Pedobacter lentus sp. nov. and *Pedobacter terricola* sp. nov., isolated from soil

Jung-Hoon Yoon, So-Jung Kang, Sooyeon Park and Tae-Kwang Oh

Correspondence

Jung-Hoon Yoon
jhyoon@kribb.re.kr

Korea Research Institute of Bioscience and Biotechnology (KRIBB), PO Box 115, Yusong, Taejeon, Korea

Two Gram-negative, non-motile, pleomorphic bacterial strains, DS-40^T and DS-45^T, were isolated from a soil sample collected from Dokdo, Korea, and their exact taxonomic positions were investigated by using a polyphasic approach. Strains DS-40^T and DS-45^T grew optimally at 25 °C and pH 6.5–7.5 in the presence of 0–1.0% (w/v) NaCl. They contained MK-7 as the predominant menaquinone and possessed iso-C_{15:0}, iso-C_{17:0} 3-OH and summed feature 3 (C_{16:1}ω7c and/or iso-C_{15:0} 2-OH) as the major fatty acids. The DNA G+C contents of strains DS-40^T and DS-45^T were 36.0 and 36.8 mol%, respectively. Strains DS-40^T and DS-45^T shared a 16S rRNA gene sequence similarity of 96.7% and demonstrated a mean DNA–DNA relatedness level of 12%. Phylogenetic analyses based on 16S rRNA gene sequences revealed that strains DS-40^T and DS-45^T were most closely phylogenetically affiliated with the genus *Pedobacter* of the family *Sphingobacteriaceae*. Strains DS-40^T and DS-45^T exhibited 16S rRNA gene sequence similarity values of 91.4–93.7 and 89.9–91.6% with respect to the type strains of *Pedobacter* and *Sphingobacterium* species, respectively. Phenotypic and chemotaxonomic properties, together with the phylogenetic data, support the assignment of strains DS-40^T and DS-45^T as two distinct species within the genus *Pedobacter*. On the basis of phenotypic, phylogenetic and genetic data, strains DS-40^T and DS-45^T represent two novel species of the genus *Pedobacter*, for which the names *Pedobacter lentus* sp. nov. and *Pedobacter terricola* sp. nov. are proposed, respectively. The respective type strains are DS-40^T (=KCTC 12875^T=JCM 14593^T) and DS-45^T (=KCTC 12876^T=JCM 14594^T).

The genus *Pedobacter* was proposed by Steyn *et al.* (1998) through the reclassification of two *Sphingobacterium* species and the description of two novel species. Since then, the number of *Pedobacter* species has increased considerably with the description of many novel members of the genus. Interestingly, most of these recently described novel *Pedobacter* species have been isolated from a variety of soils from Korea (Yoon *et al.*, 2006, 2007; Hwang *et al.*, 2006; Ten *et al.*, 2006; Kwon *et al.*, 2007). In this study, we describe two bacterial strains, DS-40^T and DS-45^T, which were isolated from soil from the island of Dokdo, Korea. Comparative 16S rRNA gene sequence analyses indicated that the two strains are phylogenetically affiliated with the family *Sphingobacteriaceae*, which includes the genera *Pedobacter* and *Sphingobacterium* (Steyn *et al.*, 1998; Bernardet *et al.*, 2002). Accordingly, the aim of the present work was to determine the exact taxonomic positions of strains DS-40^T and DS-45^T by using a polyphasic

characterization that included phenotypic and chemotaxonomic analyses, a detailed phylogenetic investigation based on 16S rRNA gene sequences and determination of the levels of genetic relatedness.

A soil sample collected from the island of Dokdo (37° 14' 12" N 131° 52' 07" E), Korea, was used as the source for the isolation of bacterial strains. Strains DS-40^T and DS-45^T were isolated by means of the standard dilution plating technique, at 25 °C on 10 × diluted nutrient agar (NA; Difco). The morphological, physiological and biochemical characteristics of strains DS-40^T and DS-45^T were investigated using routine cultivation on NA at 25 °C. Cell morphology was examined by using light microscopy (E600; Nikon) and transmission electron microscopy. Flagellation was determined by using a Philips CM-20 transmission electron microscope with cells from exponentially growing cultures: for this purpose, the cells were negatively stained with 1% (w/v) phosphotungstic acid and the grids were examined after being air-dried. Gliding motility was determined as described by Bowman (2000), using quarter-strength nutrient broth (NB; Difco) solidified with 1% (w/v) agarose and R2A agar (Difco). The Gram reaction was determined by using the bioMérieux Gram stain kit

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of strains DS-40^T and DS-45^T are EF446146 and EF446147, respectively.

The cellular fatty acid compositions of strains DS-40^T and DS-45^T are available in a supplementary table with the online version of this paper.

Table 1. Differential phenotypic characteristics of strains DS-40^T and DS-45^T and *Pedobacter* species

Taxa: 1, strain DS-40^T (*Pedobacter lentus* sp. nov.); 2, strain DS-45^T (*Pedobacter terricola* sp. nov.); 3, *Pedobacter heparinus*; 4, *Pedobacter africanus*; 5, *Pedobacter piscium*; 6, *Pedobacter cryoconitis*; 7, *Pedobacter himalayensis*; 8, *Pedobacter caeni*; 9, *Pedobacter ginsengisoli*; 10, *Pedobacter panaciterrae*; 11, *Pedobacter sandarakinus*; 12, *Pedobacter roseus*; 13, *Pedobacter aquatilis*. Data are from Steyn *et al.* (1998), Margesin *et al.* (2003), Shivaji *et al.* (2005), Vanparys *et al.* (2005), Gallego *et al.* (2006), Hwang *et al.* (2006), Ten *et al.* (2006), Yoon *et al.* (2006, 2007) and this study. All are positive for catalase, oxidase, acid phosphatase (data for *P. cryoconitis*, *P. himalayensis*, *P. ginsengisoli* and *P. panaciterrae* from this study), alkaline phosphatase (data for *P. cryoconitis*, *P. himalayensis*, *P. ginsengisoli* and *P. panaciterrae* from this study), esterase lipase (C8) (data for *P. cryoconitis*, *P. himalayensis*, *P. ginsengisoli* and *P. panaciterrae* from this study), leucine arylamidase (data for *P. cryoconitis*, *P. himalayensis*, *P. ginsengisoli* and *P. panaciterrae* from this study) and assimilation of D-glucose, D-mannose, N-acetylglucosamine, lactose and trehalose. All are negative for Gram-stain, sporulation, urease, production of H₂S (not determined for *P. roseus*) and indole, nitrate reduction and for assimilation of erythritol (data for *P. ginsengisoli* and *P. panaciterrae* from this study), L-sorbose, dulcitol, D-lyxose (data for *P. himalayensis* from this study), D-tagatose (data for *P. himalayensis*, *P. ginsengisoli* and *P. panaciterrae* from this study), D-fucose (data for *P. himalayensis* from this study), L-arabitol (data for *P. himalayensis*, *P. ginsengisoli* and *P. panaciterrae* from this study), gluconate (data for *P. himalayensis* from this study), adipate (data for *P. himalayensis* from this study), caprate (data for *P. himalayensis* from this study), phenylacetate (data for *P. himalayensis* from this study), citrate and malate. +, Positive reaction; –, negative reaction; w, weakly positive reaction; v, variable reaction; ND, not determined. Data in parentheses are for the type strain.

Characteristic	1	2	3	4	5	6	7	8	9	10	11	12	13
Cell shape	Pleomorphic	Pleomorphic	Short rods	ND	Long rods	Long rods	Long rods	Rods	Rods	Rods	Rods/long rods	Short rods	Rods
Colony colour	Pale yellow to pale orange	Pale orange	Translucent yellow	Translucent yellow	Yellow or creamy white	Creamy white	Pale white	Creamy white to yellow	White	White	Orange	Pink	Pink
Maximum growth temperature (°C)	31	34	37	37	25–30	25	25	37	30	30	33	33	30
Growth on MacConkey medium	–	–	–	–	–	–	+	ND	–	–	–	+	–
Motility	–	–	Gliding	–	–	Gliding	–	–	–	–	–	–	–
Arginine dihydrolase	–	–	–	–	–	–	+	–	–	–	–	–	–
Lysine decarboxylase	–	–	+	+	+	–	–	ND	–	–	–	ND	ND
Tryptophan deaminase	–	–	–	–	–	–	+	ND	–	–	–	ND	ND
Hydrolysis of aesculin	+	+	+	+	+	+	+	+	–	–	+	+	+
Enzyme activities (API ZYM)													
Esterase (C4)	+	+	+	–	+	w†	w†	–	+	–†	+	+	+
Lipase (C14)	–	–	–*	–	v*	–†	–†	–	–†	–†	–	–	–
Valine arylamidase	+	+	–*	v(–)	+	+	–†	–	+	+	–	+	+
Cystine arylamidase	+	+	+	–	+	–†	–†	–	+	–†	w	–	+
Trypsin	–	–	–*	–	+	–†	–†	–	–†	–†	–	+	+
α-Chymotrypsin	+	+	+	–	+	–†	–†	–	–†	–†	–	+	–
Naphthol-AS-BI-phosphohydrolase	+	+	+	+	ND	+	+	–	+	+	+	+	+
α-Galactosidase	–	–	+	–	+	–†	–†	–	+	+	–	+	–
β-Galactosidase	+	+	+	+	+	–†	–†	+	–	+	+	–	+
β-Glucuronidase	–	–	–*	–	v*	–†	–†	–	–†	–†	–	–	–
α-Glucosidase	+	+	+	+	+	+	w†	–	+	+	+	+	+

Table 1. cont.

Characteristic	1	2	3	4	5	6	7	8	9	10	11	12	13
β -Glucosidase	—	—	+	v(—)	+	+	+	—	—†	—†	+	—	+
N-Acetyl- β -glucos-aminidase	+	+	+	+	+	+	+	—	+	+	+	+	+
α -Mannosidase	—	—	+	v(w)	+	—†	—†	—	—†	—†	—	—	+
α -Fucosidase	—	—	—*	—	—*	—†	w†	—	—†	w†	—	—	—
Assimilation of:													
Glycerol	—	—	—	—	—	—	+	—	+	+	—	+	—
D-Arabinose	—	—	—	v(—)	—	—	+	—	—	+	—	—	—
L-Arabinose	+	+	+	v(+)	+	+	+	+	—	+	—	+	+
Ribose	—	—	—	v(—)	—	—	+	—	—	—	—	—	—
D-Xylose	+	+	+	v(+)	+	+	+	—	+	+	—	ND	—
L-Xylose	—	—	—	—	—	—	+	+	+	+	—	+	—
Adonitol	—	—	+	—	—	—	+	—	—	—	—	—	—
Methyl β -D-xyloside	—	—	—	—	—	—	—	—	—†	+	—	ND	—
D-Galactose	—	—	+	+	v	+	+	—	+	—	+	+	+
D-Fructose	—	—	+	v(—)	+	+	+	—	+	—	—	+	+
L-Rhamnose	+	+	+	+	v	—	+	—	—	—	—	+	+
Inositol	—	—	—	—	—	—	—	—	—	+	—	—	—
Mannitol	—	—	+	—	—	—	+	—	—	—	—	—	—
D-Sorbitol	—	—	+	—	—	—	+	—	—	—	—	—	—
Methyl α -D-mannoside	—	—	+	+	—	—	+	+	+	+	w	ND	+
Methyl α -D-glucoside	—	—	+	+	+	w	+	+	+	+	w	ND	+
Amygdalin	—	+	+	+	+	+	+	+	+	+	+	+	+
Arbutin	—	w	v(—)	v(—)	+	+	+	+	—†	+	—	ND	+
Salicin	—	—	+	v(+)	+	+	+	+	+	+	+	+	+
Cellobiose	—	+	+	+	+	+	+	+	+	+	+	+	+
Maltose	+	+	+	v(+)	+	+	+	+	+	+	+	+	+
Melibiose	—	—	+	+	+	+	+	+	+	+	+	+	+
Sucrose	—	—	+	+	+	+	+	+	+	+	+	+	+
Inulin	—	—	—	—	—	w	+	—	+	+	—	+	—
Melezitose	—	—	—	—	—	—	—	—	+	+	—	ND	+
D-Raffinose	—	—	—	—	+	+	+	+	+	+	—	+	+
Starch	+	+	—	v(—)	+	+	+	+	—	—	+	+	+
Glycogen	w	+	—	—	—	+	—	—	—	—	+	+	—
Xylitol	—	—	—	—	—	—	—	+	—	—	—	—	—
Gentiobiose	w	+	+	v(+)	+	+	+	+	w†	+	+	+	+
D-Turanose	—	—	+	+	+	+	+	—	+	+	—	ND	+
L-Fucose	—	—	+	v(—)	—	—	+	—	—†	—†	—	—	—
D-Arabitol	—	—	—	—	—	—	—†	—	—†	+	—	—	—
2-Ketogluconate	—	—	—	—	—	+	—†	—	—†	—†	—	—	—
5-Ketogluconate	—	—	—	—	—	—	—†	—	—†	—†	+	ND	—

Table 1. cont.

Characteristic	1	2	3	4	5	6	7	8	9	10	11	12	13
Susceptibility to:													
Ampicillin	+	w	-	-	ND	-	-	-	†	†	-	-	-
Chloramphenicol	+	+	+	v	ND	-	-	-	†	†	+	+	+
Gentamicin	+	+	-	-	ND	-	ND	-	†	†	-	-	-
Kanamycin	+	+	-	ND	ND	-	-	-	†	†	-	-	-
Penicillin G	+	+	+	v	ND	-	-	ND	†	†	-	-	-
Tetracycline	+	+	+	-	ND	-	-	+	†	†	+	+	+
DNA G+C content (mol%)	36.0	36.8	42.3–43.0	43.7–44.2	40.4–41.0	43.4	41.0	42.7	43.6	44.2	39.7	41.3	38

*Data from Takeuchi & Yokota (1992).

†Data from this study.

according to the manufacturer's instructions. Growth at various temperatures (4–40 °C) was measured on NA. Growth in the absence of NaCl and at various NaCl concentrations (0.5 and 1.0–8.0 %, w/v, using increments of 1.0 %) was investigated in trypticase soy broth prepared according to the formula of the Difco medium, except that NaCl was excluded. The pH range for growth was determined in NB adjusted to various pH values (pH 4.5–10.5, using increments of 0.5 pH units), prior to sterilization, by the addition of HCl or Na₂CO₃. Growth under anaerobic conditions was determined after incubation in an anaerobic chamber on NA and on NA supplemented with nitrate, both of which had been prepared anaerobically using nitrogen. Catalase and oxidase activities and hydrolysis of casein, gelatin, hypoxanthine, starch, Tweens 20, 40, 60 and 80, tyrosine, urea and xanthine were determined as described by Cowan & Steel (1965). Aesculin hydrolysis and nitrate reduction were studied as described by Lanyi (1987). The presence of flexirubin-type pigments was investigated as described by Reichenbach (1992). Susceptibility to antibiotics was tested on NA plates using antibiotic discs containing the following: polymyxin B, 100 U; streptomycin, 50 µg; penicillin G, 20 U; chloramphenicol, 100 µg; ampicillin, 10 µg; cephalothin, 30 µg; gentamicin, 30 µg; novobiocin, 5 µg; tetracycline, 30 µg; kanamycin, 30 µg; lincomycin, 15 µg; oleandomycin, 15 µg; neomycin, 30 µg; and carbenicillin, 100 µg. Assimilation of various substrates, enzyme activities and other physiological and biochemical properties were tested by using the API 20E, API 20NE, API 50 CH and API ZYM systems (bioMérieux); assimilation of various substrates was determined by inoculating the API 50 CH strip with cells suspended in AUX medium (bioMérieux).

Cell biomass for DNA extraction and for isoprenoid quinone analysis was obtained from cultivation in NB at 25 °C. Chromosomal DNA was isolated and purified according to the method described by Yoon *et al.* (1996), with the exception that RNase T1 was used in combination with RNase A to minimize contamination with RNA. The 16S rRNA gene was amplified by using PCR with two universal primers, as described previously (Yoon *et al.*, 1998). Sequencing of the amplified 16S rRNA gene and phylogenetic analysis were performed as described by Yoon *et al.* (2003). Isoprenoid quinones were extracted according to the method of Komagata & Suzuki (1987) and analysed using reversed-phase HPLC and a YMC ODS-A (250 × 4.6 mm) column. For fatty acid methyl ester analysis, cell mass of strains DS-40^T and DS-45^T was harvested from NA plates after incubation for 7 days at 25 °C. The fatty acids were extracted and fatty acid methyl esters were prepared according to the standard protocol of the MIDI/Hewlett Packard Microbial Identification System (Sasser, 1990). The DNA G+C content was determined by using the method of Tamaoka & Komagata (1984), with the modification that DNA was hydrolysed and the resultant nucleotides were analysed by reversed-phase HPLC. DNA–DNA hybridization was performed fluorometrically by

Fig. 1. Neighbour-joining phylogenetic tree, based on 16S rRNA gene sequences, showing the positions of strains DS-40^T and DS-45^T and some related taxa. Bootstrap percentages (based on 1000 replications) >50% are shown at nodes. *Flavobacterium aquatile* ATCC 11947^T (GenBank accession number M62797) was used as an outgroup. Bar, 0.01 substitutions per nucleotide position.

using the method of Ezaki *et al.* (1989) with photobiotin-labelled DNA probes and microdilution wells. Hybridization was performed with five replications for each sample. The highest and lowest values obtained for each sample were excluded and the means of the remaining three values were quoted as the DNA–DNA relatedness values.

Morphological, cultural, physiological and biochemical characteristics of strains DS-40^T and DS-45^T are given in the species description (see below) or are shown in Table 1. The almost-complete 16S rRNA gene sequences of strains DS-40^T and DS-45^T determined in this study comprised 1477 and 1474 nt, respectively, representing approximately 96% of the *Escherichia coli* 16S rRNA gene sequence. The 16S rRNA gene sequence similarity between strains DS-40^T and DS-45^T was 96.7%. Comparative 16S rRNA gene sequence analyses showed that strains DS-40^T and DS-45^T were most closely related phylogenetically to the family *Sphingobacteriaceae* (Fig. 1). In the neighbour-joining tree constructed using 16S rRNA gene sequences, strains DS-40^T and DS-45^T formed a coherent cluster at a bootstrap resampling value of 99.9%, and this cluster joined the clade comprising *Pedobacter* species (Fig. 1). Strains DS-40^T and DS-45^T exhibited 16S rRNA gene sequence similarity values of 91.4–93.7% with respect to the type strains of recognized *Pedobacter* species and showed values of 89.9–91.6% with respect to the type strains of recognized *Sphingobacterium* species. When the DNAs of strains DS-40^T and DS-45^T were used individually as labelled DNA probes for cross-hybridization, the mean level of DNA–DNA relatedness was 12%, indicating that the two strains represent different genomic species (Wayne *et al.*, 1987).

Strains DS-40^T and DS-45^T contained MK-7 (at peak area ratios of approximately 87–94%) as the predominant isoprenoid quinone. The fatty acid profiles of strains DS-40^T and DS-45^T showed the presence of large amounts of branched and hydroxy fatty acids; the major components were iso-C_{15:0}, iso-C_{17:0} 3-OH and summed feature

3 (C_{16:1ω7c} and/or iso-C_{15:0} 2-OH) (see Supplementary Table S1, available in IJSEM Online). These fatty acid profiles were similar to those of other *Pedobacter* species, although there were differences in the proportions of some fatty acids, perhaps because of differences in the analytical conditions used (e.g. cultivation, extraction and apparatus) in the analyses (Shivaji *et al.*, 2005; Vanparys *et al.*, 2005; Yoon *et al.*, 2006, 2007; Hwang *et al.*, 2006; Ten *et al.*, 2006). The DNA G+C contents of strains DS-40^T and DS-45^T were 36.0 and 36.8 mol%, respectively. There were no distinct phenotypic, and, in particular, chemotaxonomic, properties to differentiate strains DS-40^T and DS-45^T from members of the genera *Pedobacter* and *Sphingobacterium* (Takeuchi & Yokota, 1992; Steyn *et al.*, 1998; Kim *et al.*, 2006; Yoon *et al.*, 2007). In view of the higher 16S rRNA gene sequence similarities and the absence of urease and α-fucosidase activities, it seems reasonable to place strains DS-40^T and DS-45^T within the genus *Pedobacter* rather than within the genus *Sphingobacterium* (Steyn *et al.*, 1998; Shivaji *et al.*, 2005; Vanparys *et al.*, 2005; Yoon *et al.*, 2006, 2007; Gallego *et al.*, 2006; Hwang *et al.*, 2006; Ten *et al.*, 2006). Strains DS-40^T and DS-45^T were distinguishable from recognized *Pedobacter* species on the basis of several phenotypic characteristics (listed in Table 1). The 16S rRNA gene sequence similarity values were low enough to justify the allocation of strains DS-40^T and DS-45^T as two novel species that are distinct from the recognized *Pedobacter* species (Stackebrandt & Goebel, 1994). Therefore, on the basis of the data presented, strains DS-40^T and DS-45^T represent two distinct novel species within the genus *Pedobacter*, for which the names *Pedobacter lentus* sp. nov. and *Pedobacter terricola* sp. nov. are proposed, respectively.

Description of *Pedobacter lentus* sp. nov.

Pedobacter lentus (len'tus. L. masc. adj. *lentus* slow, delayed, referring to the slow growth of the micro-organism).

Cells are Gram-negative, non-spore-forming, non-flagellated cocci, oval-shaped or rods ($0.4\text{--}0.8 \times 0.4\text{--}3.0\text{ }\mu\text{m}$). Colonies on NA are circular, convex, smooth, glistening, pale yellow to pale orange in colour and $0.3\text{--}0.5\text{ mm}$ in diameter after incubation for 7 days at $25\text{ }^{\circ}\text{C}$. Optimal growth occurs at $25\text{ }^{\circ}\text{C}$; growth occurs at 4 and $31\text{ }^{\circ}\text{C}$, but not at $32\text{ }^{\circ}\text{C}$. Optimal pH for growth is $6.5\text{--}7.5$; growth occurs at pH 6.0 and 8.0, but not at pH 5.5 or 8.5. Optimal growth occurs in the presence of $0\text{--}1.0\%$ (w/v) NaCl; growth does not occur in the presence of more than 4% (w/v) NaCl. Growth does not occur under anaerobic conditions on NA or on NA supplemented with nitrate. Starch and Tweens 20, 40, 60 and 80 are hydrolysed, but casein, gelatin, tyrosine, hypoxanthine and xanthine are not. Ornithine decarboxylase is absent. Flexirubin-type pigments are absent. Sensitive to carbenicillin, cephalothin, lincomycin, neomycin, polymyxin B and streptomycin, but not to novobiocin or oleandomycin. The predominant menaquinone is MK-7. Major fatty acids ($>10\%$ of total fatty acids) are iso- $\text{C}_{15:0}$ and iso- $\text{C}_{17:0}$ 3-OH. The DNA G+C content is $36.0\text{ mol}\%$ (HPLC). Other phenotypic properties are shown in Table 1.

The type strain, DS-40^T (=KCTC 12875^T=JCM 14593^T), was isolated from soil from the island of Dokdo, Korea.

Description of *Pedobacter terricola* sp. nov.

Pedobacter terricola (ter.ri.co'la. L. masc. n. *terricola* a dweller of soil, referring to the isolation of the type strain from soil).

Cells are Gram-negative, non-spore-forming, non-flagellated cocci, oval-shaped or rods ($0.3\text{--}0.6 \times 0.5\text{--}5.0\text{ }\mu\text{m}$); occasionally, a few cells $>10.0\text{ }\mu\text{m}$ in length may occur. Colonies on NA are circular, slightly convex, smooth, glistening, pale orange in colour and $1.0\text{--}1.2\text{ mm}$ in diameter after incubation for 7 days at $25\text{ }^{\circ}\text{C}$. Optimal growth occurs at $25\text{ }^{\circ}\text{C}$; growth occurs at 4 and $34\text{ }^{\circ}\text{C}$, but not at $35\text{ }^{\circ}\text{C}$. Optimal pH for growth is $6.5\text{--}7.5$; growth occurs at pH 5.5 and 8.0, but not at pH 5.0 or 8.5. Optimal growth occurs in the presence of $0\text{--}1.0\%$ (w/v) NaCl; growth does not occur in the presence of more than 7% (w/v) NaCl. Growth does not occur under anaerobic conditions on NA or on NA supplemented with nitrate. Tweens 20, 40, 60 and 80 are hydrolysed, but casein, gelatin, starch, tyrosine, hypoxanthine and xanthine are not. Ornithine decarboxylase is absent. Flexirubin-type pigments are absent. Sensitive to carbenicillin, cephalothin, lincomycin, neomycin, streptomycin and novobiocin and slightly sensitive to polymyxin B and oleandomycin. The predominant menaquinone is MK-7. Major fatty acids ($>10\%$ of total fatty acids) are iso- $\text{C}_{15:0}$, iso- $\text{C}_{17:0}$ 3-OH and summed feature 3 ($\text{C}_{16:1\omega7c}$ and/or iso- $\text{C}_{15:0}$ 2-OH). The DNA G+C content is $36.8\text{ mol}\%$ (HPLC). Other phenotypic properties are shown in Table 1.

The type strain, DS-45^T (=KCTC 12876^T=JCM 14594^T), was isolated from soil from the island of Dokdo, Korea.

Acknowledgements

This work was supported by the 21C Frontier Program of Microbial Genomics and Applications (grant MG05-0401-2-0) and the Support and Application Project of Biological Resources (grant M10508050004-06N0805-00410) from the Ministry of Science and Technology (MOST) of the Republic of Korea.

References

- Bernardet, J.-F., Nakagawa, Y. & Holmes, B. (2002). Proposed minimal standards for describing new taxa of the family *Flavobacteriaceae* and emended description of the family. *Int J Syst Evol Microbiol* **52**, 1049–1070.
- Bowman, J. P. (2000). Description of *Cellulophaga algicola* sp. nov., isolated from the surfaces of Antarctic algae, and reclassification of *Cytophaga uliginosa* (ZoBell and Upham 1944) Reichenbach 1989 as *Cellulophaga uliginosa* comb. nov. *Int J Syst Evol Microbiol* **50**, 1861–1868.
- Cowan, S. T. & Steel, K. J. (1965). *Manual for the Identification of Medical Bacteria*. London: Cambridge University Press.
- Ezaki, T., Hashimoto, Y. & Yabuuchi, E. (1989). Fluorometric deoxyribonucleic acid-deoxyribonucleic acid hybridization in micro-dilution wells as an alternative to membrane filter hybridization in which radioisotopes are used to determine genetic relatedness among bacterial strains. *Int J Syst Bacteriol* **39**, 224–229.
- Gallego, V., Garcia, M. T. & Ventosa, A. (2006). *Pedobacter aquatilis* sp. nov., isolated from drinking water, and emended description of the genus *Pedobacter*. *Int J Syst Evol Microbiol* **56**, 1853–1858.
- Hwang, C. Y., Choi, D. H. & Cho, B. C. (2006). *Pedobacter roseus* sp. nov., isolated from a hypertrophic pond, and emended description of the genus *Pedobacter*. *Int J Syst Evol Microbiol* **56**, 1831–1836.
- Kim, K.-H., Ten, L. N., Liu, Q.-M., Im, W.-T. & Lee, S.-T. (2006). *Sphingobacterium daejeonense* sp. nov., isolated from a compost sample. *Int J Syst Evol Microbiol* **56**, 2031–2036.
- Komagata, K. & Suzuki, K. (1987). Lipid and cell wall analysis in bacterial systematics. *Methods Microbiol* **19**, 161–207.
- Kwon, S.-W., Kim, B. Y., Lee, K.-H., Jang, K.-Y., Seok, S.-J., Kwon, J.-S., Kim, W.-G. & Weon, H. Y. (2007). *Pedobacter suwonensis* sp. nov., isolated from the rhizosphere of Chinese cabbage (*Brassica campestris*). *Int J Syst Evol Microbiol* **57**, 480–484.
- Lanyi, B. (1987). Classical and rapid identification methods for medically important bacteria. *Methods Microbiol* **19**, 1–67.
- Margesin, R., Spröer, C., Schumann, P. & Schinner, F. (2003). *Pedobacter cryoconitis* sp. nov., a facultative psychrophile from alpine glacier cryoconite. *Int J Syst Evol Microbiol* **53**, 1291–1296.
- Reichenbach, H. (1992). The order Cytophagales. In *The Prokaryotes. A Handbook on the Biology of Bacteria: Ecophysiology, Isolation, Identification, Applications*, 2nd edn, pp. 3631–3675. Edited by A. Balows, H. G. Trüper, M. Dworkin, W. Harder & K. H. Schleifer. New York: Springer.
- Sasser, M. (1990). Identification of bacteria by gas chromatography of cellular fatty acids. Newark, DE: MIDI Inc.
- Shivaji, S., Chaturvedi, P., Reddy, G. S. N. & Suresh, K. (2005). *Pedobacter himalayensis* sp. nov., from the Hamta glacier located in the Himalayan mountain ranges of India. *Int J Syst Evol Microbiol* **55**, 1083–1088.
- Stackebrandt, E. & Goebel, B. M. (1994). Taxonomic note: a place for DNA-DNA reassociation and 16S rRNA sequence analysis in the present species definition in bacteriology. *Int J Syst Bacteriol* **44**, 846–849.

- Steyn, P. L., Segers, P., Vancanneyt, M., Sandra, P., Kersters, K. & Joubert, J. J. (1998). Classification of heparinolytic bacteria into a new genus, *Pedobacter*, comprising four species: *Pedobacter heparinus* comb. nov., *Pedobacter piscium* comb. nov., *Pedobacter africanus* sp. nov. and *Pedobacter saltans* sp. nov. Proposal of the family *Sphingobacteriaceae* fam. nov. *Int J Syst Bacteriol* **48**, 165–177.
- Takeuchi, M. & Yokota, A. (1992). Proposals of *Sphingobacterium faecium* sp. nov., *Sphingobacterium piscium* sp. nov., *Sphingobacterium heparinum* comb. nov., *Sphingobacterium thalpophilum* comb. nov., and two genospecies of the genus *Sphingobacterium*, and synonymy of *Flavobacterium yabuuchiae* and *Sphingobacterium spiritivorum*. *J Gen Appl Microbiol* **38**, 465–482.
- Tamaoka, J. & Komagata, K. (1984). Determination of DNA base composition by reversed-phase high-performance liquid chromatography. *FEMS Microbiol Lett* **25**, 125–128.
- Ten, L. N., Liu, Q.-M., Im, W.-T., Lee, M., Yang, D.-C. & Lee, S.-T. (2006). *Pedobacter ginsengisoli* sp. nov., a novel DNase-producing bacterium isolated from soil of a ginseng field in South Korea. *Int J Syst Evol Microbiol* **56**, 2565–2570.
- Vanparys, B., Heylen, K., Lebbe, L. & De Vos, P. (2005). *Pedobacter caeni* sp. nov., a novel species isolated from a nitrifying inoculum. *Int J Syst Evol Microbiol* **55**, 1315–1318.
- Wayne, L. G., Brenner, D. J., Colwell, R. R., Grimont, P. A. D., Kandler, O., Krichevsky, M. I., Moore, L. H., Moore, W. E. C., Murray, R. G. E. & other authors (1987). International Committee on Systematic Bacteriology. Report of the ad hoc committee on reconciliation of approaches to bacterial systematics. *Int J Syst Bacteriol* **37**, 463–464.
- Yoon, J.-H., Kim, H., Kim, S.-B., Kim, H.-J., Kim, W. Y., Lee, S. T., Goodfellow, M. & Park, Y.-H. (1996). Identification of *Saccharomonospora* strains by the use of genomic DNA fragments and rRNA gene probes. *Int J Syst Bacteriol* **46**, 502–505.
- Yoon, J.-H., Lee, S. T. & Park, Y.-H. (1998). Inter- and intraspecific phylogenetic analysis of the genus *Nocardioides* and related taxa based on 16S rRNA gene sequences. *Int J Syst Bacteriol* **48**, 187–194.
- Yoon, J.-H., Kim, I.-G., Shin, D.-Y., Kang, K. H. & Park, Y.-H. (2003). *Microbulbifer salipaludis* sp. nov., a moderate halophile isolated from a Korean salt marsh. *Int J Syst Evol Microbiol* **53**, 53–57.
- Yoon, J.-H., Lee, M.-H., Kang, S.-J., Park, S.-Y. & Oh, T.-K. (2006). *Pedobacter sandarakinus* sp. nov., isolated from soil. *Int J Syst Evol Microbiol* **56**, 1273–1277.
- Yoon, M.-H., Ten, L. N., Im, W.-T. & Lee, S.-T. (2007). *Pedobacter panaciterrae* sp. nov., isolated from soil in South Korea. *Int J Syst Evol Microbiol* **57**, 381–386.