Bowmanella pacifica sp. nov., isolated from a pyrene-degrading consortium

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A taxonomic study was carried out on a strain, designated W3-3ATT, which was isolated from a pyrene-degrading consortium, enriched from sediment of the Pacific Ocean. Phylogenetic analysis based on 16S rRNA gene sequences indicated that strain W3-3ATT belonged to the genus Bowmanella, with the highest sequence similarity (99.0 %) with Bowmanella denitrificans BD1T, whereas sequence similarities with other species were less than 93 %. The nucleotide sequence similarity of both gyrB and rpoD genes of strain W3-3ATT and B. denitrificans BD1T was 81.1 %. However, the protein sequence similarities of the gyrB and rpoD genes of strain W3-3ATT and B. denitrificans BD1T were 96.1 % and 91.0 %, respectively. Phylogenetic trees based on these housekeeping genes showed that strain W3-3ATT and B. denitrificans BD1T formed a distinct lineage in the Gammaproteobacteria. The DNA–DNA hybridization value between strain W3-3ATT and B. denitrificans BD1T was 43 %. Strain W3-3ATT could also be differentiated from B. denitrificans BD1T based on the repetitive extragenic palindromic DNA–PCR fingerprint. The G+C content of the chromosomal DNA of strain W3-3ATT was 49 mol%. The combined genotypic and phenotypic data showed that strain W3-3ATT represents a novel species of the genus Bowmanella, for which the name Bowmanella pacifica sp. nov. is proposed, with the type strain W3-3ATT (=CGMCC 1.7086T=LMG 24568T=MCCC 1A01018T).

During the screening of pyrene-degrading bacteria, an Alteromonas-like bacterium, designated strain W3-3ATT, was isolated from a pyrene-degrading consortium, enriched from sediment of the Pacific Ocean in 2002 (Wang et al., 2008), and was selected for further characterization by using a polyphasic approach, including genotypic, chemo-

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Abbreviations: gyrB, DNA gyrase subunit B gene; rpoD, DNA-directed RNA polymerase subunit D gene; rep-PCR, repetitive extragenic palindromic DNA–PCR.

The GenBank/EMBL/DDBJ accession numbers for the nucleotide sequences reported in this study are EU440951 (Bowmanella pacifica W3-3ATT, 16S rRNA gene), EU441038 (B. pacifica W3-3AT, partial gyrb gene), EU441040 (B. pacifica W3-3AT, partial rpoD gene), EU441037 (Bowmanella denitrificans BD1T, partial gyrb gene) and EU441039 (B. denitrificans BD1T, partial rpoD gene).

Transmission electron micrographs of cells of strain W3-3ATT, dendrograms showing the phylogenetic positions of strain W3-3AT and related species based on gyrB and rpoD gene sequences, and results of rep-PCR and polar lipid analysis of strain W3-3AT and B. denitrificans BD1T and a table showing the cellular fatty acid contents of strain W3-3AT and B. denitrificans BD1T are available as supplementary material with the online version of this paper.
and minimum-evolution methods of Rzhetsky & Nei (1992, 1993) were determined by using bootstrap values based on 1000 replications. As the topology of the minimum-evolution tree was similar to that obtained using the neighbouring-joining method, the data generated using minimum-evolution are not shown.

A nearly full-length 16S rRNA gene sequence (1496 nt) of strain W3-3AT was determined. As shown in Fig. 1, the phylogenetic tree based on 16S rRNA gene sequences showed that strain W3-3AT and *Bowmanella denitrificans* BD1T formed an independent monophyletic cluster, with a high level of similarity (99.0 %); similarity values between the sequence of strain W3-3AT and those of other related taxa were all less than 93 %. The high level of 16S rRNA gene similarity confirmed that strain W3-3AT belonged to the genus *Bowmanella*.

For further comparison of strain W3-3AT with *B. denitrificans* BD1T, two housekeeping genes, the DNA gyrase subunit B gene (*gyrB*) and the DNA-directed RNA polymerase subunit D gene (*rpoD*) of the two strains were sequenced using the method described by Yamamoto et al. (2000). The similarity values between the *gyrB* and *rpoD* gene sequences of strain W3-3AT and *B. denitrificans* BD1T were both 81.1 %. In addition, the protein sequence of strain W3-3AT and those of other related taxa were determined. As shown in Supplementary Figs S1 and S2 (available in IJSEM Online), phylogenetic trees based on the sequences of the two housekeeping genes showed that strain W3-3AT and *B. denitrificans* BD1T formed an independent monophyletic cluster, similar to that obtained based on the 16S rRNA gene sequences. Strain W3-3AT could be differentiated from *B. denitrificans* BD1T based on these results.

DNA–DNA hybridization experiments were performed with genomic DNA of strain W3-3AT and *B. denitrificans* BD1T using a method that was described previously (Liu & Shao, 2005). Genomic DNA from *Escherichia coli* DH5α was used as an outgroup sample. Salmon sperm DNA was used as a negative control. The results showed that strain W3-3AT and *B. denitrificans* BD1T had low DNA–DNA relatedness (43 %), demonstrating their affiliation to different species in accordance with the cut-off value of 70 % recognized by Wayne et al. (1987) for discrimination of bacterial species. Strain W3-3AT and *B. denitrificans* BD1T were compared further by using repetitive extragenic palindromic DNA–PCR fingerprint (rep-PCR). The primer BOX-A1R (5'-CTACGGCAAGGCGACGTGACG-3') was used for rep-PCR fingerprint analysis (Versalovic et al. 1991). PCR was carried out with the following cycle conditions: denaturation for 5 min at 94 °C; 35 cycles of 15 s at 94 °C, 30 s at 53 °C and 8 min at 65 °C and a final extension at 65 °C for 8 min. The PCR products were separated by using agarose (2 %, w/v) gel electrophoresis. The rep-PCR result is shown in Supplementary Fig. S3 (in IJSEM Online). Strain W3-3AT showed a rep-PCR fingerprint pattern that was different from that of *B. denitrificans* BD1T. These results further confirmed the results of the DNA–DNA hybridization.

General cell morphology was studied under an Olympus inverted microscope (Olympus IX70) using 1 day-old cultures of strain W3-3AT grown on M2 agar medium. For electron microscopy, exponential-phase cells were harvested, suspended and absorbed on a Formvar–carbon-coated grid, and stained with phosphotungstic acid. The Gram reaction and catalase and oxidase activities were carried out according to Dong & Cai (2001). The optimal temperature for growth (using 4, 10, 20, 25, 37, 42 and 55 °C) and pH (from pH 3 to 12) were determined in M2 medium. Tolerance of NaCl was tested by using Luria–Bertani (LB) medium (10 g peptone l⁻¹ and 5 g yeast l⁻¹), supplemented with NaCl concentrations of 0, 0.5, 1, 3, 5, 7, 8, 9, 10, 12 and 15 % (w/v). Other biochemical tests were carried out in duplicate using API 20NE and API ZYM strips (bioMérieux) and the Biolog GN2 MicroPlate panel, according to the manufacturers’ instructions, with the adjustment that the NaCl concentration was 3.0 %. With the exception of the Biolog test, *B. denitrificans* BD1T was tested at the same time as strain W3-3AT for comparison.

Strain W3-3AT was found to be a Gram-negative, non-pigmented, rod-shaped bacterium that was motile by...
means of at least one polar flagellum (see Supplementary Fig. S4 in IJSEM Online). The differential physiological, biochemical and chemotaxonomic characteristics between strain W3-3A<sup>T</sup> and <i>B. denitrificans</i> BD1<sup>T</sup> are given in Table 1.

Antibiotic susceptibility tests were performed by using disc-diffusion methods as described by Shieh et al. (2003). Strain W3-3A<sup>T</sup> and <i>B. denitrificans</i> BD1<sup>T</sup> were tested at the same time in this study. The two strains were sensitive to chloramphenicol (30 μg per disk; Oxoid), ciprofloxacin (5 μg), co-trimoxazole (25 μg), erythromycin (15 μg), rifampicin (5 μg), gentamicin (10 μg), norfloxacin (10 μg) and polymyxin B (30 IU); and resistant to ampicillin (10 μg), carbenicillin (100 μg), cefadroxil (30 μg), cefazolin (30 μg), cefoperazone (30 μg), cephradin (30 μg), clindamycin (2 μg), lincomycin (2 μg), metronidazole (5 μg), minocycline (30 μg), oxytetracycline (1 μg), penicillin G (10 μg), ceftriaxone (30 μg), tetracycline (30 μg) and doxycycline (30 μg). The susceptibilities to other antibiotics that differentiate the two strains are shown in Table 1.

Fatty acids of whole cells of strain W3-3A<sup>T</sup> and <i>B. denitrificans</i> BD1<sup>T</sup> grown on 216L plate medium (1 g citrate, 0.5 g; agar, 15 g; pH 7.5) at 28 °C for 48 h were extracted, saponified and esterified. Analysis of the fatty acid methyl esters was performed using GC, according to the instructions of the MIDI system (Sasser, 1997). The fatty acid profile of <i>B. denitrificans</i> BD1<sup>T</sup> was determined in parallel with strain W3-3A<sup>T</sup>. The fatty acid profiles of the two strains are shown in Supplementary Table S1 (in IJSEM Online). The major fatty acids of the two strains were C<sub>16:1ω7c/ω6c</sub> (30.4 %), C<sub>16:0</sub> (23.3 %), C<sub>17:1ω8c</sub> (7.1 %) and C<sub>18:1ω9c</sub> (13.8 %), accounting for >74 % of the total fatty acids. The amounts of summed feature 3 (C<sub>16:1ω7c/ω6c</sub>) of the two strains were different. Strain W3-3A<sup>T</sup> has one peak corresponding to summed feature 3, which accounted for the content of 30.4 %. However, <i>B. denitrificans</i> BD1<sup>T</sup> had two close peaks that corresponded to summed feature 3, which accounted for 27.7 % and 6.7 %, respectively. As the fatty acid profiles of strain W3-3A<sup>T</sup> and <i>B. denitrificans</i> BD1<sup>T</sup> were determined under the same conditions, strain W3-3A<sup>T</sup> could be distinguished from <i>B. denitrificans</i> BD1<sup>T</sup> based on the differences in proportion.

Polar lipids of strain W3-3A<sup>T</sup> and <i>B. denitrificans</i> BD1<sup>T</sup> were extracted and separated according to the methods described by Tindall (1990). The results are shown in Supplementary Fig. S5 (in IJSEM Online). The major polar lipids of strain W3-3A<sup>T</sup> and <i>B. denitrificans</i> BD1<sup>T</sup> were an unidentified aminolipid, diphosphatidylglycerol, phosphatidylglycerol and phosphatidylethanolamine. Minor amounts of phosphatidylinositol and an unidentified lipid were also detected in both strains. In the study of Jean et al. (2006), only phosphatidylglycerol and phosphatidylethanolamine were detected.

The G+C content of the chromosomal DNA was determined according to the methods described by Mesbah & Whitman (1989), using a reversed-phase HPLC. The DNA G+C content of strain W3-3A<sup>T</sup> was 49 mol%, similar to that of <i>B. denitrificans</i> BD1<sup>T</sup>.

The high level of 16S rRNA gene similarity between strain W3-3A<sup>T</sup> and <i>B. denitrificans</i> BD1<sup>T</sup> confirmed that strain W3-3A<sup>T</sup> belonged to the genus <i>Bowmanella</i>. However, strain W3-3A<sup>T</sup> could be differentiated from <i>B. denitrificans</i> BD1<sup>T</sup> based on data from the gyrB and rpoD gene sequence comparisons, DNA–DNA hybridization and rep-PCR fingerprinting. On the basis of the data described above, strain W3-3A<sup>T</sup> should be placed in a novel species of the genus <i>Bowmanella</i>, for which the name <i>Bowmanella pacifica</i> sp. nov. is proposed.

### Table 1. Differential physiological characteristics of strain W3-3A<sup>T</sup> (<i>B. pacifica</i> sp. nov.) and <i>B. denitrificans</i> BD1<sup>T</sup>

Data for <i>B. denitrificans</i> BD1<sup>T</sup> were taken from Jean et al. (2006). Characteristics are scored as: w, weakly positive; +, positive; −, negative.

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Strain W3-3A&lt;sup&gt;T&lt;/sup&gt;</th>
<th>Strain BD1&lt;sup&gt;T&lt;/sup&gt;</th>
</tr>
</thead>
<tbody>
<tr>
<td>API 20NE&lt;sup&gt;*&lt;/sup&gt;</td>
<td>N-Acetyl-glucosamine, maltose</td>
<td>–</td>
</tr>
<tr>
<td>Susceptibility to antimicrobial agents&lt;sup&gt;*&lt;/sup&gt;</td>
<td>Furazolidone (15 μg)</td>
<td>+</td>
</tr>
<tr>
<td></td>
<td>Kanamycin (30 μg), neomycin (10 μg)</td>
<td>–</td>
</tr>
<tr>
<td></td>
<td>Ofloxacin (5 μg), piperacillin (100 μg), streptomycin (10 μg), vancomycin (30 μg)</td>
<td>–</td>
</tr>
<tr>
<td>Growth in 10 % NaCl&lt;sup&gt;*&lt;/sup&gt;</td>
<td>+</td>
<td>w</td>
</tr>
<tr>
<td>Utilization of:</td>
<td>d-Galactose</td>
<td>–</td>
</tr>
<tr>
<td></td>
<td>Melibiose</td>
<td>–</td>
</tr>
<tr>
<td>DNA G + C content (mol%)</td>
<td>49</td>
<td>50</td>
</tr>
</tbody>
</table>

<sup>*</sup>The characteristics of strain BD1<sup>T</sup> were determined in this study at the same time as strain W3-3A<sup>T</sup>.

Emended description of the genus <i>Bowmanella</i> Jean et al. 2006

Major polar lipids are an unidentified aminolipid, diphosphatidylglycerol, phosphatidylglycerol and phosphatidylethanolamine. Minor amounts of phosphatidylinositol and an unidentified lipid are also detected.

Description of <i>Bowmanella pacifica</i> sp. nov.

<i>Bowmanella pacifica</i> (pa.ci’fi.ca. L. fem. adj. pacificus, pertaining to the Pacific Ocean).

Cells are rod-shaped, 0.6–0.8 μm wide and 1.1–1.3 μm long, and motile by means of a single polar flagellum. Positive for oxidase, catalase, gelatinase, β-glucosidase (aesculin hydrolysis) and β-galactosidase, but negative for...
Gram reaction, indole production, urease and arginine dihydrolase. On M2 agar medium, produces smooth grey-
growing colonies after 72 h incubation at 28 °C, non-pigmented and slightly raised in the centre. In moderate halophilic;
grows in 0–10 % NaCl (optimum, 0.5–7 %) and at 10–
42 °C (optimum, 25–37 °C), but not at 4 or 45 °C. Growth
occurs at pH 6–10 (optimum, pH 8). Capable of
denitrification; does not ferment glucose. Principal fatty
acids are C16:1ω7c/ω6c, C16:0, C17:1ω9c C18:1ω7c. Among
the 95 carbon sources in the Biolog GN2 system,
potential reactions were obtained for utilization of acetic
acid, trehalose, gentiobiose, glycolyl l-aspartic acid, inosine,
lactulose, l-alanine, l-proline, sucrose, turanose, z-D-
lactose, cellobiose, dextrin, D-fructose, D-mannose, meli-
biose, glycogen, glycolyl l-glutamic acid, l-alaninamide, l-
alanyl glycinyl l-asparagine, l-glutamic acid, l-leucine,
maltose, N-acetyl-D-glucosamine, Tween 40, Tween 80, z-
cyclodextrin, z-D-glucose, β-hydroxybutyric acid and methyl
β-D-glucone. With API ZYM, positive for acid
phosphatase, alkaline phosphatase, esterase lipase (C8),
leucine aminopeptidase, N-acetyl-β-glucosaminidase,
naphthol-AS-Bl-phosphoamidase and valine aminopepti-
dase; weakly positive for cystine aminopeptidase, esterase
(C4), trypsin and z-chymotrypsin; and negative for lipase
(C14), z-fucosidase, z-galactosidase, z-glucosidase, z-
mannosidase, β-galactosidase, β-glucosidase and β-glucur-
onidase. Sensitive to chloramphenicol (30 μg), ciprofox-
acin (5 μg), co-trimoxazole (25 μg), erythromycin (15 μg),
furazolidone (15 μg), gentamicin (10 μg), norfloxacin
(10 μg), polymyxin B (30 IU) and rifampicin (5 μg); resistant
to ampicillin (10 μg), carbenicillin (100 μg), cefalexin
(30 μg), cefazolin (30 μg), cefoperazone (30 μg), cephradin
(30 μg), clindamycin (2 μg), kanamycin (30 μg), lincomycin
(2 μg), metronidazole (5 μg), minocycline (30 μg), neomycin
(10 μg), ofloxacin (5 μg), oxacillin (1 μg), penicillin G (10 μg),
piperacillin (100 μg), ceftriaxone (30 μg), streptomycin (10 μg),
tetracycline (30 μg), vancomycin (30 μg) and doxycycline (30 μg). The G+C content of the DNA of the type strain is 49 mol %.
Characteristics used to distinguish strain W3-3AT from
B. denitrificans BD1T are given in Table 1.

The type strain, W3-3A(1) (=CGMCC 1.7086T=LMG 24568T=CGMCC 1A01018T), was isolated from marine
sediment samples collected in 2002 from the Pacific Ocean.

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References

Ausbubel, F. M., Brent, R., Kingston, R. E., Moore, D. D., Seidman, J. G.,
Biology: a Compendium of Methods from Current Protocols in


Ivanova, E. P., Kripianova, E. A., Mikhailov, V. V., Levanova, G. F.,
Garagulya, A. D., Gorskhova, N. M., Vysotskii, M. V., Nicolau, D. V.,
Yumoto, N. & other authors (1998). Phenotypic diversity of
Pseudoalteromonas citrea from different marine habitats and emenda-

denitrificans gen. nov., sp. nov., a denitrifying bacterium isolated from
seawater from An-Ping Harbour, Taiwan. Int J Syst Evol Microbiol 56,
2463–2467.

alkane-degrading bacterium isolated from sea water and deep-sea

Mesbah, M. & Whitman, W. B. (1989). Measurement of deoxyguano-
sine/thymidine ratios in complex mixtures by high-performance
liquid chromatography for determination of the mole percentage
guanine+cytosine of DNA. J Chromatogr 479, 297–306.

testing minimum evolution trees. Mol Biol Evol 9, 945–967.

minimum-evolution method of phylogenetic inference.

method for reconstructing phylogenetic trees. Mol Biol Evol 4,
406–425.


Vibrio ruber sp. nov., a red, facultatively anaerobic, marine bacterium

Evolutionary Genetics Analysis (MEGA) software version 4.0. Mol.
Biol Evol 24, 1596–1599.

Tindall, B. J. (1990). Lipid composition of Halobacterium lacsuspro-

repetitive DNA sequences in eubacteria and application to finger-

A pyrene-degrading consortium from deep-sea sediment of the west
pacific and its key member Cycloclastics sp. P1. Environ Microbiol 10,

Wayne, L. G., Brenner, D. J., Colwell, R. R., Grimont, P. A. D., Kandler, O.,
authors (1987). International Committee on Systematic Bacteriology.
Report of the ad hoc committee on reconciliation of approaches to

intrageneric structure reconstructed from the nucleotide sequences
of gyrB and rpoD genes. Microbiology 146, 2385–2394.