Polaromonas aquatica sp. nov., isolated from tap water

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Two Gram-negative, rod-shaped, non-spore-forming bacteria (CCUG 39402T and CCUG 39797), isolated from different water sources, were investigated in a polyphasic study. The two isolates shared 100 % 16S rRNA gene sequence similarity and it was shown that they belonged to the Betaproteobacteria, most closely related to Polaromonas vacuolata (97-8 %) and Polaromonas naphthalenivorans (97-8 %). A polyamine pattern with 2-hydroxyputrescine and putrescine, as well as ubiquinone Q-8, were in agreement with characteristics of Betaproteobacteria. The presence of diphosphatidylglycerol, phosphatidylglycerol and phosphatidylethanolamine, and major fatty acids C16:1ω7c, C16:0 and C17:0 cyclo supported the affiliation of the two strains to the genus Polaromonas. The results of DNA–DNA hybridization and physiological and biochemical tests allowed genotypic and phenotypic differentiation of the two isolates from the two Polaromonas species with validly published names. They therefore represent a novel species, for which the name Polaromonas aquatica sp. nov. is proposed, with the type strain CCUG 39402T (=CIP 108776T).

The genus Polaromonas was proposed by Irgens et al. (1996) and until 2004 contained only one species, Polaromonas vacuolata. A second species, Polaromonas naphthalenivorans, was recently described by Jeon et al. (2004).

In a polyphasic taxonomic study, isolates CCUG 39402T and CCUG 39797 were investigated to assess their taxonomic position. Strain CCUG 39402T was isolated in 1998 on blood agar at 30 °C from tap water from a paper mill in Sweden. Strain CCUG 39797 was recovered from municipal drinking water in Sweden. Both isolates showed beige-coloured colonies on nutrient agar at 30 °C. Subcultivation was done on tryptone soy agar (TSA) at 30 °C for 24 h. Growth at 37 °C was also observed on nutrient agar and R2A agar, but not on SS agar (all from Oxoid).

Gram-staining was performed as described by Gerhardt et al. (1994). Cell morphology was studied under a Zeiss light microscope at ×1000, with cells grown for 3 days at 28 °C on TSA. The 16S rRNA gene was analysed as described by Kämpfer et al. (2003). Phylogenetic analysis was performed using the ARB software package (Strunk et al., 2000) and also MEGA version 2.1 (Kumar et al., 2001), after multiple alignment of data by CLUSTAL_X (Thompson et al., 1997). Distances (distance options according to the Kimura-2 model) and clustering with the neighbour-joining method and maximum-parsimony were performed by using bootstrap values based on 1000 replications (results not shown). The 16S rRNA gene sequences of strains CCUG 39402T and CCUG 39797 were continuous stretches of 1406 and 1407 bp, respectively. Sequence similarity calculations, following neighbour-joining analysis, indicated that the two sequences were identical. The closest relatives of the two strains were P. vacuolata (97-8 %) and P. naphthalenivorans (97-8 %). Lower sequence similarities (<97-0 %) were found with described species with validly published names from other genera of the Betaproteobacteria (Fig. 1).

Analyses of the fatty acids (Kämpfer & Kroppenstedt, 1996) of the novel strains and other Polaromonas species are detailed in Supplementary Table S1 in IJSEM Online. The fatty acid profiles of the two strains were very similar and were composed mainly of C16:1ω7c, C16:0 and C17:0 cyclo; in addition, the hydroxylated fatty acid C8:0 3-OH was detected. For P. naphthalenivorans, C10:0 3-OH was detected, which is in accordance with the report of Jeon et al. (2004). However, for P. vacuolata, C8:0 3-OH was found.

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of strains CCUG 39402T and CCUG 39797 are AM039830 and AM039831.

Contents of major fatty acids of P. aquatica sp. nov. and other Polaromonas species are available as supplementary material in IJSEM Online.
which was not detected in the original report of Irgens et al. (1996). It should be noted that the fatty acid profiles (Supplementary Table S1) were obtained on the basis of whole-cell extracts, grown on different culture media. This prevents a quantitative comparison of the results, but does give an indication of the presence or absence of diagnostic fatty acids.

Quinones, polar lipids, polyamines and cell-wall diamino acid were extracted from biomass which was grown on PYE medium (1 l: 3 g peptone from casein, 3 g yeast extract, pH 7-2). Quinone system and polar lipid profiles were analysed as described by Tindall (1990) and Altenburger et al. (1996). CCUG 39402\(^T\) and CCUG 39797 showed a quinone system with ubiquinone Q-8 predominant and traces of Q-9. Strains CCUG 39402\(^T\) (Fig. 2) and CCUG 39797 exhibited a polar lipid profile consisting of the major lipid phosphatidylethanolamine, moderate amounts of diphosphatidylglycerol and phosphatidylglycerol, and minor to trace amounts of phosphatidylserine, six unknown polar lipids, three unknown phospholipids and three unknown aminolipids. The presence of phosphatidylethanolamine, diphasphatidylglycerol and phosphatidylglycerol and lack of glycolipids were in agreement with the characteristics reported for \textit{P. naphthalenivorans} (Jeon et al., 2004). Polyamines were analysed as described previously (Busse & Auling, 1988; Busse et al., 1997). Both strains were characterized by the presence of the \textit{Betaproteobacteria}-specific diamine 2-hydroxyputrescine and putrescine. The content of 2-hydroxyputrescine in the two strains was significantly higher [69–77 \(\mu\)mol (g dry weight)\(^{-1}\)] than in any other species analysed so far (Busse & Auling, 1988; Auling et al., 1991) and might be a characteristic of this species.
Other polyamines were only detected in minor to trace amounts. The cell-wall diamino acid of the two strains, which was analysed according to Schleifer (1985), was meso-diaminopimelic acid.

Results of the physiological characterization are given in Table 1 and the species description, with methods as described previously (Kämpfer et al., 1991). Production of acid from sugars was examined in phenol red broth (Merck) according to the instructions of the manufacturer at room temperature for 7 days. Neither strain exhibited acid production with any sugar tested (see species description below). The presence of catalase was tested with H₂O₂.

DNA–DNA hybridization experiments were performed with the two strains and type strains of both established Polaromonas species using the method described by Ziemke et al. (1998), except that, for nick translation, 2 μg DNA was labelled during a 3 h incubation at 15 °C. The two isolates showed DNA–DNA hybridization values of 97·8 % (reciprocal analysis 89·7 %), clearly indicating that the two strains belong to the same species. Strain CCUG 39402ᵀ showed relatively low DNA–DNA hybridization values to P. vacuolata 34-Pᵀ (9 %, reciprocal 8 %) and P. naphthalenivorans DSM 15660ᵀ (5 %, reciprocal 14 %). The hybridization values of strain CCUG 39797 to P. vacuolata 34-Pᵀ (18 %, reciprocal 17 %) and P. naphthalenivorans DSM 15660ᵀ (8 %, reciprocal 10 %) were also very low. On the basis of these genotypic and phenotypic results, the two strains represent a novel species of the genus Polaromonas.

Comparison of the genomic fingerprints of CCUG 39402ᵀ and CCUG 39797 after ERIC-PCR, which was analysed as reported previously (Wieser & Busse, 2000), showed two bands of identical sizes at approximately 600 bp in each fingerprint (results not shown). This observation indicates that representatives of this species might be rapidly identified using ERIC-PCR.

Table 1. Physiological characteristics of strains of Polaromonas species

<table>
<thead>
<tr>
<th>Assimilation of:</th>
<th>1</th>
<th>2</th>
<th>3</th>
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<td>+*</td>
<td>−</td>
</tr>
<tr>
<td>Acetate</td>
<td>−</td>
<td>−</td>
<td>+* (⁺)</td>
<td>−</td>
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<tr>
<td>Propionate</td>
<td>−</td>
<td>−</td>
<td>+*</td>
<td>−</td>
</tr>
<tr>
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<td>−</td>
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</tr>
<tr>
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<td>(+) (⁺) +</td>
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<td>−</td>
<td>+</td>
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<td>+</td>
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<td>L-Alanine, β-alanine, L-aspartate</td>
<td>−</td>
<td>−</td>
<td>+*</td>
<td>−</td>
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</table>

*The test (based on a different method) was also performed by Irgens et al. (1996) and gave congruent results.

Description of Polaromonas aquatica sp. nov.

Polaromonas aquatica (aqu*a*tica. L. fem. adj. aquatica aquatic, from water).

Cells are motile, non-spore-forming rods (approx. 1–2 μm in length). Gram-negative, oxidase- and catalase-positive, showing an oxidative metabolism. Good growth occurs on R2A, TSA, PYE and nutrient agar at 25–30 °C; beige, translucent and shiny colonies with entire edges form within 24 h, with a diameter of approximately 2 mm. The quinone system is ubiquinone Q-8 with traces of Q-9. The fatty acid profile is largely composed of C₁₆:0 7c, C₁₆:0 and C₁₇:0 cyclo, and C₈:0 3-OH. The polar lipid profile consists of the major component phosphatidylethanolamine, moderate amounts of diphasphatidylglycerol and phosphatidylglycerol and minor to trace amounts of phosphatidylserine, six unknown polar lipids, three unknown phospholipids and three unknown aminolipids. The polyamine pattern contains the major components 2-hydroxyputrescine [69–77 μmol (g dry weight)⁻¹] and putrescine [58–76 μmol (g dry weight)⁻¹] and traces of spermidine [<1 μmol (g dry weight)⁻¹]. The cell-wall diamino acid is meso-diaminopimelic acid. Only a few carbon sources are utilized. Carbon source utilization (including differentiating characteristics for all Polaromonas species) is indicated in Table 1. Negative for production of acid from D-fructose, mannose, D-glucose, L-arabinose, raffinose and rhamnose.

The type strain is strain CCUG 39402ᵀ (=CIP 108776ᵀ). The type strain and a reference strain (CCUG 39797) were isolated from tap water in Sweden.

Acknowledgements

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References


