ORIGINAL PAPER

Arthrobacter sulfonylureivorans sp. nov., isolated from a sulfonylurea herbicides degrading consortium enriched with birch forest soil

Xiaoyan Han[1,2] · Qi Zhang[3] · Qingyun Ma[1] · Delong Kong[1] · Yiqing Zhou[1] · Xu Jiang[1,5] · Wei Zhang[3] · Zhiyong Ruan[1,4]

Abstract

A gram-stain positive, aerobic, motile, rod-shaped bacterium, designated strain LAM7117[T], was isolated from a sulfonylurea herbicides degrading consortium enriched with birch forest soil. The optimal temperature and pH for the growth of strain LAM7117[T] were 35 °C and 7.5, respectively. Strain LAM7117[T] could grow in the presence of NaCl with concentration up to 9% (w/v). Strain LAM7117[T] formed a distinct phylogenetic subclade within the genus *Arthrobacter* in the phylogenetic trees built with 16S rRNA gene sequences and shared the highest similarity with *A. crystallopoietes* JCM 2522[T] (97.7%). The values of digital DNA–DNA relatedness and Avery Nucleotide Identity based on the genome sequences between LAM7117[T] and *A. crystallopoietes* JCM 2522[T] were 21.4 and 77.4%, respectively. The genomic DNA G + C content was 65.9 mol%. The major cellular fatty acids were anteiso-$C_{15:0}$, iso-$C_{16:0}$ and anteiso-$C_{17:0}$. The cell wall peptidoglycan contained the amino acids as glycine, lysine, alanine and glutamic acid. The major polar lipids present in strain LAM7117[T] were diphosphatidylglycerol, phosphatidylglycerol, phosphatidyl inositol, two unidentified glycolipids and one unidentified lipid. The predominant menaquinones of strain LAM7117[T] were MK-8 and MK-9. Based on the phenotypic characteristics, chemotaxonomic data and genotypic analyses, strain LAM7117[T] should be classified as a novel species of genus *Arthrobacter*, for which the name *Arthrobacter sulfonylureivorans* sp. nov. is proposed. The type strain is LAM7117[T] (=JCM 32824[T] = CGMCC 1.16681[T]).

Abbreviations
JCM   Japan collection of microorganisms
ANI   Average nucleotide identity

✉ Wei Zhang
zw0991@sohu.com

✉ Zhiyong Ruan
ruanzhiyong@caas.cn

Extended author information available on the last page of the article

Introduction

The genus *Arthrobacter* belongs to the family *Micrococcaceae* and was proposed by Conn and Dimmick (1947). Strains of the genus *Arthrobacter* have been isolated from various environmental sources, such as soil, clinical environments, marine sediment, cheese, mural paintings, water, sewage, the air, cyanobacterial mat and filtration substrate (Skyring and Quadling 1970; Pindi et al. 2010; Li et al. 2004). At the time of writing, the genus *Arthrobacter* comprises 100 species with validly published names (www.bacterio.net/arthrobacter.html). Members of this genus are aerobic, catalase-positive, Gram-stain positive with a high DNA G + C content in the range of 55–72 mol% (Xiang et al. 2011; Wang et al. 2015). The cell-wall peptidoglycan type is A3α or A4α, and the major polar lipids are diphosphatidylglycerol, phosphatidylglycerol, phosphatidylinositol and dimannosylglyceride. Those species with peptidoglycan type A3α usually contain MK-9(H_2) as the predominant menaquinone, while MK-9(H_2)/MK-8(H_2) or MK-8(H_2) comprise the major menaquinones in those species with peptidoglycan