Arthrobacter siderocapsulatus was proposed by Dubinina & Zhdanov (1975) to accommodate motile iron bacteria isolated from lake water. The authors considered the species would previously have been designated 'Siderocapsa eusphaera' and its assignment to the genus Arthrobacter was based primarily on morphological features in the developmental cycle and its capacity for Mn and Fe oxidation. The name was subsequently included in the Approved Lists of Bacterial Names (Skerman et al., 1980). However, it was later listed as a species incertae sedis in Bergey’s Manual of Systematic Bacteriology (Keddie et al., 1986). Some of the phenotypic properties of A. siderocapsulatus differ from Arthrobacter sensu stricto (Jones & Keddie, 1992; Koch et al., 1995): cells are Gram-negative, able to grow under microaerophilic conditions and produce acid from glucose. Collins (1986) also pointed out that the organism is misclassified as it has ubiquinone-9 and straight-chain saturated, monounsaturated, cyclopropane ring and 3-hydroxy fatty acids, which are typical of Gram-negative bacteria. Similar results were reported by Amadi & Alderson (1992). In the present investigation, 16S rDNA sequence and phenotypic data were employed to elucidate the taxonomic position of A. siderocapsulatus.

A. siderocapsulatus NCIMB 11286T (= BKM-B N 1122) was grown on Tryptic Soy Agar (TSA; Difco) at 30°C. The primary structure of the 16S rDNA was determined following the method of Chun & Goodfellow (1995). An almost complete sequence was obtained (1442 bp). A similarity search against nucleotide sequences held in the GenBank database using the BLAST program indicated that the 16S rDNA sequence of A. siderocapsulatus NCIMB 11286T was almost identical to that of the type strain of Pseudomonas putida (accession no. D37923; Yamamoto & Hara-yama, 1995) (99.85% nucleotide similarity, corresponding to two nucleotide differences). To rule out the possibility of contamination, we also determined the 16S rDNA sequence of A. siderocapsulatus DSM 7314T, and found the two sequences to be identical.

Phenotypic profiles of A. siderocapsulatus NCIMB 11286T and P. putida KCTC 1751T (= ATCC 12633T) were investigated in duplicate using API 20NE (BioMérieux) and BIOLOG GN2 kits, following the manufacturers’ instructions. The two strains showed identical reactions for tests included in the API 20NE kit. Similarly, among 95 carbon sources included in the BIOLOG kit, a clear discrepancy was found for only one substrate, namely malonic acid; a positive reaction was recorded for all tests, except for assimilation of malonic acid. The two strains also showed almost identical cellular fatty acid profiles. On the basis of evidence presented in this and earlier studies, it is proposed that Arthrobacter siderocapsulatus is a later subjective synonym of Pseudomonas putida (Trevisan 1889) Migula 1895AL.

Keywords: Arthrobacter siderocapsulatus, Pseudomonas putida, 16S rDNA sequencing, reclassification
was recorded for *P. putida* KCTC 1751T but not for *A. siderocapsulatus* NCIMB 11286T. The two type strains were then subjected to cellular fatty acid analysis using the Sherlock Microbial Identification System (MIDI), following the manufacturer’s instructions. They showed almost identical cellular fatty acid profiles (Table 1). The fatty acid profile of *A. siderocapsulatus* NCIMB 11286T was slightly different from those reported by Collins (1986) and Amadi & Alderson (1992). This discrepancy may be attributed to the growth media and culture conditions used for fatty acid analysis.

In addition to the new findings presented in this study, the original description of *A. siderocapsulatus* by Dubinina & Zhdanov (1975) provides further evidence for its assignment to *P. putida*; the cells are Gram-negative, rods or cocci (pleomorphic), motile by polar lophotrichous flagella, catalase-positive, and have DNA with a G+C content of 60.8 mol% (Palleroni, 1992). Published chemotaxonomic properties (Collins, 1986; Amadi & Alderson, 1992) of *A. siderocapsulatus* also matched those of *P. putida* strains (Oyaizu & Komagata, 1983). Thus it is clear from genetic, chemical and phenotypic evidence that *A. siderocapsulatus* NCIMB 11286T belongs to *P. putida*. We therefore propose that *Arthrobacter siderocapsulatus* Dubinina & Zhdanov 1975AL is a later subjective synonym of *Pseudomonas putida* (Trevisan 1889) Migula 1895AL.

### References


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**Table 1.** Cellular fatty acid composition (%) of *A. siderocapsulatus* NCIMB 11286T and *P. putida* KCTC 1751T

<table>
<thead>
<tr>
<th>Fatty acids</th>
<th>NCIMB 11286T</th>
<th>KCTC 1751T</th>
</tr>
</thead>
<tbody>
<tr>
<td>10:0 3-OH</td>
<td>3.8</td>
<td>3.7</td>
</tr>
<tr>
<td>12:0</td>
<td>1.9</td>
<td>3.2</td>
</tr>
<tr>
<td>12:0 2-OH</td>
<td>5.0</td>
<td>4.0</td>
</tr>
<tr>
<td>12:0 3-OH</td>
<td>4.6</td>
<td>4.3</td>
</tr>
<tr>
<td>16:1</td>
<td>32.6</td>
<td>35.9</td>
</tr>
<tr>
<td>16:0</td>
<td>27.4</td>
<td>27.0</td>
</tr>
<tr>
<td>17:0 cyclo</td>
<td>1.7</td>
<td>1.6</td>
</tr>
<tr>
<td>18:1</td>
<td>21.6</td>
<td>19.4</td>
</tr>
</tbody>
</table>

Only values over 1% are given.

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J. Chun and others