Parapedobacter luteus sp. nov. and *Parapedobacter composti* sp. nov., isolated from cotton waste compost

Soo-Jin Kim,¹ Hang-Yeon Weon,¹ Yi-Seul Kim,¹ Seung-Hee Yoo,¹ Byung-Yong Kim,¹ Rangasamy Anandham² and Soon-Wo Kwon¹

Correspondence
Soon-Wo Kwon
swkwon@rda.go.kr

¹Korean Agricultural Culture Collection (KACC), National Agrobiodiversity Center, Suwon 441-707, Republic of Korea

²Agricultural Microbiology, Department of Agricultural Microbiology, Agricultural College and Research Institute, Madurai, India

Two aerobic, Gram-reaction-negative, non-spore-forming bacterial strains, 4M29^T and 4M40^T, were isolated from cotton composts. The two strains grew in the presence of 0–5 % (w/v) NaCl (optimum growth in the absence of NaCl), at pH 6.0–8.0 (optimum, pH 7.0) and at 15–45 °C (optimum, 30 °C). The strains shared 97.1 % 16S rRNA gene sequence similarity. Strains 4M29^T and 4M40^T showed the next highest levels of 16S rRNA gene sequence similarity to *Parapedobacter koreensis* Jip14^T (95.6 and 94.4 %, respectively) and *Parapedobacter soli* DCY14^T (95.2 and 93.8 %). The level of DNA–DNA relatedness between strains 4M29^T and 4M40^T was 38 %. The two strains contained iso-C_{15:0}, summed feature 3 (comprising iso-C_{15:0} 2-OH and/or C_{16:1}ω7c) and iso-C_{17:0} 3-OH as major fatty acids, MK-7 as the major respiratory quinone, homospermidine as the only polyamine and phosphatidylethanolamine as the major polar lipid. The DNA G + C contents of strains 4M29^T and 4M40^T were 47.6 and 48.6 mol%, respectively. On the basis of phylogenetic and phenotypic data, strains 4M29^T and 4M40^T are considered to represent two novel species of the genus *Parapedobacter*, for which the names *Parapedobacter luteus* sp. nov. (type strain 4M29^T = KACC 10955^T = JCM 15977^T) and *Parapedobacter composti* sp. nov. (type strain 4M40^T = KACC 10972^T = JCM 15978^T) are proposed.

The genus *Parapedobacter* was erected with the description of *Parapedobacter koreensis* to accommodate a single strain isolated from dried rice straw (Kim *et al.*, 2007). A second species of the genus isolated from soil, *Parapedobacter soli*, was subsequently described (Kim *et al.*, 2008). The genus belongs to the family *Sphingobacteriaceae* together with the genera *Sphingobacterium* (Yabuuchi *et al.*, 1983), *Pedobacter* (Steyn *et al.*, 1998), *Mucilaginibacter* (Pankratov *et al.*, 2007), *Olivibacter* (Ntougias *et al.*, 2007), *Pseudosphingobacterium* (Vaz-Moreira *et al.*, 2007), *Nubsella* (Asker *et al.*, 2008) and *Solitalea* (Weon *et al.*, 2009). Members of the genus *Parapedobacter* are Gram-reaction-negative, rod-shaped, non-motile bacteria with iso-C_{15:0}, iso-C_{17:0} 3-OH and summed feature 3 (comprising iso-C_{15:0} 2-OH and/or C_{16:1}ω7c) as major fatty acids, menaquinone 7 as the

predominant respiratory quinone and sphingolipid as a characteristic polar lipid.

During the course of a study on the bacterial diversity of cotton waste composts used for the cultivation of the oyster mushroom (*Pleurotus ostreatus*), we previously isolated several novel bacterial strains by means of the plating technique on trypticase soy agar (TSA, pH 7.0; Difco) at 30 °C. In the present study, we report the taxonomic characterization of two of these bacterial strains, designated 4M29^T and 4M40^T.

The 16S rRNA genes of strains 4M29^T and 4M40^T were amplified by PCR with primers fD1 and rP2 (Weisburg *et al.*, 1991), and the entire PCR fragment was then directly sequenced (Hiraishi, 1992). 16S rRNA gene sequences were aligned by using the MEGALIGN program (DNASTAR). A phylogenetic tree was constructed by using the software package MEGA version 3.1 (Kumar *et al.*, 2004). Distances (options according to Kimura's two-parameter model) and clustering (via the neighbour-joining and maximum-parsimony methods) were determined by using bootstrap values based on 1000 replicates. The level of 16S rRNA gene

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of strains 4M29^T and 4M40^T are FJ754320 and FJ754321, respectively.

Thin-layer chromatograms showing the polar lipid profiles of strains 4M29^T, 4M40^T and *Parapedobacter koreensis* Jip14^T are available as supplementary material with the online version of this paper.

sequence similarity between strains 4M29^T and 4M40^T was 97.1 %. Strains 4M29^T and 4M40^T showed the next highest 16S rRNA gene sequence similarities to *Parapedobacter koreensis* Jip14^T (95.6 and 95.2 %, respectively) and *Parapedobacter soli* DCY14^T (94.4 and 93.8 %). The two strains showed sequence similarities of <92 % with the type strains of other related taxa. In the neighbour-joining phylogenetic tree (Fig. 1), the novel strains clustered with *Parapedobacter koreensis* Jip14^T and *Parapedobacter soli* DCY14^T with 100 % bootstrap support. This topology was also recovered in the maximum-parsimony tree.

DNA–DNA hybridization experiments between the two new isolates were carried out according to the method of Seldin & Dubnau (1985). Probe labelling was conducted by using the non-radioactive DIG High Prime DNA labelling and detection starter kit II (Roche Molecular Biochemicals). Reassociation was conducted at 65 °C. The hybridized DNA was visualized by using the DIG luminescent detection kit (Roche) and DNA–DNA relatedness was quantified by using a densitometer (Bio-Rad). The level of DNA–DNA relatedness between strains 4M29^T and 4M40^T was 38 %.

For quantitative analysis of cellular fatty acids, strains 4M29^T and 4M40^T were grown under the same conditions that had been used for *Parapedobacter koreensis* Jip14^T and *Parapedobacter soli* DCY14^T, i.e. on TSA plates at 30 °C for 2 days. Cells were harvested and cellular fatty acids were

saponified, methylated and extracted as described for use of the Sherlock Microbial Identification System (MIDI, 1999). Fatty acids were analysed by GC (Hewlett Packard 6890) and were identified by using the Microbial Identification software package (Sasser, 1990). Isoprenoid quinones were analysed by HPLC as described by Groth *et al.* (1996). Polyamines were analysed by HPLC (Shimadzu LC-10A), with the chromatograph equipped with a fluorescence detector (Shimadzu RF-10AXL) and reversed-phase column [Akzo Nobel; Kromasil ODS (250 × 4.6 mm)] as described previously (Busse & Auling, 1988; Busse *et al.*, 1997). Polar lipids of strains 4M29^T and 4M40^T and *Parapedobacter koreensis* Jip14^T were analysed according to Minnikin *et al.* (1984). DNA G+C contents were determined by HPLC of deoxyribonucleosides as described by Mesbah *et al.* (1989), by using a reversed-phase column (Supelcosil LC-18 S; Supelco).

The predominant cellular fatty acids of strains 4M29^T and 4M40^T were iso-C_{15:0}, summed feature 3 (comprising iso-C_{15:0} 2-OH and/or C_{16:1}ω7c) and iso-C_{17:0} 3-OH. The complete fatty acid compositions of the novel strains and of the type strains of the two recognized *Parapedobacter* species are detailed in Table 1. The fatty acid profiles of strains 4M29^T and 4M40^T were similar to those of *Parapedobacter koreensis* Jip14^T and *Parapedobacter soli* DCY14^T but differed based on the presence or proportions of anteiso-C_{13:0}, 10-methyl C_{16:0}, anteiso-C_{17:0},

Fig. 1. Neighbour-joining phylogenetic tree based on 16S rRNA gene sequences, showing the positions of strains 4M29^T and 4M40^T, the type strains of recognized *Parapedobacter* species and representative members of the family *Sphingobacteriaceae*. The sequence of *Bacteroides caccae* ATCC 43185^T was used as an outgroup. Numbers at nodes indicate bootstrap values, expressed as percentages of 1000 replications; only values >70 % are shown. Dots indicate that the corresponding branches were also recovered in the maximum-parsimony tree. Bar, 0.02 accumulated changes per nucleotide.

iso-C_{17:1}ω9c and ECL 13.566. The two novel strains possessed MK-7 as the major menaquinone, in agreement with all members of the family *Sphingobacteriaceae*. The only polyamine of strains 4M29^T and 4M40^T was homospermidine. Homospermidine is the major polyamine in members of the family *Sphingobacteriaceae*. The major polar lipid of strains 4M29^T and 4M40^T and *Parapedobacter koreensis* Jip14^T was phosphatidylethanolamine, and several unknown polar lipids were also detected; these three strains also contained sphingolipid, the characteristic polar lipid of members of the family *Sphingobacteriaceae* (see Supplementary Fig. S1 in IJSEM Online). The DNA G + C contents of strains 4M29^T and 4M40^T were 47.6 and 48.6 mol%, respectively.

Phenotypic characteristics including Gram staining, catalase and oxidase activities and hydrolysis of CM-cellulose, casein, chitin, DNA, tyrosine, Tween 80 and starch were assessed according to the methods of Smibert & Krieg (1994). Cell morphology and motility and the presence of flagella were observed by phase-contrast and transmission electron microscopy. For the latter, cells were negatively

Table 1. Cellular fatty acid profiles (%) of strains 4M29^T and 4M40^T and the type strains of recognized *Parapedobacter* species

Strains: 1, 4M29^T; 2, 4M40^T; 3, *P. koreensis* Jip14^T (data from Kim *et al.*, 2007); 4, *P. soli* DCY14^T (Kim *et al.*, 2008). All strains were grown on TSA at 30 °C for 2 days. Fatty acids amounting to <1 % in all strains are not shown. tr, Trace (<1 %); –, not detected.

Fatty acid	1	2	3	4
anteiso-C _{13:0}	–	–	–	11.4
C _{14:0}	tr	tr	1.1	–
C _{15:0} 3-OH	–	–	1.7	–
iso-C _{15:0}	48.5	42.9	33.6	29.3
iso-C _{15:0} 3-OH	2.4	3.1	2.3	3.7
C _{15:1} ω6c	–	–	1.1	–
C _{16:0}	1.6	tr	6.0	2.7
C _{16:0} 2-OH	tr	–	1.1	–
C _{16:0} 3-OH	tr	tr	1.9	2.3
10-Methyl C _{16:0}	–	–	7.1	–
anteiso-C _{17:0}	–	–	–	3.1
iso-C _{17:0} 3-OH	13.3	17.6	14.4	16.3
iso-C _{17:1} ω9c	7.1	11.0	–	7.1
C _{18:0}	–	–	–	1.2
ECL 13.566	2.5	5.4	tr	–
ECL 16.580	–	–	–	1.1
ECL 16.582	1.4	1.7	tr	–
Summed feature 3*	18.1	14.2	27.8	19.4
Summed feature 8*	–	–	–	1.2

*Summed features are groups of two or three fatty acids that could not be separated by GLC with the Microbial Identification System (MIDI). Summed feature 3 comprised iso-C_{15:0} 2-OH and/or C_{16:1}ω7c. Summed feature 8 comprised C_{19:1}ω11c and/or unknown ECL 18.756.

stained with 0.5 % uranyl acetate. Growth under anaerobic conditions was tested in a GasPak (BBL) jar at 30 °C for 15 days on TSA. Flexirubin-type pigments were revealed based on the colour shift that occurred after exposure of the colonies to a 20 % (w/v) KOH solution (Reichenbach, 1992). Growth was assessed at 5, 10, 15, 20, 25, 30, 33, 35, 40, 45 and 50 °C on R2A agar (Reasoner & Geldreich, 1985). The pH range for growth was determined in R2A broth that was buffered at pH 4.0–10.0 (at intervals of 1.0 pH unit) with citrate/phosphate or Tris/HCl buffer (Breznak & Costilow, 1994). NaCl tolerance was tested in R2A broth supplemented with 0, 1, 2, 3, 5 and 7 % (w/v) NaCl. Other biochemical tests were carried out by using the API 20 NE, API ID 32GN and API ZYM test kits according to the manufacturer's instructions (bioMérieux).

Strains 4M29^T and 4M40^T could be differentiated based on colony colour, hydrolysis of Tween 80, assimilation of D-ribose and L-proline and the presence of cystine arylamidase, α-chymotrypsin and α-fucosidase activities. Differential characteristics between strains 4M29^T and 4M40^T, *Parapedobacter koreensis* Jip14^T and *Parapedobacter soli* DCY14^T are provided in Table 2. On the basis of phenotypic data and phylogenetic inference, strains 4M29^T and 4M40^T are considered to represent two novel species of the genus *Parapedobacter*, for which the names *Parapedobacter luteus* sp. nov. and *Parapedobacter composti* sp. nov., respectively, are proposed.

Description of *Parapedobacter luteus* sp. nov.

Parapedobacter luteus (lu'te.us. L. masc. adj. *luteus* golden yellow, reflecting the colour of colonies).

Cells are aerobic, Gram-reaction-negative, non-motile, non-spore-forming rods (0.5 µm in diameter and 1.3–2.5 µm long). On R2A agar, colonies are circular with regular margins, convex and yellow. Growth occurs at 15–45 °C, at pH 6.0–8.0 and in the presence of 0–5 % NaCl. Optimum growth occurs at 30 °C, at pH 7.0 and in the absence of NaCl. Catalase- and oxidase-positive. Flexirubin-type pigments are produced. Nitrate is not reduced. Starch and Tween 80 are hydrolysed, but casein, chitin, CM-cellulose, DNA and tyrosine are not. Positive for aesculin hydrolysis, but negative for indole production, glucose fermentation, arginine dihydrolase and urease activities and gelatin hydrolysis (API 20 NE). Assimilates D-glucose, L-arabinose, D-mannose, N-acetylglucosamine, maltose, L-rhamnose, sucrose, glycogen, salicin, melibiose and L-proline, but not D-mannitol, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, phenylacetic acid, D-ribose, inositol, itaconic acid, suberic acid, sodium malonate, sodium acetate, lactic acid, L-alanine, potassium 5-ketogluconate, 3-hydroxybenzoic acid, L-serine, L-fucose, D-sorbitol, propionic acid, valeric acid, L-histidine, potassium 2-ketogluconate, 3-hydroxybutyric acid or 4-hydroxybenzoic acid (API 20 NE and API ID 32GN). Positive for alkaline phosphatase, leucine arylamidase, valine arylamidase, cystine arylamidase, trypsin, α-chymotrypsin, acid phosphatase, naphthol-AS-BI-

Table 2. Differential phenotypic characteristics between strains 4M29^T and 4M40^T and the type strains of recognized *Parapedobacter* species

Strains: 1, 4M29^T; 2, 4M40^T; 3, *P. koreensis* Jip14^T (unless indicated, data from Kim *et al.*, 2007, 2008); 4, *P. soli* DCY14^T (Kim *et al.*, 2008).

Characteristic	1	2	3	4
Colony colour*	Y	WH	LY†	Y
Flexirubin pigments	+	—	+†	+†
Growth at 42 °C	+	+	+	—
Hydrolysis of Tween 80	+	—	—†	—†
Assimilation of:				
L-Arabinose	+	+	—	+
D-Mannitol	—	—	+	+
L-Rhamnose	+	+	—	+
D-Ribose	—	+	+	+
Inositol	—	—	+	—
Glycogen	+	+	—	+
L-Serine	—	—	+	—
Melibiose	+	+	—	+
L-Fucose	—	—	+	—
D-Sorbitol	—	—	+	+
L-Proline	+	—	—	—
Enzyme activities				
Valine arylamidase	+	+	+	—
Cystine arylamidase	+	—	+	—
Trypsin	+	+	+	—
α -Chymotrypsin	+	—	+	—
α -Mannosidase	+	+	—	+
α -Fucosidase	—	+	—	—
DNA G + C content (mol%)	47.6	48.6	45.6	50.1

*LY, Light yellow; WH, white; Y, yellow.

†Data from the present study.

phosphohydrolase, α -galactosidase, β -galactosidase, α -glucosidase, β -glucosidase, *N*-acetyl- β -glucosaminidase and α -mannosidase activities, but negative for esterase (C4), esterase lipase (C8), lipase (C14), β -glucuronidase and α -fucosidase activities (API ZYM). The major fatty acids (>13 % of the total) are iso-C_{15:0}, iso-C_{17:0} 3-OH and summed feature 3 (comprising iso-C_{15:0} 2-OH and/or C_{16:1}ω7c). The complete fatty acid composition of the type strain is given in Table 1. The predominant isoprenoid quinone is MK-7. The major polar lipid is phosphatidylethanolamine; sphingolipid, an unknown phospholipid, an unknown aminolipid and several unknown polar lipids are also detected. The only polyamine is homospermidine. The DNA G + C content of the type strain is 47.6 mol%.

The type strain, 4M29^T (=KACC 10955^T =JCM 15977^T), was isolated from cotton waste compost in Korea.

Description of *Parapedobacter composti* sp. nov.

Parapedobacter composti (com.pos'ti. L. gen. n. *composti* of/ from compost).

Cells are aerobic, Gram-reaction-negative, non-motile, non-spore-forming rods (0.2–0.5 µm in diameter and 1.2–5 µm long). On R2A agar, colonies are circular with regular margins, convex and white. Growth occurs at 15–45 °C, at pH 6.0–8.0 and in the presence of 0–5 % NaCl. Optimum growth occurs at 30 °C, at pH 7.0 and in the absence of NaCl. Catalase- and oxidase-positive. Flexirubin-type pigments are not produced. Nitrate is not reduced. Starch is hydrolysed, but casein, chitin, CM-cellulose, DNA, Tween 80 and tyrosine are not. Positive for aesculin hydrolysis, but negative for indole production, glucose fermentation, arginine dihydrolase and urease activities and gelatin hydrolysis (API 20 NE). Assimilates D-glucose, L-arabinose, D-mannose, *N*-acetylglucosamine, maltose, L-rhamnose, D-ribose, sucrose, glycogen, salicin and melibiose, but not D-mannitol, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, phenylacetic acid, inositol, itaconic acid, suberic acid, sodium malonate, sodium acetate, lactic acid, L-alanine, potassium 5-ketogluconate, 3-hydroxybenzoic acid, L-serine, L-fucose, D-sorbitol, propionic acid, valeric acid, L-histidine, potassium 2-ketogluconate, 3-hydroxybutyric acid, 4-hydroxybenzoic acid or L-proline (API 20 NE and API ID 32GN). Positive for alkaline phosphatase, leucine arylamidase, valine arylamidase, trypsin, acid phosphatase, naphthol-AS-BI-phosphohydrolase, α -galactosidase, α -glucosidase, β -glucosidase, *N*-acetyl- β -glucosaminidase, α -mannosidase and α -fucosidase activities, but negative for esterase (C4), esterase lipase (C8), lipase (C14), cystine arylamidase, α -chymotrypsin, β -galactosidase and β -glucuronidase activities (API ZYM). The major fatty acids (>14 % of the total) are iso-C_{15:0}, iso-C_{17:0} 3-OH and summed feature 3 (comprising iso-C_{15:0} 2-OH and/or C_{16:1}ω7c). The complete fatty acid composition of the type strain is given in Table 1. The predominant isoprenoid quinone is MK-7. The major polar lipid is phosphatidylethanolamine; sphingolipid, an unknown aminolipid and several unknown polar lipids are also detected. The only polyamine is homospermidine. The DNA G + C content of the type strain is 48.6 mol%.

The type strain, 4M40^T (=KACC 10972^T =JCM 15978^T), was isolated from cotton waste compost in Korea.

Acknowledgements

This work was supported by the National Academy of Agricultural Science (NAAS), Rural Development Administration, Republic of Korea.

References

- Asker, D., Beppu, T. & Ueda, K. (2008). *Nubsella zeaxanthinifaciens* gen. nov., sp. nov., a zeaxanthin-producing bacterium of the family *Sphingobacteriaceae* isolated from freshwater. *Int J Syst Evol Microbiol* 58, 601–606.
- Breznak, J. A. & Costilow, R. N. (1994). Physicochemical factors in growth. In *Methods for General and Molecular Bacteriology*, pp. 137–

154. Edited by P. Gerhardt, R. G. E. Murray, W. A. Wood & N. R. Krieg. Washington, DC: American Society for Microbiology.
- Busse, H.-J. & Auling, G. (1988).** Polyamine pattern as a chemotaxonomic marker within the *Proteobacteria*. *Syst Appl Microbiol* **11**, 1–8.
- Busse, H.-J., Bunka, S., Hensel, A. & Lubitz, W. (1997).** Discrimination of members of the family *Pasteurellaceae* based on polyamine patterns. *Int J Syst Bacteriol* **47**, 698–708.
- Groth, I., Schumann, P., Weiss, N., Martin, K. & Rainey, F. A. (1996).** *Agrococcus jenensis* gen. nov., sp. nov., a new genus of actinomycetes with diaminobutyric acid in the cell wall. *Int J Syst Bacteriol* **46**, 234–239.
- Hiraishi, A. (1992).** Direct automated sequencing of 16S rDNA amplified by polymerase chain reaction from bacterial cultures without DNA purification. *Lett Appl Microbiol* **15**, 210–213.
- Kim, M. K., Na, J. R., Cho, D. H., Soung, N. K. & Yang, D. C. (2007).** *Parapedobacter koreensis* gen. nov., sp. nov. *Int J Syst Evol Microbiol* **57**, 1336–1341.
- Kim, M. K., Kim, Y. A., Kim, Y. J., Soung, N. K., Yi, T. H., Kim, S. Y. & Yang, D. C. (2008).** *Parapedobacter soli* sp. nov., isolated from soil of a ginseng field. *Int J Syst Evol Microbiol* **58**, 337–340.
- Kumar, S., Tamura, K. & Nei, M. (2004).** MEGA 3: integrated software for molecular evolutionary genetics analysis and sequence alignment. *Brief Bioinform* **5**, 150–163.
- Mesbah, M., Premachandran, U. & Whitman, W. B. (1989).** Precise measurement of the G + C content of deoxyribonucleic acid by high-performance liquid chromatography. *Int J Syst Bacteriol* **39**, 159–167.
- MIDI (1999).** *Sherlock Microbial Identification System Operating Manual*, version 3.0. Newark, DE: MIDI Inc.
- Minnikin, D. E., O'Donnell, A. G., Goodfellow, M., Alderson, G., Athalye, M., Schaal, A. & Parlett, J. H. (1984).** An integrated procedure for the extraction of bacterial isoprenoid quinones and polar lipids. *J Microbiol Methods* **2**, 233–241.
- Ntougias, S., Fasseas, C. & Zervakis, G. I. (2007).** *Olivibacter sitiensis* gen. nov., sp. nov., isolated from alkaline olive-oil mill wastes in the region of Sitia, Crete. *Int J Syst Evol Microbiol* **57**, 398–404.
- Pankratov, T. A., Tindall, B. J., Liesack, W. & Dedysh, S. N. (2007).** *Mucilagibacter paludis* gen. nov., sp. nov. and *Mucilagibacter gracilis* sp. nov., pectin-, xylan- and laminarin-degrading members of the family *Sphingobacteriaceae* from acidic *Sphagnum* peat bog. *Int J Syst Evol Microbiol* **57**, 2349–2354.
- Reasoner, D. J. & Geldreich, E. E. (1985).** A new medium for the enumeration and subculture of bacteria from potable water. *Appl Environ Microbiol* **49**, 1–7.
- Reichenbach, H. (1992).** The order *Cytophagales*. In *The Prokaryotes*, 2nd edn, vol. 4, 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.
- Seldin, L. & Dubnau, D. (1985).** Deoxyribonucleic acid homology among *Bacillus polymyxa*, *Bacillus macerans*, *Bacillus azotofixans*, and other nitrogen-fixing *Bacillus* strains. *Int J Syst Bacteriol* **35**, 151–154.
- Smibert, R. M. & Krieg, N. R. (1994).** Phenotypic characterization. In *Methods for General and Molecular Bacteriology*, pp. 607–654. Edited by P. Gerhardt, R. G. E. Murray, W. A. Wood & N. R. Krieg. Washington, DC: American Society for Microbiology.
- 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.
- Vaz-Moreira, I., Nobre, M. F., Nunes, O. C. & Manaia, C. M. (2007).** *Pseudosphingobacterium domesticum* gen. nov., sp. nov., isolated from home-made compost. *Int J Syst Evol Microbiol* **57**, 1535–1538.
- Weisburg, W. G., Barns, S. M., Pelletier, D. A. & Lane, D. J. (1991).** 16S ribosomal DNA amplification for phylogenetic study. *J Bacteriol* **173**, 697–703.
- Weon, H. Y., Kim, B. Y., Lee, C. M., Hong, S. B., Jeon, Y. A., Koo, B. S. & Kwon, S. W. (2009).** *Solitalea koreensis* gen. nov., sp. nov. and the reclassification of [*Flexibacter*] *canadensis* as *Solitalea canadensis* comb. nov. *Int J Syst Evol Microbiol* **59**, 1969–1975.
- Yabuuchi, E., Kaneko, T., Yano, I., Moss, C. W. & Miyoshi, N. (1983).** *Sphingobacterium* gen. nov., *Sphingobacterium spiritivorum* comb. nov., *Sphingobacterium multivorum* comb. nov., *Sphingobacterium mizutae* sp. nov., and *Flavobacterium indologenes* sp. nov.: glucose-nonfermenting gram-negative rods in CDC groups IIK-2 and IIb. *Int J Syst Bacteriol* **33**, 580–598.