**Arthrobacter deserti** sp. nov., isolated from a desert soil sample

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A Gram-stain-positive, non-motile, rod-shaped, catalase-positive and oxidase-negative bacterium, designated YIM CS25T, was isolated from a soil sample collected from Turpan desert in Xinjiang Uyghur Autonomous Region, north-western China. The isolate grew at 15–40 °C, at pH 6.0–8.0 and with 0–6 % (w/v) NaCl. The phylogenetic trees based on 16S rRNA gene sequences revealed that strain YIM CS25T belonged to the genus *Arthrobacter* and was closely related to *Arthrobacter halodurans* JSM 078085T (95.89 % similarity). The peptidoglycan type contained lysine, alanine and glutamic acid. The major whole-cell sugars were galactose, glucose and ribose. The isolate contained diphosphatidylglycerol, phosphatidylglycerol and phosphatidylinositol as the major polar lipids and MK-9 (H2) as the predominant menaquinone. The major cellular fatty acids were anteiso-C15 : 0, iso-C15 : 0, anteiso-C17 : 0, iso-C16 : 0 and anteiso-C17 : 1 ω9c. The genomic DNA G+C content was 68.3 mol%. On the basis of phylogenetic, phenotypic and chemotaxonomic analysis, strain YIM CS25T is considered to represent a novel species of the genus *Arthrobacter*, for which the name *Arthrobacter deserti* sp. nov. is proposed. The type strain is YIM CS25T (=KCTC 39544T=CGMCC 1.15091T).

The genus *Arthrobacter*, first proposed by Conn & Dimmick (1947), consists of a group of Gram-stain-positive, catalase-positive, aerobic and asporogenous rod-shaped bacteria that display a coryneform morphology (Keddie et al., 1986). The description of the genus *Arthrobacter* was later emended by Koch et al. (1995), with the reclassification of *Micrococcus agilis* as *Arthrobacter agilis*. Members of the genus *Arthrobacter* show a rod–coccus cell cycle, aerobic metabolism, little or no acid production from glucose, have lysine in the peptidoglycan and a high DNA G+C content of 55–72 mol% (Keddie et al., 1986; Busse et al., 2012; Wang et al., 2015). According to the peptidoglycan type and menaquinone composition, two main groups of species referred to as the 'globiformis' group and the 'nicotianae' group are distinguished within the genus *Arthrobacter* (Stackebrandt et al., 1983). The 'globiformis' group, including the type species *Arthrobacter globiformis* and the majority of other *Arthrobacter* species, contains peptidoglycan of the A3 type and

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**Abbreviation:** OPA, o-phthalaldehyde.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain YIM CS25T is KT946776.

One supplementary table and five supplementary figures are available with the online Supplementary Material.
menaquinone MK-9(H₂), while members of the ‘nicotianae’ group possess peptidoglycan variation A4γ and unsaturated menaquinones with 8–10 isoprenoid units (Schleifer & Kandler, 1972). At the time of writing, the genus *Arthrobacter* embraces 87 species with validly published names. Strains of the genus *Arthrobacter* have been isolated from some particular environments, such as alpine ice cave (Margesin et al., 2004), sewage (Kim et al., 2008) and contaminated soil (Arora & Jain, 2013). It has been reported that some species isolated from polluted environments were able to degrade poisonous substances or contaminants such as nitrophenols and chlorophenols (Kotoucková et al., 2004; Arora & Jain, 2013). During the course of a study on the microbial diversity of Turpan desert, a novel strain designated YIM CS25ᵀ was isolated from a soil sample. The results of a polyphasic taxonomic study indicated that strain YIM CS25ᵀ represents a novel species of the genus *Arthrobacter*.

Strain YIM CS25ᵀ was isolated from a soil sample collected from Turpan desert, north-western China (42° 12′ 33″ N 89° 17′ 47″ E). Two grams of the soil sample was diluted to 10⁻² and 10⁻⁴, spread on tryptic soy agar (TSA; Difco) supplemented with 100 mg nystatin l⁻¹, and incubated at 28 °C for 2 weeks. Colonies were picked and further purified on T5 agar medium (0.05 % tryptone, 0.1 % glucose, 0.2 % yeast extract, 0.1 % CaCO₃, 0.1 % trace salt, 1.5 % agar, pH 7.0). The purified strain was preserved as glycerol suspensions (25 %, v/v) at −80 °C.

Genomic DNA extraction and PCR amplification of the 16S rRNA gene were carried out as described by Li et al. (2007). The 16S rRNA gene sequence was purified and cloned using a PCR purification kit (Sangon Biotech) and pEASY-T1 cloning kit (Transgen Biotechnology) to obtain a complete sequence. The almost complete sequence of the 16S rRNA gene was determined by Sangon Biotech and compared with available 16S rRNA gene sequences of cultured species using the EzTaxon-e server (Kim et al., 2012). Multiple alignments of 16S rRNA gene sequences were carried out using the CLUSTAL X program (Thompson et al., 1997). Neighbour-joining (Saitou & Nei, 1987), maximum-likelihood (Felsenstein, 1981) and maximum-parsimony (Fitch, 1971) methods were employed to reconstruct the phylogenetic trees. Phylogenetic and molecular evolutionary analyses were performed using the software package MEGA version 6.0 (Tamura et al., 2013). Bootstrap analysis with 1000 replications (Felsenstein, 1985) was performed to assess the topology of the phylogenetic trees. The evolutionary distances were calculated using Kimura’s two-parameter model (Kimura, 1980). The DNA G+C content was determined by the thermal denaturation method (Marmur & Doty, 1962) with *Escherichia coli* JM-109 as the reference strain and was determined by HPLC.

Phylogenetic analyses based on the nearly complete 16S rRNA gene sequence of strain YIM CS25ᵀ (1491 bp) showed that the new isolate shared highest sequence similarities with *Citrococcus yambaruensis* PS9 (95.93 %) and *Arthrobacter halodurans* JSM 078085ᵀ (95.89 %). However, in the phylogenetic tree reconstructed by the neighbour-joining algorithm (Fig. 1), strain YIM CS25ᵀ clustered with *A. halodurans* JSM 078085ᵀ. This phylogenetic relationship was also confirmed in the trees generated with the maximum-parsimony (Fig. S1, available in the online Supplementary Material) and maximum-likelihood (Fig. S2) algorithms. The genomic DNA G+C content of strain YIM CS25ᵀ was 68.3 mol%, which was within the range reported for members of the genus *Arthrobacter* (55–72 mol%) (Busse et al., 2012).

Cell morphology of strain YIM CS25ᵀ was observed under a light microscope (model BH2; Olympus) and scanning electron microscope (ESEM-TMP; Philips) with cells grown on T5 medium. Gram staining was performed according to the standard Gram staining procedure and was confirmed by the KOH lysis test (Gregersen, 1978). Cell motility was studied using the hanging-drop technique (Bernardet et al., 2002). The temperature range for growth was investigated on T5 agar at different temperatures (4, 10, 15, 20, 28, 30, 37, 40, 45, 50, 55 and 60 °C). NaCl tolerance at various concentrations (0–10 %, w/v, at intervals of 1 %) were tested on T5 agar at 28 °C. Growth at pH 4.0–10.0 (in 0.5 pH unit intervals) was examined in T5 broth with the pH adjusted as described by Xu et al. (2005). Tests for the utilization of different carbon sources were carried out by using GEN III MicroPlates (Biolog). Catalase activity was detected by the production of bubbles with the addition of 3 % (v/v) H₂O₂; oxidase activity was tested by using 1 % N,N,N’,N’-tetramethyl-p-phenylenediamine. Hydrolysis of starch, gelatin, casein, urea and Tweenes (20, 40, 60, 80) was determined as described by Cowan & Steel (1965). Tests for nitrite reduction and H₂S production were performed as recommended by Smibert & Krieg (1994). Other physiological and biochemical properties were analysed using API 50CH/B, API 20NE and API ZYM strips (bioMérieux) according to the manufacturer’s instructions.

Strain YIM CS25ᵀ was aerobic, Gram-stain-positive, catalase-positive and oxidase-negative. Cells were non-sporulating, non-motile and rod-to-coccus-shaped (Fig. S3). Growth occurred at temperatures ranging from 15 to 40 °C (optimum 28 °C). The pH range for growth was pH 6.0–8.0 (optimum pH 7.0). Strain YIM CS25ᵀ was able to grow in the presence of 0–6 % (w/v) NaCl (optimum 0–4 %). Detailed phenotypic characteristics of strain YIM CS25ᵀ are given in the species description and compared with those of the reference strain *A. halodurans* JSM 078085ᵀ in Table 1.

For chemotaxonomic analyses, several characteristics such as cellular fatty acids were investigated using standard methods. Biomass for fatty acid analysis was obtained from cells growing on TSA at 28 °C for 2 days. The fatty acid methyl esters were analysed using the Microbial Identification System (MIDI Sherlock Version 6.0,
ACTINO) as described by Sasser (1990). Polar lipids were extracted and separated by two-dimensional TLC and identified using described procedures (Minnikin et al., 1979; Collins & Jones, 1980; Minnikin et al., 1984). Menaquinones were extracted according to the method of Collins et al. (1977) and were determined by HPLC (Kroppenstedt, 1982). Purified cell-wall preparations were obtained and hydrolysed as described by Kim & Lee (2011), and the detailed protocol was as follows: 2 g of wet cell material was suspended in 0.05 M phosphate buffer (pH 7.2) and the bacterial cells were broken ultrasonically. After centrifugation at 40 000 g for 20 min three times, the supernatant was transferred to a new tube, which was then centrifuged at 40 000 g for 25 min. After precipitated debris had been obtained, a 4 % SDS solution (6 ml) was added and the resuspended material was transferred to a glass tube and maintained at 100 °C for 40 min until it became colourless. It was then centrifuged at 40 000 g for 25 min at room temperature and washed with water. Hydrolysis of the purified cell walls was carried out by using 6 M HCl at 100 °C for 16 h. Amino acids in cell-wall hydrolysates were analysed by using pre-column derivatization with o-phthalaldehyde (OPA) by using HPLC as described by Tang et al. (2009). Eight amino acid standards (10 µl, 0.2 mM; Sigma) and 10 µl hydrolysed purified cell wall of strain YIM CS25T were dissolved in 30 µl 0.1 M borax buffer and 10 µl OPA (Agilent Technologies) was added and allowed to react for 50 s at

![Fig. 1. Neighbour-joining phylogenetic tree based on 16S rRNA gene sequences showing the relationship of strain YIM CS25T to related species of the genus *Arthrobacter*. *Rhodococcus ruber* DSM 43338T was used as an outgroup (not shown). Filled circles at nodes indicate generic branches that were also recovered by using the maximum-parsimony and maximum-likelihood algorithms. Bootstrap values (≥70 %) based on 1000 replications are shown at branch nodes. Bar, 0.005 nucleotide substitutions per site.](http://ijs.microbiologyresearch.org)
The major cellular fatty acids of strain YIM CS25<sup>T</sup> were anteiso-C<sub>15:0</sub> (51.4 %), iso-C<sub>15:0</sub> (18.9 %), anteiso-C<sub>17:0</sub> (8.7 %), iso-C<sub>16:0</sub> (5.0 %) and anteiso-C<sub>17:1</sub>ω<sub>9c</sub> (4.3 %). The detailed fatty acid profiles are shown in Table S1. The polar lipids consisted of diphosphatidylglycerol, phosphatidylglycerol, phosphatidylinositol, one unknown glycolipid, one unidentified phospholipid and an unidentified polar lipid (Fig. S4). The predominant menaquinone was MK-9(H<sub>2</sub>), which is common to the genus Arthrobacter. The purified amino acids in cell-wall hydrolysates were lysine, alanine and glutamic acid (Fig. S5), which is consistent with <i>Arthrobacter halodurans</i> JSM 078085<sup>T</sup>, whose peptidoglycan type was A4z (L-Lys–L-Ala–L-Glu) (Chen et al., 2009). The major whole-cell sugars were galactose, glucose and ribose. On the basis of phylogenetic, phenotypic and chemotaxonomic analysis, the isolated strain is distinct from other related species within the genus <i>Arthrobacter</i>. It is thus suggested that strain YIM CS25<sup>T</sup> represents a novel species of the genus <i>Arthrobacter</i>, for which the name <i>Arthrobacter deserti</i> sp. nov. is proposed.

### Description of Arthrobacter deserti sp. nov.

<i>Arthrobacter deserti</i> (des.erti. L. gen. n. deserti of a desert, referring to where the type strain was isolated).

Cells are Gram-stain-positive, aerobic, non-motile and exhibit a rod–coccus cycle. Colonies on T5 agar are white. Growth occurs at 15–40 °C, at pH 6.0–8.0 and in the presence of 0–6% (w/v) NaCl. Positive for catalase, and hydrolyses aesculin, Tween 40 and gelatin, but negative for oxidase, urease and hydrolysis of Tweens (20, 60, 80) and starch. Utilizes the following carbon sources: dextrin, maltose, trehalose, cellobiose, sucrose, turanose, raffinose, α-D-glucose, D-mannose, D-fructose, D-galactose, L-arabino-\(\text{\text{-}}\)\(\text{\text{-}}\)\(\text{\text{-}}\)\text{-}D-mannopyranoside, methyl α-D-\(\text{\text{-}}\)\(\text{\text{-}}\)\text{-}D-mannopyranoside, methyl α-D-glucopyranoside and L-glutamic acid, citric acid, D-malic acid, L-malic acid, bromosuccinic acid, acetoacetic acid, propionic acid and acetic acid. According to the results of API 20NE and 50CH strips, positive for assimilation of gluconate, adipate, malate, citrate, phenylacetate, erythritol, amylgdalin, arbutin and melibiose. However, negative for nitrate reduction, indole.

### Table 1. Differential physiological characteristics between strain YIM CS25<sup>T</sup> and its closest phylogenetic neighbour in the genus Arthrobacter, <i>Arthrobacter halodurans</i> JSM 078085<sup>T</sup>

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>YIM CS25&lt;sup&gt;T&lt;/sup&gt;</th>
<th>A. halodurans JSM 078085&lt;sup&gt;T&lt;/sup&gt;</th>
</tr>
</thead>
<tbody>
<tr>
<td>Colony colour</td>
<td>White</td>
<td>Yellow</td>
</tr>
<tr>
<td>Temperature for growth (°C)</td>
<td>15–40</td>
<td>4–37</td>
</tr>
<tr>
<td>pH range for growth</td>
<td>6–8</td>
<td>6–9</td>
</tr>
<tr>
<td>NaCl tolerance (% w/v)</td>
<td>0–6</td>
<td>0–10</td>
</tr>
<tr>
<td>Hydrolysis of Tween 80</td>
<td>−</td>
<td>+</td>
</tr>
<tr>
<td>Nitrate reduction</td>
<td>−</td>
<td>+</td>
</tr>
<tr>
<td>Acid phosphatase</td>
<td>+</td>
<td>−</td>
</tr>
<tr>
<td>Utilization of D-serine</td>
<td>−</td>
<td>+</td>
</tr>
<tr>
<td>Acid production from (API 50CH):</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Glycerol, 1,2,3,4-butanetetrol</td>
<td>+</td>
<td>−</td>
</tr>
<tr>
<td>Ribose, mannitol, arbutin, L-arabinose</td>
<td>+</td>
<td>−</td>
</tr>
<tr>
<td>Amygdalin, methyl α-D-mannoside</td>
<td>+</td>
<td>−</td>
</tr>
<tr>
<td>Methyl α-D-glucoside, cellobiose, melibiose</td>
<td>+</td>
<td>−</td>
</tr>
<tr>
<td>N-Acetylglosamine, trehalose, raffinose</td>
<td>+</td>
<td>−</td>
</tr>
<tr>
<td>Turanose, tagatose, glucosate</td>
<td>+</td>
<td>−</td>
</tr>
<tr>
<td>DNA G+C content (mol%)</td>
<td>68.3</td>
<td>63.3</td>
</tr>
</tbody>
</table>

On the basis of phylogenetic, phenotypic and chemotaxonomic analysis, the isolated strain is distinct from other related species within the genus Arthrobacter. It is thus suggested that strain YIM CS25<sup>T</sup> represents a novel species of the genus Arthrobacter, for which the name Arthrobacter deserti sp. nov. is proposed.
production, glucose acidification and arginine hydrodase.
In the API ZYM strip, positive for alkaline phosphatase,
esterase (C4), esterase lipase (C8), acid phosphatase,
naphthol-AS-BI-phosphohydrolase and α-glucosidase.
The predominant menaquinone is MK-9(H2). Polar
lipids consist of diphasphatidylglycerol, phosphatidylgly-
cerol, phosphatidylinositol, one unknown glycolipid, one
unidentified phospholipid and an unknown polar lipid.
Anteiso-C15:0, iso-C15:0 anteiso-C17:0, iso-C16:0 and ante-
iso-C17:1ω9C are the major cellular fatty acids (>4%).
The peptidoglycan type contains lysine, alanine and
glutamic acid, and the cell-wall sugars are galactose,
glucose and ribose.

The type strain, YIM CS25T (=KCTC 39544T=CGMCC
1.15091T), was isolated from Turpan desert in Xinjiang
Uyghur Autonomous Region, north-western China. The
genomic DNA G+C content of the type strain is 68.3 mol%.

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