolated from Birch Forest Soil

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Abstract

A novel actinomycete, designated strain LAM7112^T, was isolated from soil sample collected from a birch forest in Xinjiang Uygur Autonomous Region, China. The new isolate was found to be able to grow at 20–45 °C (optimum: 35 °C), pH 5.0–10.0 (optimum: 7.0) and in the presence of 0–10.0% (optimum: 3.0%) (w/v) NaCl. The isolate formed very scantily irregular sporangia containing motile spores on the substrate mycelium. Phylogenetic analysis of 16S rRNA gene sequences indicated that the new isolate was closely related to members of the family *Micromonosporaceae*, with highest similarities to *Actinoplanes ferrugineus* X-14695^T (97.4%), *Micromonospora zamorensis* DSM 45600^T (97.3%) and *Micromonospora aurantiaca* ATCC 27029^T (97.3%). In the phylogenetic trees, strain LAM7112^T formed a stable phylogenetic subclade within the genus *Actinoplanes*. The genomic DNA G + C content was 70.0 mol%. The major fatty acids (> 10%) were determined to be iso-C_{16:0}, anteiso-C_{15:0} and anteiso-C_{17:0}. The predominant menaquinones were identified as MK-9 (H₂), MK-9 (H₄) and MK-9 (H₆). The major polar lipids were found to be diphosphatidylglycerol, phosphatidylinositol and phosphatidylethanolamine. The diagnostic amino acid of the cell wall peptidoglycan was determined to be *meso*-diaminopimelic acid. The diagnostic sugars in cell hydrolysates were determined to be glucose and ribose. On the basis of its phenotypic, phylogenetic and chemotaxonomic characteristics, strain LAM7112^T (= CGMCC 4.7580^T = JCM 32512^T) is proposed to represent the type strain of a novel species of the genus *Actinoplanes*, for which the name *Actinoplanes solisilvae* is proposed.

Qingyun Ma and Qi Zhang have contributed equally to this study and share first authorship.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain LAM7112^T is MF784352. The GenBank accession number for the draft genome sequence of strain LAM7112^T is RJAC00000000.

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Introduction

Tetracycline is a broad-spectrum antibiotic widely used for human and animal health [19]. Because antibiotics cannot be absorbed or metabolized entirely by the animal, antibiotics administered are excreted into the environment. Tetracycline compounds and their transformation products can disrupt the structure and function of natural microbial communities and cause the emergence of antibiotic resistance among bacteria. In order to get effective tetracycline degrading microbial resources, an investigation study on soil samples collected from a birch (*Betula platyphylla*) forest in

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