NOTE

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 2362^T was very similar to that of *B. andropogonis* LMG 2129^T (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 2362^T and LMG 2363 and *B. andropogonis* strains LMG 2126, LMG 2129^T, 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 2362^T (accession no. AB021422; Anzai *et al.*, 2000) and *B. andropogonis* LMG 2129^T (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 2362^T and *B. andropogonis*

Fig. 1. Electrophoretic protein patterns of a selection of strains investigated. The *M*_r markers used (lane at the bottom) were (from left to right): lysozyme (*M*_r 14500), trypsin inhibitor (20000), trypsinogen (24000), glyceraldehyde-3-phosphate dehydrogenase (36000), egg albumin (45000), bovine albumin (60000) and β -galactosidase (116000).

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.

Strain*	13:1 AT 12-13	14:0	16:0	17:0 cyclo	16:1 2-OH	16:0 2-OH	16:0 3-OH	18:1 ω 7c	19:0 cyclo ω 8c	18:1 2-OH	Summed feature 2†	Summed feature 3†
[<i>P.</i>] <i>woodsii</i> (3)	1.2 $\pm$ 0.2	4.6 $\pm$ 0.2	14.8 $\pm$ 1.0	2.7 $\pm$ 1.7	4.2 $\pm$ 0.8	5.8 $\pm$ 0.6	4.9 $\pm$ 0.1	30.2 $\pm$ 5.0	5.7 $\pm$ 3.5	1.5 $\pm$ 0.3	6.0 $\pm$ 0.4	17.8 $\pm$ 1.5
<i>B. andropogonis</i> (4)	1.2 $\pm$ 0.1	4.7 $\pm$ 0.2	14.5 $\pm$ 0.9	5.2 $\pm$ 0.7	4.0 $\pm$ 1.1	6.1 $\pm$ 0.7	4.8 $\pm$ 0.3	23.5 $\pm$ 1.3	12.0 $\pm$ 2.0	1.7 $\pm$ 0.4	6.0 $\pm$ 0.6	15.1 $\pm$ 1.1

* Numbers in parentheses represent the number of strains.

† Summed feature 2 comprises 14:0 3-OH, 16:1 iso I, an unidentified fatty acid with equivalent chain length value of 10.928, or 12:0 ALDE, or any combination of these fatty acids. Summed feature 3 comprises 16:1 ω 7c or 15 iso 2-OH, or both.

LMG 2129^T, indicating that both strains belonged to the same species. The 16S rDNA sequence of [*P.*] *woodsii* strain LMG 2362^T was very similar to that of *B. andropogonis* LMG 2129^T (99.0% 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, 18:1 ω 7c and summed feature 3 (comprising 16:1 ω 7c or 15 iso 2-OH, 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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