Pedobacter insulae sp. nov., isolated from soil

Jung-Hoon Yoon, So-Jung Kang, Hyun Woo Oh and Tae-Kwang Oh

Correspondence

Jung-Hoon Yoon
jhyoon@kribb.re.kr

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

A Gram-negative, non-motile, rod-shaped bacterium, DS-139^T, was isolated from a soil sample collected from Dokdo, Korea, and subjected to a polyphasic taxonomic analysis. Strain DS-139^T grew optimally at 25 °C and pH 6.5–7.5 in the presence of 0–0.5 % (w/v) NaCl. It contained MK-7 as the predominant menaquinone and iso-C_{15:0}, C_{16:1ω7c} and/or iso-C_{15:0} 2-OH and iso-C_{17:0} 3-OH as the major fatty acids. The DNA G+C content was 39.4 mol%. Phylogenetic analyses based on 16S rRNA gene sequences revealed that strain DS-39^T belongs to the genus *Pedobacter* in the family *Sphingobacteriaceae*. The similarity values between the 16S rRNA gene sequence of strain DS-139^T and those of the type strains of recognized *Pedobacter* species, except *Pedobacter saltans*, were in the range 93.9–96.7 %. The differential phenotypic properties, together with the phylogenetic distinctiveness, were sufficient to assign strain DS-139^T to a species that is separate from recognized *Pedobacter* species. On the basis of the phenotypic and phylogenetic data, therefore, strain DS-139^T represents a novel species of the genus *Pedobacter*, for which the name *Pedobacter insulae* sp. nov. is proposed. The type strain is DS-139^T (=KCTC 12820^T =DSM 18684^T).

The genus *Pedobacter* was proposed by Steyn *et al.* (1998) with the reclassification of two *Sphingobacterium* species and the description of two novel species. At the time of writing, the genus comprises 13 species with validly published names: *Pedobacter heparinus*, *P. piscium*, *P. africanus* and *P. saltans* (Steyn *et al.*, 1998), *P. cryoconitis* (Margesin *et al.*, 2003), *P. himalayensis* (Shivaji *et al.*, 2005), *P. caeni* (Vanparys *et al.*, 2005), *P. sandarakinus* (Yoon *et al.*, 2006), *P. roseus* (Hwang *et al.*, 2006), *P. aquatilis* (Gallego *et al.*, 2006), *P. ginsengisoli* (Ten *et al.*, 2006), *P. panaciterrae* (Yoon *et al.*, 2007) and *P. suwonensis* (Kwon *et al.*, 2007). In this study, we report on the taxonomic characterization of a bacterial strain, DS-139^T, that is phylogenetically closely related to the genus *Pedobacter*.

A soil sample collected from Dokdo (37° 14' 12" N 131° 52' 07" E), an island in Korea, was used as the source for the isolation of bacterial strains. Strain DS-139^T was isolated by means of the standard dilution plating technique, at 25 °C on 10-fold-diluted nutrient agar (Difco). The morphological, physiological and biochemical characteristics of strain DS-139^T were investigated using routine cultivation on trypticase soy agar (TSA; Difco) at 25 °C. The cell morphology was examined using light microscopy (E600; Nikon) and transmission electron microscopy. Flagellation was determined by using a Philips CM-20 transmission electron microscope to investigate cells from exponentially

growing cultures. 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 trypticase soy broth (TSB; Difco) solidified with 1 % (w/v) agarose and R2A agar (Difco). The Gram reaction was determined by using the bioMérieux Gram stain kit according to the manufacturer's instructions. Growth at various temperatures (4–40 °C) was measured on TSA. Growth in the absence of NaCl and at various NaCl concentrations (0.5 %, w/v, and 1.0–5.0 %, w/v, in 1.0 % increments) was investigated in trypticase soy broth prepared according to the formula of the Difco medium except that no NaCl was used. The pH range for growth was determined in nutrient broth (Difco) adjusted to various pH values (pH 4.5–10.5 in 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 TSA and on TSA supplemented with nitrate, both of which had been prepared anaerobically using nitrogen. Catalase and oxidase activities and the hydrolysis of casein, gelatin, hypoxanthine, starch, Tweens 20, 40, 60 and 80, tyrosine, urea and xanthine were determined as described by Cowan & Steel (1965). DNase activity was examined by using DNase test agar with methyl green (Difco). Aesculin hydrolysis and nitrate reduction were studied as described previously (Lanyi, 1987). The presence of flexirubin-type pigments was investigated as described by Reichenbach (1992). Antibiotic susceptibility was tested on TSA plates,

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain DS-139^T is EF100697.

Table 1. Differential phenotypic characteristics of strain DS-139^T and some phylogenetically related *Pedobacter* species

Species: 1, *P. insulae* sp. nov. (strain DS-139^T); 2, *P. heparinus*; 3, *P. africanus*; 4, *P. piscium*; 5, *P. cryoconitis*; 6, *P. himalayensis*; 7, *P. caeni*; 8, *P. ginsengisoli*; 9, *P. panaciterrae*. Data are from Steyn *et al.* (1998), Margesin *et al.* (2003), Shivaji *et al.* (2005), Vanparrys *et al.* (2005), Ten *et al.* (2006), Yoon *et al.* (2006) and this study. All species are positive for catalase, oxidase, acid phosphatase^{abcd}, alkaline phosphatase^{abcd} and leucine arylamidase^{abcd} and for assimilation of D-glucose, D-mannose, D-cellobiose, N-acetylglucosamine, amygdalin^c, lactose, melibiose, sucrose and trehalose. All species stain Gram-negative and are negative for sporulation, urease, production of indole and H₂S, nitrate reduction, assimilation of erythritol^{bd}, L-sorbose, dulcitol, D-lyxose^c, D-tagatose^{bcd}, D-fucose^c, L-arabitol^{bcd}, gluconate^c, 5-ketogluconate^{bcd}, adipate^c, caprate^c, phenylacetate^c, citrate and malate and for susceptibility to ampicillin^{bd} (no data for *P. piscium*) and kanamycin^{bd} (no data for *P. africanus* or *P. piscium*). +, Positive; –, negative; w, weakly positive; v, variable (data in parentheses are for the type strain); ND, no data available.

Characteristic	1	2	3	4	5	6	7	8	9
Cell shape	Rod	Short rod	ND	Long rod	Long rod	Long rod	Rod	Rod	Rod
Colony colour*	LY	TY	TY	Y/CWH	CWH	WH	CWH–Y	WH	WH
Maximum growth temperature (°C)	31	37	37	25–30	25	25	37	30	30
Growth on MacConkey agar	–	–	–	–	–	+	ND	–	–
Gliding motility	–	+	–	–	+	–	–	–	–
Arginine dihydrolase	–	–	–	–	–	+	–	–	–
Lysine decarboxylase	–	+	+	+	–	–	ND	–	–
Tryptophan deaminase	–	–	–	–	–	+	ND	–	–
Hydrolysis of aesculin	+	+	+	+	+	+	+	–	–
Enzyme activity (API ZYM)									
Esterase (C4)	–	+†	–	+†	W ^{a†}	W ^b	–	+ ^c	– ^d
Esterase lipase (C8)	–	+	+	+	+ ^a	+ ^b	+	+ ^c	+ ^d
Lipase (C14)	–	–†	–	v†	– ^a	– ^b	–	– ^c	– ^d
Valine arylamidase	+	–†	v (–)	+†	+ ^a	– ^b	–	+ ^c	+ ^d
Cystine arylamidase	–	+†	–	+†	– ^a	– ^b	–	+ ^c	– ^d
Trypsin	–	–†	–	+†	– ^a	– ^b	–	– ^c	– ^d
α-Chymotrypsin	+	+†	–	+†	– ^a	– ^b	–	– ^c	– ^d
α-Galactosidase	–	+†	–	+†	– ^a	– ^b	–	+ ^c	+ ^d
β-Galactosidase	–	+	+	+	– ^a	– ^b	+	–	+
β-Glucuronidase	–	–†	–	v†	– ^a	– ^b	–	– ^c	– ^d
α-Glucosidase	+	+	+	+	+ ^a	W ^b	–	+ ^c	+ ^d
β-Glucosidase	–	+†	v (–)	+†	+	+	–	– ^c	– ^d
N-Acetyl-β-glucosaminidase	+	+	+	+	+ ^a	+ ^b	–	+ ^c	+ ^d
α-Mannosidase	–	+†	v (w)	+†	– ^a	– ^b	–	– ^c	– ^d
α-Fucosidase	–	–†	–	–†	– ^a	W ^b	–	– ^c	W ^d
Assimilation of:									
Glycerol	+	–	–	–	–	+	–	+	+
D-Arabinose	–	–	v (–)	–	–	+	–	–	+
L-Arabinose	+	+	v (+)	+	+	+	+	–	+
Ribose	–	–	v (–)	–	–	+	–	–	–
D-Xylose	+	+	v (+)	+	+	+	–	+	+
L-Xylose	–	–	–	–	–	+	+	+	+
Adonitol	+	+	–	–	–	+	–	–	–
Methyl β-D-xyloside	–	–	–	–	–	–	–	– ^c	+ ^d
D-Galactose	–	+	+	v	+	+	–	+	–
D-Fructose	–	+	v (–)	+	+	+	–	+	–
Assimilation of:									
L-Rhamnose	w	+	+	v	–	+	–	–	–
Inositol	–	–	–	–	–	–	–	–	+
Mannitol	–	+	–	–	–	+	–	–	–
D-Sorbitol	–	+	–	–	–	+	–	–	–
Methyl α-D-mannoside	w	+	+	–	–	+	+	+ ^c	+ ^d
Methyl α-D-glucoside	+	+	+	+	w	+	+	+ ^c	+ ^d
Arbutin	+	v (–)	v (–)	+	+	+	+	– ^c	+ ^d
Salicin	+	+	v (+)	+	+	+	+	+	+
Maltose	+	+	v (+)	+	+	+	+	+	+
Inulin	–	–	–	–	w	+	–	+	+

Table 1. cont.

Characteristic	1	2	3	4	5	6	7	8	9
D-Melezitose	—	—	—	—	—	—	—	+ ^c	+ ^d
D-Raffinose	—	—	—	+	+	+	+	+	+
Starch	+	—	v (—)	+	+	+	+	—	—
Glycogen	+	—	—	—	+	—	—	—	—
Xylitol	—	—	—	—	—	—	+	—	—
Gentiobiose	+	+	v (+)	+	+	+ ^b	+	w ^c	+ ^d
D-Turanose	w	+	+	+	+	+ ^b	—	+ ^c	+ ^d
L-Fucose	—	+	v (—)	—	—	+	—	— ^c	— ^d
D-Arabitol	—	—	—	—	—	— ^b	—	— ^c	+ ^d
2-Ketogluconate	—	—	—	—	+	— ^b	—	— ^c	— ^d
Susceptibility to antibiotics									
Chloramphenicol	+	+	v	ND	—	—	—	+ ^c	+ ^d
Penicillin G	+	+	v	ND	—	—	ND	— ^c	+ ^d
Tetracycline	+	+	—	ND	—	—	+	+ ^c	+ ^d
DNA G + C content (mol%)	39.4	42.3–43.0	43.7–44.2	40.4–41.0	43.4	41.0	42.7	43.6	44.2

*CWH, Creamy white; LY, light yellow; TY, translucent yellow; WH, white; Y, yellow.

†Data from Takeuchi & Yokota (1992).

‡Data obtained in this study for the type strains of the following species: a, *P. cryoconitis*; b, *P. ginsengisoli*; c, *P. himalayensis*; d, *P. panaciterrae*.

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); the cells were suspended in AUX medium according to the manufacturer's instructions to inoculate the API 50 CH system.

The type strains of four *Pedobacter* species were used as reference strains for phenotypic characterization: *P. cryoconitis* KACC 11394^T and *P. himalayensis* KACC 11499^T were obtained from the Korean Agricultural Culture Collection (KACC), Suwon, Korea, and *P. ginsengisoli* KCTC 12576^T and *P. panaciterrae* KCTC 12594^T were obtained from the Korean Collection for Type Cultures (KCTC), Taejeon, Korea.

Cell biomass for DNA extraction and for isoprenoid quinone analysis was obtained from cultivation in TSB at 25 °C. Chromosomal DNA was isolated and purified according to the method described by Yoon *et al.* (1996), except that RNase T1 was used in combination with RNase A to minimize contamination with RNA. The 16S rRNA gene was amplified by using a 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, biomass of strain DS-139^T was harvested from TSA plates after incubation for 7 days at 25 °C. The fatty acid methyl esters were extracted and 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.

Morphological, cultural, physiological and biochemical characteristics of strain DS-139^T are given in the species description and in Table 1. The almost-complete 16S rRNA gene sequence of strain DS-139^T, determined in this study, comprised 1475 nt (approx. 96 % of the *Escherichia coli* 16S rRNA gene sequence). 16S rRNA gene sequence analyses showed that strain DS-139^T was most closely related phylogenetically to the genus *Pedobacter* within the family *Sphingobacteriaceae* (Fig. 1). In the neighbour-joining tree based on 16S rRNA gene sequences, strain DS-139^T formed a distinct phylogenetic lineage within the cluster comprising *Pedobacter* species (Fig. 1). Strain DS-139^T exhibited 16S rRNA gene sequence similarity values ranging from 93.9 % (*P. aquatilis* AR 107^T) to 96.7 % (*P. caeni* LMG 22862^T) with respect to the type strains of *Pedobacter* species (except *P. saltans* DSM 12145^T) and showed less than 90.4 % sequence similarity with respect to other species.

Strain DS-139^T contained MK-7 (at a peak area ratio of approximately 96 %) as the predominant isoprenoid quinone. The fatty acid profile comprised the following (of those making up >1.0 % of total fatty acids): branched fatty acids iso-C_{15:0} (26.0 %), iso-C_{17:1ω9c} (6.9 %), anteiso-C_{17:1ω9c} (4.7 %), anteiso-C_{15:0} (3.2 %), iso-C_{16:1}

Fig. 1. Neighbour-joining phylogenetic tree, based on 16S rRNA gene sequences, showing the positions of strain DS-139^T and some related taxa. Bootstrap percentages (from 1000 replications) are shown at nodes only if they are $\geq 50\%$. *Cytophaga hutchinsonii* ATCC 33406^T was used as the outgroup. Bar, 0.01 substitutions per nucleotide position.

(2.1%) and iso- $C_{16:0}$ (2.0%); summed feature 3, comprising $C_{16:1\omega 7c}$ and/or iso- $C_{15:0}$ 2-OH (19.1%); hydroxy fatty acids iso- $C_{17:0}$ 3-OH (11.6%), $C_{17:0}$ 2-OH (8.9%), iso- $C_{16:0}$ 3-OH (3.1%), iso- $C_{15:0}$ 3-OH (2.1%) and $C_{15:0}$ 2-OH (1.5%); and unsaturated fatty acids $C_{15:1\omega 6c}$ (1.1%) and $C_{16:1\omega 5c}$ (1.0%). This fatty acid profile was similar to those of recognized *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; Shivaji *et al.*, 2005; Vanparys *et al.*, 2005; Yoon *et al.*, 2006; Hwang *et al.*, 2006; Ten *et al.*, 2006). The DNA G+C content of strain DS-139^T was 39.4 mol%. These chemotaxonomic properties are in agreement with the result of a monothetic phylogenetic classification that placed strain DS-139^T within the genus *Pedobacter* (Steyn *et al.*, 1998; Margesin *et al.*, 2003; Shivaji *et al.*, 2005; Vanparys *et al.*, 2005; Yoon *et al.*, 2006; Hwang *et al.*, 2006; Ten *et al.*, 2006). Strain DS-139^T differs from some phylogenetically related *Pedobacter* species in several phenotypic characteristics, as shown in Table 1. The phylogenetic distinctiveness of DS-139^T, together with the differential phenotypic properties, is sufficient to show that the strain is distinct from recognized *Pedobacter* species (Stackebrandt & Goebel, 1994). Therefore, on the basis of the data presented, strain DS-139^T represents a novel species of the genus *Pedobacter*, for which the name *Pedobacter insulae* sp. nov. is proposed.

Description of *Pedobacter insulae* sp. nov.

Pedobacter insulae (in.su'lae. L. fem. gen. n. *insulae* of an island, referring to the source of isolation of the type strain).

Cells are Gram-negative, non-spore-forming, non-flagellated rods ($0.3\text{--}0.5 \times 0.7\text{--}6.0$ μm); occasionally cells greater than 10.0 μm in length occur. Colonies on TSA are circular, convex, smooth, glistening, light yellow in colour and 1.0–2.0 mm in diameter after incubation for 7 days at 25 °C. Optimal growth occurs at 25 °C; growth occurs at 4 and 31 °C, but not at 32 °C. The optimal pH for growth is 6.5–7.5; growth occurs at pH 6.0 and 10.0, but not at pH 5.5 or 10.5. Optimal growth occurs in the presence of 0–0.5% (w/v) NaCl; growth does not occur in the presence of more than 2% (w/v) NaCl. Growth does not occur under anaerobic conditions on TSA or on TSA supplemented with nitrate. DNase-positive. Starch, tyrosine and Tweens 20, 40, 60 and 80 are hydrolysed, but casein, gelatin, hypoxanthine and xanthine are not. Ornithine decarboxylase is absent. Naphthol-AS-BI-phosphohydrolase is present. Flexirubin-type pigments are absent. Susceptible to carbenicillin, cephalothin, gentamicin, lincomycin, novobiocin, oleandomycin and streptomycin, but not to neomycin or polymyxin B. The predominant menaquinone is MK-7. The major fatty acids ($>10\%$ of total fatty acids) are iso- $C_{15:0}$, $C_{16:1\omega 7c}$ and/or iso- $C_{15:0}$ 2-OH and iso- $C_{17:0}$ 3-OH. The DNA G+C content is 39.4 mol% (HPLC). Other phenotypic properties are shown in Table 1.

The type strain, DS-139^T (=KCTC 12820^T =DSM 18684^T), was isolated from a soil at Dokdo, an island in 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

- 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.
- 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.
- 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*, MIDI Technical Note 101. 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 thalophilum* 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.
- 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.