Pedobacter aquatilis sp. nov., isolated from drinking water, and emended description of the genus *Pedobacter*

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A Gram-negative, rod-shaped, non-spore-forming bacterium (strain AR107^T) was isolated from the drinking water distribution system of Seville (Spain). A polyphasic taxonomic study of the isolate resulted in its identification as a member of the genus *Pedobacter*. On the basis of 16S rRNA gene sequence comparisons, strain AR107^T was shown to belong to the phylum *Bacteroidetes*, being related to members of the genus *Pedobacter*. It showed 95.2 % sequence similarity with respect to the type strains of *Pedobacter heparinus* and *Pedobacter piscium*, and 94.1 % similarity with respect to the type strain of *Pedobacter himalayensis*. The predominant fatty acids were iso-C_{15:0}, iso-C_{17:0} 3-OH and summed feature 3 (iso-C_{15:0} 2-OH and/or C_{16:1} ω7c), which supports the affiliation of strain AR107^T to the genus *Pedobacter*. The DNA G + C content of this strain was 38 mol%. On the basis of the phenotypic, phylogenetic and genotypic results, strain AR107^T represents a novel species, for which the name *Pedobacter aquatilis* sp. nov. is proposed. The type strain is AR107^T (= CCM 7347^T = CECT 7114^T = JCM 13454^T).

The genus *Pedobacter* belongs to the family *Sphingobacteriaceae* and currently includes seven species: *Pedobacter heparinus* (the type species) (Steyn *et al.*, 1998), *Pedobacter africanus* (Steyn *et al.*, 1998), *Pedobacter caeni* (Vanparys *et al.*, 2005), *Pedobacter cryoconitis* (Margesin *et al.*, 2003), *Pedobacter himalayensis* (Shivaji *et al.*, 2005), *Pedobacter piscium* (Steyn *et al.*, 1998) and *Pedobacter saltans* (Steyn *et al.*, 1998). Members of this genus have been isolated from soil, fish, a nitrifying inoculum and glacier samples from the Tyrolean Alps (Austria) and a Himalayan mountain (Steyn *et al.*, 1998; Margesin *et al.*, 2003; Shivaji *et al.*, 2005).

The culturable bacterial population from tap water collected at different points of the distribution system of Seville (Spain) was studied in order to monitor the water quality in microbiological terms. Samples (25 l) of drinking water were concentrated by using a tangential flow filtration system (Filtron) and plated on plate count agar (Difco) and R2A (Difco) (Reasoner & Geldreich, 1985). Plates were incubated at 28 °C for 7 days and different morphological colonies were subsequently plated in order to obtain pure cultures. During the sampling campaign of January 2004, strain AR107^T was isolated on R2A medium.

The 16S rRNA gene of strain AR107^T was amplified using the universal primers 16F27 and 16R1488, as described previously by Mellado *et al.* (1995). Sequencing was

performed by NBT-Newbiotechnic (Seville, Spain), using an automated DNA sequencer (model 3100; Applied Biosystems). Alignment of the 16S rRNA gene sequence was carried out using the ARB software program (Ludwig *et al.*, 2004). Phylogenetic trees were inferred by using three tree-making algorithms: maximum parsimony (Kluge & Farris, 1969), neighbour joining (Saitou & Nei, 1987) and maximum likelihood (Felsenstein, 1991). The almost-complete 16S rRNA gene sequence of strain AR107^T (1450 bp) was compared by using BLAST with sequences of related organisms retrieved from the GenBank/EMBL/DBJ databases: the analysis showed that members of the genus *Pedobacter* were its closest phylogenetic neighbours. The sequence similarity values with respect to the type strains of species of the genus *Pedobacter* were generally between 94.1 % (with the type strain of *P. himalayensis*) and 95.2 % (with the type strains of *P. heparinus* and *P. piscium*), although the 16S rRNA gene sequence similarity with respect to the type strain of *P. saltans* was only 90.0 %. The maximum-parsimony phylogenetic tree constructed includes this strain in a separate branch within the genus *Pedobacter* (Fig. 1). When neighbour-joining and maximum-likelihood algorithms were used, similar phylogenetic trees were obtained (not shown), indicating the congruence of the phylogenetic position obtained for strain AR107^T. According to the phylogenetic data, the isolate belongs to the genus *Pedobacter*, but does not show 16S rRNA gene sequence similarity values higher than 95.2 % with respect to the species of the genus *Pedobacter*,

The GenBank/EMBL/DBJ accession number for the 16S rRNA gene sequence of strain AR107^T is AM114396.

Fig. 1. Maximum-parsimony tree, based on 16S rRNA gene sequence comparisons, showing the position of strain AR107^T and the type strains of *Pedobacter* and *Sphingobacterium* species. Bootstrap percentage values higher than 70% (from 1000 resamplings) are indicated at branching points. GenBank accession numbers are shown in parentheses. Bar, 2% sequence divergence.

indicating that this strain represents a novel species of this genus (Stackebrandt & Goebel, 1994).

Chromosomal DNA was isolated and purified according to the method described by Marmur (1961). The G+C content of genomic DNA was determined by the thermal denaturation method of Marmur & Doty (1962), using the equation of Owen & Hill (1979). The DNA G+C content of this strain is 38 mol%, a value that is within the range described for the genus *Pedobacter* (Steyn *et al.*, 1998).

The shape and motility of cells of strain AR107^T from a culture grown for 24 h in liquid R2A medium were observed under a phase-contrast microscope ($\times 1000$). Growth at different temperatures (4–40 °C), pH values (pH 3–12) and NaCl concentrations (0–5% NaCl) was tested on solid and liquid R2A medium. The isolate was also tested for its ability to grow on MacConkey agar (Difco), nutrient agar and TSA (Difco). Oxidase activity was determined by using a 1% solution of tetramethyl-*p*-phenylenediamine (Difco) (Kovács, 1956). Acid and gas production from glucose, lactose and sucrose were determined in Kligler's iron agar (Difco). Catalase activity was tested by picking a young colony and mixing it into a drop of H₂O₂. The methyl red and Voges–Proskauer reactions were tested in Clark–Lubs medium (Scharlau). Indole production was determined with Kovács' reagent in 1% tryptone broth. The Simmons' citrate test was performed (Simmons' citrate agar; Sigma). Medium containing 0.5% peptone, 0.5% NaCl and 0.001% phenol red was used (Cowan & Steel, 1974) for the determination of acid production from different carbohydrates. Nitrate reduction was tested for on nitrate broth containing 0.2% KNO₃ (Skerman, 1967). Urease activity was studied in Christensen's medium (Christensen, 1946). Hydrolysis of gelatin, starch and DNA was tested on the corresponding agar media (Scharlau). Tween 80 hydrolysis was tested in R2A medium containing 1% Tween 80 and 0.02% CaCl₂. Casein hydrolysis was tested in R2A medium supplemented with 2% skimmed milk (Difco) (Cowan & Steel, 1974). The presence of flexirubin-type pigments was examined as described by Bernardet *et al.* (2002). API 20NE and API ZYM strips (bioMérieux) were inoculated according to the manufacturer's instructions and incubated at 28 °C. An API 50 CH strip (bioMérieux) was inoculated as described by Kersters *et al.* (1984) and incubated at 28 °C. Antibiotic susceptibilities were determined according to the conventional Kirby–Bauer method (Bauer *et al.*, 1966).

Differential characteristics with respect to other species of *Pedobacter* are shown in Table 1 (see the species description for further details).

Fatty acid, polar lipid and quinone analyses were carried out by the Identification Service of the Deutsche Sammlung von Mikroorganismen und Zellkulturen (Braunschweig, Germany). Cells were cultured for 24 h at 28 °C on TSA medium at pH 7.0 (Miller, 1982; Kämpfer & Kroppenstedt, 1996). The predominant fatty acids of strain AR107^T were iso-C_{15:0}, iso-C_{17:0} 3-OH and summed feature 3 (iso-C_{15:0} 2-OH and/or C_{16:1} ω7c) (Table 2). Significant amounts of these fatty acids are characteristic of members of the family *Sphingobacteriaceae* (Steyn *et al.*, 1998). Like other members of the genus *Pedobacter*, strain AR107^T contains sphingolipids and MK-7 was the predominant menaquinone system.

As the phenotypic, genotypic and chemotaxonomic features of strain AR107^T are similar to those of *Pedobacter* species, and the phylogenetic results clearly show that it is also closely related to species of this genus, we propose to include it in a novel species, for which the name *Pedobacter aquatilis* sp. nov. is proposed. As *P. aquatilis* and the three most recently described species possess traits different from those described for the previously identified *Pedobacter* species, we also propose an emended description for the genus *Pedobacter*.

Emended description of *Pedobacter* Steyn *et al.* 1998

The genus description is as given by Steyn *et al.* (1998) and emended by Vanparys *et al.* (2005), with the following changes. Colonies on TSA have different pigmentations, from dirty yellow to creamy white or pink. Voges–Proskauer, gelatin hydrolysis and arginine dihydrolase tests are variable. Some strains grow on MacConkey agar. Isolated from soil, activated sludge, fish, glacier water, glacier cryoconite and drinking water. The type species is *Pedobacter heparinus*.

Description of *Pedobacter aquatilis* sp. nov.

Pedobacter aquatilis (a.qua.ti'lis. L. masc. adj. *aquatilis* aquatic, growing in water).

Gram-negative rods, 0.8–1 × 2–6 μm in size, occurring singly, in pairs or in short chains. Non-spore-forming. Cells are non-motile. Colonies on TSA plates are pale pink, round

Table 1. Differential characteristics of strain AR107^T and species of the genus *Pedobacter*

All taxa are positive for catalase, oxidase, phosphatase, β -galactosidase, aesculin hydrolysis and assimilation of D-glucose, D-mannose and N-acetylglucosamine. All strains are negative for reduction of nitrate, indole production, urease activity and assimilation of erythritol, L-sorbose, dulcitol and inositol. Unless otherwise indicated, data for reference species are taken from Vanparys *et al.* (2005) (*P. caeni*), Shivaji *et al.* (2005) (*P. himalayensis* and *P. cryoconitis*) and Steyn *et al.* (1998) (*P. heparinus*, *P. africanus*, *P. piscium* and *P. saltans*). +, Positive; –, negative; V, variable; NA, data not available.

Characteristic	Strain AR107 ^T	<i>P. caeni</i>	<i>P. himalayensis</i>	<i>P. cryoconitis</i>	<i>P. heparinus</i>	<i>P. africanus</i>	<i>P. piscium</i>	<i>P. saltans</i>
Habitat	Drinking water	Nitrifying inoculum	Glacier water	Glacier cryoconite	Soil	Soil, sludge	Fish	Soil
Colony pigmentation	Pink	Creamish white to yellow	Pale white	Creamish white	Translucent yellow	Translucent yellow	Yellow or creamish white	Light yellow
Temperature for growth (°C)								
Range	4–30	NA	4–25	1–25	5–30	NA	5–30	NA
Maximum	30	37	25	25	37*	37	25–30	25–30
Growth on MacConkey agar	–	NA	+	–	–	–	–	–
Gelatin hydrolysis	–	–	+	+	–	V	–	–
Arginine dihydrolase	–	–	+	–	–	–	NA	–
β -Glucosidase	+	–	+	+	–/+*	V	+	+
Lipase (C14)	–	–	–	–	–/–*	–	V*	–
Esterase lipase	+	+	NA	NA	+	+	+	+
Esterase	+	–	NA	NA	–/+*	–	+	–
Leucine arylamidase	+	+	NA	NA	+	+	+	+
Valine arylamidase	+	–	NA	NA	–/–*	V	+	V
Cystine arylamidase	+	–	NA	NA	–/+*	–	+	–
Trypsin	+	–	NA	NA	–/–*	–	+	–
α -Chymotrypsin	–	–	NA	NA	–/+*	–	+	–
Naphthol-AS-BI-phosphohydrolase	+	–	NA	NA	+	+	NA	NA
α -Galactosidase	–	–	NA	NA	–/+*	–	+	–
β -Glucuronidase	–	–	NA	NA	–/–*	–	V*	V
α -Glucosidase	+	–	NA	NA	+	+	+	+
N-Acetyl- β -glucosaminidase	+	–	NA	NA	+	+	+	+
α -Mannosidase	+	–	NA	NA	–/+*	V	+	–
α -Fucosidase	–	–	NA	NA	–	–	–	–
Assimilation of:								
D-Melezitose	+	–	–	–	–	–	–	–
D-Arabinose	–	–	+	–	–	V	–	V
L-Arabinose	+	+	+	+	+	V	+	+
Ribose	–	–	+	–	–	V	–	–
D-Galactose	+	–	+	+	+	+	V	+
L-Rhamnose	+	–	+	–	+	+	V	+
D-Cellobiose	+	+	+	+	+	+	+	–

Table 1. cont.

Characteristic	Strain AR107 [†]	<i>P. caeni</i>	<i>P. himalayensis</i>	<i>P. cryoconitis</i>	<i>P. heparinus</i>	<i>P. africanus</i>	<i>P. piscium</i>	<i>P. saltans</i>
Sucrose	+	+	+	+	+	+	+	V
D-Trehalose	+	+	+	+	+	+	+	V
D-Maltose	+	+	+	+	+	V	+	+
Inulin	–	–	+	+	–	–	–	–
Glycogen	–	–	–	+	–	–	–	–
Salicin	+	+	+	+	+	V	+	+
Mannitol	–	–	+	–	+	–	–	–
Glycerol	–	–	+	–	–	–	–	+
D-Xylose	–	–	+	+	+	V	+	+
D-Adonitol	–	–	+	–	+	–	–	+
D-Galactose	+	–	+	+	+	+	V	+
D-Fructose	+	–	+	+	+	V	+	V
D-Sorbitol	–	–	+	–	+	–	–	–
Arbutin	+	+	+	+	V	V	+	+
D-Raffinose	+	+	+	+	–	–	+	V
Starch	+	+	+	+	–	V	+	–
Xylitol	–	+	–	–	–	–	–	–
L-Fucose	–	–	+	+	+	V	–	–
Acid production from:								
D-Arabinose	–	NA	–	–	V	V	V	V
D-Glucose	–	NA	–	–	V/+ [*]	V	+ [*]	V
D-Mannose	–	NA	+	–	–	–	NA	NA
DNA G+C content (mol%)	38	42·7	41	43·4	42–43	43–45	40–43	36–38

^{*}Data from Takeuchi & Yokota (1992).

[†]Data from Vanparys *et al.* (2005).

Table 2. Cellular fatty acid composition (%) of strain AR107^T and *Pedobacter* species

Taxa: 1, strain AR107^T (data from this study); 2, *P. caeni*; 3, *P. africanus*; 4, *P. heparinus* (data in columns 2–4 from Vanparys *et al.*, 2005); 5, *P. himalayensis*; 6, *P. cryoconitis* (data in columns 5 and 6 from Shivaji *et al.*, 2005); 7, *P. piscium*; 8, *P. saltans* (data in columns 7 and 8 from Steyn *et al.*, 1998). –, Not detected; tr, trace (<1.0%). Summed feature 3 contains iso-C_{15:0} 2-OH and/or C_{16:1}ω7c.

Fatty acid	1	2	3	4	5	6	7	8
C _{14:0}	1.0	2.5	1.2	1.1	1.0	1.0	1.3	tr
C _{15:0}	1.6	—	—	—	—	—	—	1.4
C _{15:1} ω6c	2.1	—	tr	—	—	—	—	1.4
iso-C _{15:0}	28.9	21.3	33.3	27.9	33.0	15.0	26.2	31.4
anteiso-C _{15:0}	tr	tr	1.0	tr	—	—	2.6	2.9
C _{15:0} 2-OH	tr	tr	tr	tr	—	—	—	—
iso-C _{15:0} 3-OH	2.7	3.3	2.1	3.6	1.5	1.9	2.5	2.8
C _{16:0}	1.9	3.0	2.2	2.2	7.3	9.1	3.3	4.0
C _{16:1} ω5c	3.2	2.5	1.3	1.9	—	—	3.5	tr
C _{16:0} 3-OH	3.5	2.8	1.6	2.2	—	—	4.5	tr
iso-C _{17:1} ω9c	2.6	2.2	6.5	6.4	4.0	8.6	1.6	6.6
anteiso-C _{17:1} ω9c	—	tr	—	—	—	—	1.2	—
C _{17:0} 2-OH	tr	1.3	tr	2.7	—	—	—	—
iso-C _{17:0} 3-OH	13.6	12.1	16.1	14.0	6.0	4.2	9.2	12.7
Summed feature 3	30.7	39.9	26.5	31.7	22	29	42.1	28.5

and convex and 1–2 mm in diameter after 48 h at 28 °C. Pigments do not give the typical flexirubin reaction with 20 % KOH. Strictly aerobic. Does not grow in the presence of ≥2 % NaCl. Growth occurs at temperatures between 4 and 30 °C (optimal temperature 25–28 °C) and at pH 5–9 (optimal pH 6–7). Good growth occurs in R2A and TSA media but not on MacConkey agar medium. Positive for oxidase and catalase activities. Negative for urease activity. Negative for indole and in the methyl red and Voges–Proskauer tests. Does not produce H₂S from thiosulfate. Starch, aesculin and Tween 80 are hydrolysed but casein, DNA and gelatin are not. Negative result in the Simmons' citrate test. Nitrate is not reduced. Acid is not produced oxidatively from D-galactose, D-mannose, D-glucose, D-arabinose, fructose or D-maltose. Negative for glucose fermentation. L-Arabinose, D-galactose, D-mannose, D-glucose, D-fructose, L-rhamnose, methyl α-D-mannopyranoside, methyl α-D-glucopyranoside, N-acetylglucosamine, amygdalin, arbutin, salicin, D-cellobiose, D-maltose, D-lactose, D-melibiose, sucrose, D-trehalose, D-melezitose, D-raffinose, starch, gentiobiose and D-turanose are used as carbon sources. Glycerol, erythritol, D-arabinose, D-ribose, D-xylose, L-xylose, D-adonitol, methyl β-D-xylopyranoside, L-sorbose, dulcitol, inositol, D-mannitol, D-sorbitol, inulin, glycogen, xylitol, D-lyxose, D-tagatose, D-fucose, L-fucose, D-arabitol, L-arabitol, potassium gluconate, potassium 2-ketogluconate, potassium 5-ketogluconate, capric acid, adipic acid, malate, trisodium citrate and phenylacetic acid are not used as carbon sources. Alkaline and acid phosphatase, esterase (C4), esterase lipase (C8), leucine arylamidase, valine arylamidase, cystine arylamidase, trypsin, naphthol-AS-BI-phosphohydrolase, β-galactosidase, α-glucosidase, β-glucosidase, N-acetyl-β-glucosaminidase

and α-mannosidase are present. Arginine dihydrolase, lipase (C14), α-chymotrypsin, α-galactosidase, β-glucuronidase and α-fucosidase are not present. Resistant to the following antibiotics (μg per disc unless otherwise indicated): novobiocin (30), ampicillin (10), neomycin (10), nalidixic acid (30), streptomycin (10) bacitracin (10 U), penicillin (10 U), kanamycin (30), cefazolin (30) and gentamicin (10). Shows an intermediate reaction to the following antibiotics (μg per disc): chloramphenicol (30), tetracycline (30), erythromycin (15) and rifampicin (30). The fatty acid composition is shown in Table 2. Sphingolipids are present. MK-7 is the major respiratory quinone. The DNA G + C content is 38 mol%.

The type strain, strain AR107^T (=CCM 7347^T=CECT 7114^T=JCM 13454^T), was isolated from drinking water.

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