Algoriphagus lutimaris sp. nov., isolated from a tidal flat sediment

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A Gram-negative, non-motile, non-spore-forming bacterial strain, S1-3^T, was isolated from a tidal flat sediment on the west coast of Korea and its taxonomic position was investigated. Strain S1-3^T grew optimally at 30 °C and in the presence of 2 % (w/v) NaCl. Strain S1-3^T contained MK-7 as the predominant menaquinone and C_{16:1}ω7c and/or iso-C_{15:0} 2-OH and iso-C_{15:0} as the major fatty acids. The DNA G + C content was 41.4 mol%. Phylogenetic analyses based on 16S rRNA gene sequences revealed that strain S1-3^T fell within the clade comprising *Algoriphagus* species, clustering with *Algoriphagus halophilus* IMSNU 14013^T, with which it exhibited 99.6 % 16S rRNA gene sequence similarity. The 16S rRNA gene sequence similarity between strain S1-3^T and the type strains of other *Algoriphagus* species was 94.0–97.1 %. Differential phenotypic properties and phylogenetic and genetic distinctiveness of strain S1-3^T demonstrated that this strain is distinguishable from the other *Algoriphagus* species as well as *A. halophilus*. On the basis of phenotypic, chemotaxonomic, phylogenetic and genetic data, strain S1-3^T is considered to represent a novel species of the genus *Algoriphagus*, for which the name *Algoriphagus lutimaris* sp. nov. is proposed. The type strain is S1-3^T (=KCTC 22630^T =CCUG 57608^T).

The genus *Algoriphagus* was first proposed by Bowman *et al.* (2003) and belongs phylogenetically to the phylum *Bacteroidetes* (Nedashkovskaya *et al.*, 2007). Since the proposal of the genus, further descriptions of novel species and reclassifications of members of the genera *Hongiella* and *Chimaericella* have increased the number of species belonging to the genus *Algoriphagus* considerably (Nedashkovskaya *et al.*, 2004, 2007; Van Trappen *et al.*, 2004; Yoon *et al.*, 2005a, b, 2006; Copa-Patiño *et al.*, 2008; Liu *et al.*, 2009). At the time of writing, the genus *Algoriphagus* comprised 17 species with validly published names and members have been isolated from sea ice, seawater, algae, marine sediments, soil and fresh water (Nedashkovskaya *et al.*, 2007; Copa-Patiño *et al.*, 2008; Liu *et al.*, 2009). In this study, we report on the taxonomic characterization of an *Algoriphagus*-like bacterial strain, S1-3^T, which was isolated from a tidal flat sediment on the west coast of Korea.

Strain S1-3^T was isolated by means of the standard dilution-plating technique at 25 °C on marine agar 2216 (MA; Difco). *Algoriphagus halophilus* KCTC 12051^T, which was used as a reference strain for phenotypic characteriza-

tion, fatty acid analysis and DNA–DNA hybridization, was obtained from the Korean Collection for Type Cultures. The morphological, physiological and biochemical characteristics of strain S1-3^T were investigated after cultivation on MA at 30 °C. Cell morphology was examined by light microscopy (Nikon E600) 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 investigated as described by Bowman (2000). The Gram reaction was determined by using the bioMérieux Gram-stain kit according to the manufacturer's instructions. Growth in the absence of NaCl and in the presence of 0.5, 1.0, 2.0 and 3.0 % (w/v) NaCl was investigated with trypticase soy broth (Difco) that had been prepared according to the manufacturer's instructions except that NaCl was added to the desired final concentration and 0.45 % (w/v) MgCl₂·6H₂O or 0.06 % (w/v) KCl were used as supplements. Growth at 2.0–10.0 % (w/v) NaCl (in increments of 1.0 %) was investigated in marine broth 2216 (MB; Difco). Growth at 4, 10, 20, 25, 28, 30, 35, 37, 40 and 45 °C was measured on MA. The pH range for growth was determined in MB that was adjusted to pH 4.5–9.5 (in increments of 0.5 pH units) by the addition of HCl or Na₂CO₃. Growth under anaerobic conditions was determined after incubation in a Forma

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain S1-3^T is FJ669216.

Maximum-likelihood and maximum-parsimony trees based on 16S rRNA gene sequences are available as supplementary material with the online version of this paper.

anaerobic chamber on MA and on MA supplemented with potassium nitrate (0.1 %, w/v), both of which had been prepared anaerobically in a nitrogen atmosphere. Catalase and oxidase activities were determined as described by Cowan & Steel (1965). Hydrolysis of casein, starch, hypoxanthine, tyrosine and xanthine was tested on MA, using the substrate concentrations described by Cowan & Steel (1965). Hydrolysis of aesculin, gelatin, Tweens 20, 40, 60 and 80 and urea and nitrate reduction were investigated as described by Lányi (1987) with the modification that artificial seawater was used for medium preparation. The artificial seawater contained (l^{-1} distilled water) 23.6 g NaCl, 0.64 g KCl, 4.53 g $MgCl_2 \cdot 6H_2O$, 5.94 g $MgSO_4 \cdot 7H_2O$ and 1.3 g $CaCl_2 \cdot 2H_2O$ (Bruns *et al.*, 2001). H_2S production was tested as described by Bruns *et al.* (2001). The presence of flexirubin-type pigments was investigated as described by Reichenbach (1992). For pigment absorption-spectrum analysis, strain S1-3^T was cultivated aerobically in the dark at 30 °C in MB. The culture was centrifuged, washed twice using a MOPS buffer (0.01 M MOPS/NaOH, 0.1 M KCl, 0.001 M $MgCl_2$, pH 7.5) and disrupted by sonication with a Branson Sonifier 450. After removal of cell debris by centrifugation, the absorption spectrum of the supernatant was examined on a Beckman Coulter DU800 spectrophotometer. Acid production from carbohydrates was determined as described by Leifson (1963). Utilization of substrates as sole carbon and energy sources was tested as described by Baumann & Baumann (1981) using supplementation with 2 % (v/v) Hutner's mineral base (Cohen-Bazire *et al.*, 1957) and 1 % (v/v) vitamin solution (Staley, 1968). Susceptibility to antibiotics was tested on MA plates using antibiotic discs containing the following (μ g unless otherwise stated): polymyxin B (100 U), streptomycin (50), penicillin G (20 U), chloramphenicol (100), ampicillin (10), cephalothin (30), gentamicin (30), novobiocin (5), tetracycline (30), kanamycin (30), lincomycin (15), oleandomycin (15), neomycin (30) and carbenicillin (100). Other physiological and biochemical tests were performed with the API 20E and API ZYM systems (bioMérieux).

Cell biomass of strain S1-3^T for DNA extraction and for isoprenoid quinone analysis was obtained from cultures grown for 3 days in MB at 30 °C. Chromosomal DNA was isolated and purified according to the method described previously (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 sequence was amplified by PCR using two universal primers as described previously (Yoon *et al.*, 1998). Sequencing and phylogenetic analysis were performed as described previously (Yoon *et al.*, 2003). The identification of phylogenetic neighbours was achieved using the EzTaxon server (<http://www.eztaxon.org/>; Chun *et al.*, 2007). Isoprenoid quinones were extracted according to the method of Komagata & Suzuki (1987) and analysed using reversed-phase HPLC and a YMC ODS-A (250 $\times$ 4.6 mm) column. For fatty acid methyl ester analysis, cell mass of

Table 1. Differential phenotypic characteristics of *Algoriphagus lutimaris* sp. nov. S1-3^T and *A. halophilus* JC 2051^T

Strains: 1, *A. lutimaris* sp. nov. S1-3^T; 2, *A. halophilus* JC 2051^T (unless indicated, data from Yi & Chun, 2004; Nedashkovskaya *et al.*, 2004). Both strains are Gram-negative and rod-shaped and positive for catalase, oxidase, hydrolysis of aesculin and gelatin, utilization of cellobiose, D-glucose, D-fructose, maltose, D-mannose, salicin, sucrose, trehalose and D-xylose, acid production from L-arabinose, D-glucose, lactose, maltose, D-mannose, raffinose and L-rhamnose, activity of alkaline phosphatase, esterase lipase (C8), leucine arylamidase, cystine arylamidase, trypsin, α -chymotrypsin, acid phosphatase, naphthol-AS-BI-phosphohydrolase and N-acetyl- β -glucosaminidase and susceptibility to carbenicillin, chloramphenicol, lincomycin and oleandomycin. Both strains are negative for flagellation, gliding motility, production of flexirubin-type pigments, nitrate reduction, H_2S and indole production, arginine dihydrolase, hydrolysis of agar, cellulose, starch, urea, tyrosine and xylan (data for the latter two substrates obtained in this study for *A. halophilus* KCTC 12051^T), utilization of acetate, citrate, formate, L-glutamate, succinate, benzoate, L-malate and pyruvate, acid production from myo-inositol, D-mannitol, D-ribose and D-sorbitol, activity of lipase (C14), α -galactosidase, β -glucuronidase, α -mannosidase and α -fucosidase and susceptibility to ampicillin, penicillin G, cephalothin, gentamicin, kanamycin, neomycin, novobiocin, polymyxin B and streptomycin. +, Positive; w, weakly positive; –, negative.

Characteristic	1	2
Wavelength of maximum absorption peak (nm)	467	475
NaCl requirement for growth	–*	+
Optimal growth temperature (°C)	30	35
Hydrolysis of:		
Casein	+	–
DNA	+	–
Utilization of:†		
L-Arabinose	–	w
D-Galactose	–	+
Acid production from:†		
Cellobiose	–	+
D-Fructose	–	+
D-Galactose	+	–
Melezitose	–	+
Melibiose	–	+
Sucrose	–	+
Trehalose	+	–
D-Xylose	–	+
Enzyme activity (API ZYM)†		
Esterase (C4)	–	+
Valine arylamidase	–	w
β -Galactosidase	–	+
α -Glucosidase	–	+
β -Glucosidase	–	+
Susceptibility to tetracycline	–	+
DNA G + C content (mol%)	41.4	42

*Growth in the absence of NaCl occurs when Mg^{2+} ions are added.

†Data for *A. halophilus* KCTC 12051^T from this study.

strain S1-3^T and *A. halophilus* KCTC 12051^T was harvested from MA plates after incubation for 3 days at 30 °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 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 the method of Ezaki *et al.* (1989) using photobiotin-labelled genomic DNA probes for cross-hybridization experiments in microdilution wells. Hybridization was performed with five replications for each sample. The highest and lowest values obtained in each sample were excluded and the means of the remaining three values were quoted as DNA–DNA relatedness values.

Morphological, cultural, physiological and biochemical characteristics of strain S1-3^T are given in the species description and in Table 1. Sonicated cell extracts of strain S1-3^T showed an absorption peak maximum at 467 nm, which indicates the presence of carotenoids. Flexirubin-type pigments were not produced, as shown by the negative KOH test result. An almost-complete 16S rRNA gene sequence of strain S1-3^T, comprising 1475 nt (approx. 96% of the *Escherichia coli* 16S rRNA sequence), was determined in this study. In the neighbour-joining phylogenetic tree based on 16S rRNA gene sequences, strain S1-3^T fell within the clade comprising *Algoriphagus* species and formed a coherent cluster with *A. halophilus* IMSNU 14013^T with a bootstrap resampling value of 100% (Fig. 1). The close relationship between strain S1-3^T and *A. halophilus* IMSNU 14013^T was also found in trees constructed using the maximum-likelihood and maximum-parsimony algorithms (Supplementary Fig. S1,

available in IJSEM Online). The 16S rRNA gene sequence similarity between strain S1-3^T and *A. halophilus* IMSNU 14013^T was 99.6%. Strain S1-3^T exhibited 16S rRNA gene sequence similarity of 94.0–97.1% to the type strains of the other *Algoriphagus* species and less than 92.5% to the type strains of the other species used in the phylogenetic analysis.

The predominant isoprenoid quinone detected in strain S1-3^T was menaquinone-7 (MK-7), which is the same as that found in other members of the genus *Algoriphagus* (Nedashkovskaya *et al.*, 2004, 2007). The cellular fatty acid profiles of strain S1-3^T and *A. halophilus* KCTC 12051^T obtained in this study are shown in Table 2. The major fatty acids (>10% of total fatty acids) in strain S1-3^T were C_{16:1}ω7c and/or iso-C_{15:0} 2-OH and iso-C_{15:0}. The fatty acid profiles were similar in the two strains, though there were differences in the proportions of some fatty acids. The DNA G+C content of strain S1-3^T was 41.4 mol%. The chemotaxonomic analysis showed that strain S1-3^T shared properties found in *Algoriphagus* species and was in agreement with the finding from the phylogenetic analysis that strain S1-3^T may be a member of the genus *Algoriphagus* (Bowman *et al.*, 2003; Nedashkovskaya *et al.*, 2004, 2007).

The mean DNA–DNA relatedness value between strain S1-3^T and *A. halophilus* KCTC 12051^T was 48%, which indicates that the two strains are members of different genomic species (Wayne *et al.*, 1987). Strain S1-3^T was distinguishable from *A. halophilus* KCTC 12051^T by differences in several phenotypic characteristics, most of which were determined using the same methods in this study (Table 1). The phylogenetic distinctiveness of strain S1-3^T, together with the genetic distinctiveness and differential phenotypic properties, are sufficient to show that this strain is separate from other *Algoriphagus* species

Fig. 1. Neighbour-joining phylogenetic tree based on 16S rRNA gene sequences showing the relative positions of *Algoriphagus lutimaris* sp. nov. S1-3^T, other *Algoriphagus* species and some other related taxa. Bootstrap values (>50%) based on 1000 replications are shown at branch nodes. Filled circles indicate that the corresponding nodes were also recovered in maximum-likelihood and maximum-parsimony trees. *Cytophaga hutchinsonii* ATCC 33406^T was used as an outgroup. Bar, 0.01 substitutions per nucleotide position.

Table 2. Cellular fatty acid compositions of strain S1-3^T and *A. halophilus* KCTC 12051^T

Strains: 1, *A. lutimaris* sp. nov. S1-3^T; 2, *A. halophilus* KCTC 12051^T. Data were obtained in this study and are percentages of total fatty acids; fatty acids representing <0.5% in both strains are omitted. ECL, Equivalent chain-length; —, not detected.

Fatty acid	1	2
Straight-chain		
C _{15:0}	2.2	—
C _{16:0}	1.1	—
Branched		
anteiso-C _{11:0}	1.5	1.9
iso-C _{15:0}	21.3	25.1
anteiso-C _{15:0}	2.6	3.2
iso-C _{16:0}	4.6	5.0
iso-C _{16:1}	1.2	3.2
iso-C _{17:1} ω ₉ c	9.4	10.3
Unsaturated		
C _{15:1} ω ₆ c	0.7	0.5
C _{16:1} ω ₅ c	3.9	3.5
C _{17:1} ω ₆ c	3.2	1.8
Hydroxy		
C _{16:0} 3-OH	1.4	—
iso-C _{15:0} 3-OH	2.2	2.5
iso-C _{16:0} 3-OH	1.4	2.0
iso-C _{17:0} 3-OH	9.3	7.1
Summed features*		
3	23.5	19.4
4	2.7	3.9
Unknown ECL 13.565	—	2.0

*Summed feature represent two or three fatty acids that cannot be separated by the Microbial Identification System. Summed feature 3 consisted of C_{16:1}ω₇c and/or iso-C_{15:0} 2-OH. Summed feature 4 consisted of iso-C_{17:1} I and/or anteiso-C_{17:1} B.

as well as *A. halophilus* (Stackebrandt & Goebel, 1994). Therefore, on the basis of the phenotypic, chemotaxonomic, phylogenetic and genetic data, strain S1-3^T is considered to represent a novel species of the genus *Algoriphagus*, for which the name *Algoriphagus lutimaris* sp. nov. is proposed.

Description of *Algoriphagus lutimaris* sp. nov.

Algoriphagus lutimaris (lu.ti.ma'ris. L. n. *lutum* mud; L. gen. n. *maris* of the sea, marine; N.L. gen. n. *lutimaris* of a marine mud).

Cells are Gram-staining-negative, non-spore-forming, non-flagellated and short rods or rods (0.4–0.7 × 0.8–4.5 μm); a few cells longer than 10 μm are also observed. Colonies on MA are circular, convex, smooth, glistening, reddish-orange in colour and 1.0–1.5 mm in diameter after incubation for 3 days at 30 °C. Growth occurs at 4 (weak) and 40 °C (optimum 30 °C) but not at 45 °C, at pH 5.0 (optimum pH 7.0–8.0) but not at pH 4.5 and with 0–8.0 %

(w/v) NaCl (optimum 2 % NaCl). Mg²⁺ ions are required for growth. Growth does not occur under anaerobic conditions on MA or on MA supplemented with nitrate. Tweens 20, 40, 60 and 80 are hydrolysed. The predominant menaquinone is MK-7. The major fatty acids (>10 % of total fatty acids) are C_{16:1}ω₇c and/or iso-C_{15:0} 2-OH and iso-C_{15:0}. Other phenotypic properties are shown in Table 1. The DNA G+C content of the type strain is 41.4 mol% (HPLC).

The type strain, S1-3^T (=KCTC 22630^T =CCUG 57608^T), was isolated from sediment of a tidal flat at Saemankum on the west coast of Korea.

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References

- Baumann, P. & Baumann, L. (1981). The marine Gram-negative eubacteria: genera *Photobacterium*, *Beneckea*, *Alteromonas*, *Pseudomonas*, and *Alcaligenes*. In *The Prokaryotes*, pp. 1302–1331. Edited by M. P. Starr, H. Stolp, H. G. Trüper, A. Balows & H. G. Schlegel. Berlin: Springer.
- 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.
- Bowman, J. P., Nichols, C. M. & Gibson, J. A. E. (2003). *Algoriphagus ratkowskyi* gen. nov., sp. nov., *Brumimicrobium glaciale* gen. nov., sp. nov., *Cryomorpha ignava* gen. nov., sp. nov. and *Crocinitomix catalasitica* gen. nov., sp. nov., novel flavobacteria isolated from various polar habitats. *Int J Syst Evol Microbiol* **53**, 1343–1355.
- Bruns, A., Rohde, M. & Berthe-Corti, L. (2001). *Muricauda ruestringensis* gen. nov., sp. nov., a facultatively anaerobic, appendaged bacterium from German North Sea intertidal sediment. *Int J Syst Evol Microbiol* **51**, 1997–2006.
- Chun, J., Lee, J.-H., Jung, Y., Kim, M., Kim, S., Kim, B. K. & Lim, Y. W. (2007). EzTaxon: a web-based tool for the identification of prokaryotes based on 16S ribosomal RNA gene sequences. *Int J Syst Evol Microbiol* **57**, 2259–2261.
- Cohen-Bazire, G., Sistrom, W. R. & Stanier, R. Y. (1957). Kinetic studies of pigment synthesis by nonsulfur purple bacteria. *J Cell Comp Physiol* **49**, 25–68.
- Copa-Patiño, J. L., Arenas, M., Soliveri, J., Sánchez-Porro, C. & Ventosa, A. (2008). *Algoriphagus hitonicola* sp. nov., isolated from an athallassohaline lagoon. *Int J Syst Evol Microbiol* **58**, 424–428.
- 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.

- Komagata, K. & Suzuki, K. (1987). Lipid and cell-wall analysis in bacterial systematics. *Methods Microbiol* **19**, 161–207.
- Lányi, B. (1987). Classical and rapid identification methods for medically important bacteria. *Methods Microbiol* **19**, 1–67.
- Leifson, E. (1963). Determination of carbohydrate metabolism of marine bacteria. *J Bacteriol* **85**, 1183–1184.
- Liu, Y., Li, H., Jiang, J.-T., Liu, Y.-H., Song, X.-F., Xu, C.-J. & Liu, Z.-P. (2009). *Algoriphagus aquatilis* sp. nov., isolated from a freshwater lake. *Int J Syst Evol Microbiol* **59**, 1759–1763.
- Nedashkovskaya, O. I., Vancanneyt, M., Van Trappen, S., Vandemeulebroecke, K., Lysenko, A. M., Rohde, M., Falsen, E., Frolova, G. M., Mikhailov, V. V. & Swings, J. (2004). Description of *Algoriphagus aquimarinus* sp. nov., *Algoriphagus chordae* sp. nov. and *Algoriphagus winogradskyi* sp. nov., from sea water and algae, transfer of *Hongiella halophila* Yi and Chun 2004 to the genus *Algoriphagus* as *Algoriphagus halophilus* comb. nov. and emended descriptions of the genera *Algoriphagus* Bowman *et al.* 2003 and *Hongiella* Yi and Chun 2004. *Int J Syst Evol Microbiol* **54**, 1757–1764.
- Nedashkovskaya, O. I., Kim, S. B., Kwon, K. K., Shin, D. S., Luo, X., Kim, S.-J. & Mikhailov, V. V. (2007). Proposal of *Algoriphagus vanfongensis* sp. nov., transfer of members of the genera *Hongiella* Yi and Chun 2004 emend. Nedashkovskaya *et al.* 2004 and *Chimaericella* Tiago *et al.* 2006 to the genus *Algoriphagus*, and emended description of the genus *Algoriphagus* Bowman *et al.* 2003 emend. Nedashkovskaya *et al.* 2004. *Int J Syst Evol Microbiol* **57**, 1988–1994.
- 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*. Newark, DE: MIDI Inc.
- 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.
- Staley, J. T. (1968). *Prosthecomicrobium* and *Ancalomicrobium*: new prosthecate freshwater bacteria. *J Bacteriol* **95**, 1921–1942.
- Tamaoka, J. & Komagata, K. (1984). Determination of DNA base composition by reversed-phase high-performance liquid chromatography. *FEMS Microbiol Lett* **25**, 125–128.
- Van Trappen, S., Vandecandelaere, I., Mergaert, J. & Swings, J. (2004). *Algoriphagus antarcticus* sp. nov., a novel psychrophile from microbial mats in Antarctic lakes. *Int J Syst Evol Microbiol* **54**, 1969–1973.
- 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.
- Yi, H. & Chun, J. (2004). *Hongiella manitolivorans* gen. nov., sp. nov., *Hongiella halophila* sp. nov. and *Hongiella ornithinivorans* sp. nov., isolated from tidal flat sediment. *Int J Syst Evol Microbiol* **54**, 157–162.
- 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., Kang, S.-J., Jung, S.-Y., Lee, C.-H. & Oh, T.-K. (2005a). *Algoriphagus yeomjeoni* sp. nov., isolated from a marine solar saltern of the Yellow Sea, Korea. *Int J Syst Evol Microbiol* **55**, 865–870.
- Yoon, J.-H., Kang, S.-J. & Oh, T.-K. (2005b). *Algoriphagus locisalis* sp. nov., isolated from a marine solar saltern. *Int J Syst Evol Microbiol* **55**, 1635–1639.
- Yoon, J.-H., Lee, M.-H., Kang, S.-J. & Oh, T.-K. (2006). *Algoriphagus terrigena* sp. nov., isolated from soil. *Int J Syst Evol Microbiol* **56**, 777–780.