Genotypic and chemotaxonomic evidence for the reclassification of *Pseudomonas woodsii* (Smith 1911) Stevens 1925 as *Burkholderia andropogonis* (Smith 1911) Gillis et al. 1995

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It was reported before that *Pseudomonas woodsii* and *Burkholderia andropogonis* are phenotypically indistinguishable and probably represent the same taxon, for which the name *B. andropogonis* has been proposed. In the present study, it was found that *P. woodsii* and *B. andropogonis* strains were indistinguishable by whole-cell protein electrophoresis and have a highly similar cellular fatty acid composition. A high DNA–DNA binding value of 95% was found between the type strains of both species. In addition, the 16S rDNA sequence of *P. woodsii* strain LMG 2362T was very similar to that of *B. andropogonis* LMG 2129T (99.0%). The chemotaxonomic and genotypic data confirm that *P. woodsii* and *B. andropogonis* represent the same species, for which it is proposed to retain the name *B. andropogonis*.

Keywords: *Pseudomonas woodsii*, *Burkholderia andropogonis*, taxonomy

[Bacterium] *andropogonis* was described by Smith (1911) as the causative agent of stripe disease of sorghum (*Andropogon* sp.) and leaf spot of velvet bean (*Stizolobium deeringianum*). In the same publication, [Bacterium] *woodsii* was described as an important pathogen of carnation (*Dianthus caryophyllus*). Both species were transferred to the genus *Pseudomonas*: the former by Stevens (1925) and the latter by Stapp (1928). Later it was shown that [Pseudomonas] *andropogonis* and [Pseudomonas] *woodsii* both belonged to the solanacearum rRNA branch of the pseudomonads (rRNA group II) (Palleroni, 1984; De Vos et al., 1985). Based on DNA–rRNA hybridizations, [P.] *andropogonis* was transferred to the genus *Burkholderia* by Gillis et al. (1995) and the same authors stated that [P.] *woodsii* and *Burkholderia andropogonis* could be considered as synonyms because of the nearly identical phenotypic characteristics of both organisms. Here we present additional genotypic and chemotaxonomic evidence for this synonymy.

[P.] *woodsii* strains LMG 1279, LMG 2362T and LMG 2363 and *B. andropogonis* strains LMG 2126, LMG 2129T, LMG 2328 and LMG 6872 have been described previously (Gillis et al., 1995). These strains were grown aerobically on Trypticase Soy Agar (BBL) and incubated at 28 °C unless otherwise indicated. DNA was prepared as described by Pitcher et al. (1989) and DNA–DNA hybridizations were performed with photobiotin-labelled probes in microplate wells as described by Ezaki et al. (1989), using a HTS7000 Bio Assay Reader (Perkin-Elmer) for the fluorescence measurements. The hybridization temperature was 50 °C. The 16S rDNA sequences of [P.] *woodsii* LMG 2362T (accession no. AB021422; Anzai et al., 2000) and *B. andropogonis* LMG 2129T (accession no. X67037; Li et al., 1993) were retrieved from the GenBank database and compared with published 16S rDNA sequences of other pseudomonads. Phylogenetic analysis was performed using the GeneCompar 2.1 software package (Applied Maths). For SDS-PAGE of whole-cell proteins, strains were grown on nutrient agar (Oxoid CM3) supplemented with 0·04% (w/v) KH2PO4 and 0·24% (w/v) Na2HPO4, 12H2O (pH 6·8) and incubated aerobically at 28 °C. Preparation of whole-cell proteins and SDS-PAGE was performed as described previously (Pot et al., 1994). For fatty acid methyl ester analysis, a loopful of well-grown cells was harvested after an incubation period of 24 h at 28 °C, and fatty acid methyl esters were prepared, separated and identified using the Microbial Identification System (Microbial ID) as described before (Vandamme et al., 1992).

A high DNA–DNA binding value of 95% was found between [P.] *woodsii* LMG 2362T and *B. andropogonis*.
LMG 2129<sup>T</sup>, indicating that both strains belonged to the same species. The 16S rRNA sequence of [P.]
woodsii strain LMG 2362<sup>T</sup> was very similar to that of [B. andropogonis] LMG 2129<sup>T</sup> (99.4% similarity when the 1419 common bases were compared and with the exclusion of all unknown bases). Similarity levels towards other Burkholderia species were between 95.8% and 92.2%. In addition, the protein patterns of the [P.]
woodsii and [B. andropogonis] strains were highly similar (Fig. 1). Minor quantitative differences in cellular fatty acid composition occur between [P.]
woodsii and [B. andropogonis] strains, but their overall fatty acid composition was very similar (Table 1). The predominant fatty acids in all strains investigated were 16:0, 18:1ω7c and summed feature 3 (comprising 16:1ω7c or 15 iso 2-0H, or both).

The data from our polyphasic taxonomic study are in agreement with the previously published phenotypic data (Gillis et al., 1995) and confirm that [P.]
woodsii and [B. andropogonis] represent the same species. Based on Rule 42 of the International Code of Nomenclature of Bacteria (Lapage et al., 1992), we propose to retain the name Burkholderia andropogonis for this taxon.

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Table 1. Fatty acid composition of the strains studied

Expressed as a percentage. Those fatty acids for which the mean amount for all taxa was less than 1% are not given. Mean percentages and standard deviations are given.

<table>
<thead>
<tr>
<th>Strain*</th>
<th>13:1 AT 12–13</th>
<th>14:0</th>
<th>16:0</th>
<th>17:0 cyclo</th>
<th>16:1 2-0H</th>
<th>16:0 2-0H</th>
<th>16:0 3-0H</th>
<th>18:1ω7c</th>
<th>19:0 cyclo c&lt;sub&gt;9&lt;/sub&gt;c</th>
<th>18:1 2-0H</th>
<th>Summed feature 2 †</th>
<th>Summed feature 3 ‡</th>
</tr>
</thead>
</table>
| [P.]
woodsii (3) | 12±2 | 46±2 | 148±10 | 27±1 | 42±8 | 58±6 | 49±1 | 30±5 | 15±3 | 60±4 | 17±4 |
| B. andropogonis (4) | 12±1 | 47±2 | 145±9 | 52±7 | 46±1 | 61±0 | 48±0 | 25±1 | 120±20 | 17±0 | 60±4 | 15±1 |

* Numbers in parentheses represent the number of strains.
† Summed feature 2 comprises 14:0 3-0H, 16:1 iso I, an unidentified fatty acid with equivalent chain length value of 10 – 14, or any combination of these fatty acids. Summed feature 3 comprises 16:1ω7c or 15 iso 2-0H, or both.

Fig. 1. Electrophoretic protein patterns of a selection of strains investigated. The M<sub>r</sub> markers used (lane at the bottom) were (from left to right): lysozyme (M<sub>r</sub> 14500), trypsin inhibitor (M<sub>r</sub> 24000), glyceraldehyde-3-phosphate dehydrogenase (M<sub>r</sub> 36000), egg albumin (M<sub>r</sub> 45000), bovine albumin (M<sub>r</sub> 60000) and β-galactosidase (M<sub>r</sub> 116000).

References


