Catellibacterium aquatile sp. nov., isolated from fresh water, and emended description of the genus *Catellibacterium* Tanaka *et al.* 2004

Ying Liu,¹ Cheng-Jun Xu,² Jia-Tong Jiang,¹ Ying-Hao Liu,¹
Xue-Feng Song,² Hao Li² and Zhi-Pei Liu¹

Correspondence

Zhi-Pei Liu

liuzhp@sun.im.ac.cn

¹State Key Laboratory of Microbial Resources, Institute of Microbiology,
Chinese Academy of Sciences, Beijing 100101, PR China

²Water Supply Company of Daqing Petroleum Administration, No. 49, Aiguo Road,
Ranghulu District, Daqing 163453, PR China

A Gram-negative, rod-shaped, non-pigmented, non-spore-forming bacterial strain that was motile by a single polar flagellum, designated A1-9^T, was isolated from Daqing reservoir in north-east China and its taxonomic position was studied using a polyphasic approach. Strain A1-9^T was non-halophilic, strictly aerobic and heterotrophic and lacked carotenoids, internal membranes and genes for photosynthesis (*puf* genes). Strain A1-9^T grew at 10–40 °C (optimum, 25–30 °C) and pH 5.5–9.0 (optimum, pH 6.0–6.5) and tolerated up to 1.0 % NaCl (w/v). Neither phototrophic nor fermentative growth was observed. The predominant ubiquinone was Q-10 and the major fatty acid was C_{18:1ω7c} (70 %). The DNA G + C content was 64.4 mol% (*T_m*). Phylogenetic analyses based on the 16S rRNA gene sequence revealed that strain A1-9^T, together with *Catellibacterium nectarophilum* AST4^T, formed a deep line within the '*Rhodobacter* clade' of the family *Rhodobacteraceae* and strain A1-9^T showed 94.2 % 16S rRNA gene sequence similarity to *C. nectarophilum* AST4^T. On the basis of phenotypic, chemotaxonomic and phylogenetic data, strain A1-9^T is considered to represent a novel species of the genus *Catellibacterium*, for which the name *Catellibacterium aquatile* sp. nov. is proposed. The type strain is A1-9^T (=CGMCC 1.7029^T =NBRC 104254^T).

The genus *Catellibacterium*, belonging to the '*Rhodobacter* clade' of the family *Rhodobacteraceae* of the class *Alphaproteobacteria*, was proposed by Tanaka *et al.* (2004). At the time of writing, the genus includes only one species, *Catellibacterium nectarophilum*, which was isolated from activated sludge and requires a diffusible compound from other bacterial cultures for vigorous growth (Tanaka *et al.*, 2004). Since 2008, many novel bacteria belonging to '*Rhodobacter* clade' have been isolated from various environments, such as *Rhodobacter megahophilus* from soil (Arunasri *et al.*, 2008), *Rhodobacter maris* and *Rhodobacter aestuarii* from marine environments (Venkata Ramana *et al.*, 2008, 2009), *Rhodobacter ovatus* from a polluted pond (Srinivas *et al.*, 2008), *Rhodovulum kholense* from mud (Anil Kumar *et al.*, 2008), *Rhodovulum lacipunecei* (Chakravarthy *et al.*, 2009), *Paracoccus halophilus* from marine sediment (Liu *et al.*, 2008), *Paracoccus aestuarii* from tidal-flat sediment (Roh *et al.*, 2009),

Paracoccus saliphilus from a salt lake (Wang *et al.*, 2009) and *Rhodobaca barguzinensis* from sediments of a soda lake (Boldareva *et al.*, 2008). Their wide distribution and metabolic diversity (such as heterotrophic, phototrophic and chemically autotrophic metabolism) suggest that members of this clade may play important roles in various ecosystems, especially aquatic environments. In a survey of the bacterial diversity of Daqing reservoir in north-east China, a bacterial strain, designated A1-9^T, was obtained, and database comparisons (<http://www.ncbi.nlm.nih.gov/>) showed that it was related to members of the '*Rhodobacter* clade', especially to members of the genus *Catellibacterium* (Tanaka *et al.*, 2004). In this communication, we report the isolation and taxonomic characterization of this strain.

The sample was collected from Daqing reservoir [sample site GPS position 46° 47' 40.9" N 125° 06' 46.9" E, depth 2.0 m, pH 8.5, 23 °C, chemical oxygen demand (COD_{Cr}) 15 mg l⁻¹, biological oxygen demand (BOD) 10 mg l⁻¹, total nitrogen (TN) 0.8 mg l⁻¹ and total phosphorus (TP) 0.07 mg l⁻¹]. For isolation of bacterial strains, the serially 10-fold diluted water sample was spread onto low-organic Luria–Bertani [LOLB, containing 1.0 g tryptone (Difco),

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain A1-9^T is EU313813.

A transmission electron micrograph of cells of strain A1-9^T is available as supplementary material with the online version of this paper.

0.5 g yeast extract and 10.0 g NaCl l⁻¹; pH 8.0] agar plates and incubated at 30 °C for 2 days. A bacterial strain, designated A1-9^T, was obtained. Subcultures were performed using YP medium [per litre distilled water: 3.0 g tryptone (Difco), 3.0 g yeast extract (Difco), 0.5 g MgSO₄ · 7H₂O, 0.3 g NaCl, 15 g agar, pH 7.0] or the strain was stored as glycerol stocks (15 %, w/v) at -80 °C.

Growth on several bacteriological media was tested: YP agar, R2A agar, trypticase soy agar (TSA; Difco), nutrient agar, Luria-Bertani (LB) agar and LOLB agar. Abundant growth was observed on YP agar, R2A agar and LOLB agar, but no growth was seen on the other media.

The Gram stain was performed as described by Gerhardt *et al.* (1994). Cell morphology was observed by phase-contrast microscopy and scanning electron microscopy (FEI QUANTA 200). Gliding motility was determined by the hanging drop method according to Dong & Cai (2001) and flagellation was confirmed by transmission electron microscopy (H600; Hitachi) after negative staining with 1 % (w/v) phosphotungstic acid. Colony morphology was observed on YP agar. Catalase and oxidase activities, H₂S production and hydrolysis of casein, starch and Tweens 20, 40, 60 and 80 were determined using standard methods (Cowan & Steel, 1965; Bruns *et al.*, 2001). Growth at 4, 10, 16, 20, 25, 30, 35, 40 and 45 °C, pH 5.0–9.5 (in increments

of 0.5 pH units) and 0, 0.5, 1.0, 1.5, 2.0, 2.5, 3.0 % NaCl was determined in YP liquid medium. Carbon source assimilation was determined using Biolog GN2 plates (MicroStation). Acid production from various substrates was determined using bioMérieux 50CHB/E strips according to the manufacturer's instructions. The activity of enzymes was determined using the API ZYM system (bioMérieux) following the manufacturer's instructions. *C. nectarophilum* JCM 11959^T was analysed in parallel. Other physiological tests were performed using the API 20NE system (bioMérieux) according to the manufacturer's instructions. Susceptibility to antibiotics was determined on YP agar plates using filter-paper discs (Beijing Pharmaceutical Company) containing various antibiotics as specified in the species description. All of the above tests were performed in triplicate.

The morphological, physiological and biochemical characteristics of strain A1-9^T are shown in Table 1 or are given in the genus and species descriptions. Strain A1-9^T was strictly aerobic and heterotrophic. Cells were Gram-negative, non-spore-forming rods, motile by a single polar flagellum, 0.5–0.6 µm wide and 1.0–1.6 µm long (Supplementary Fig. S1, available in IJSEM Online). Colonies on YP agar were transparent, smooth, circular and convex, 1–2 mm in diameter after incubation for 2 days at 30 °C. Strain A1-9^T

Table 1. Properties that differentiate strain A1-9^T from *C. nectarophilum* JCM 11959^T

Data are from this study unless indicated. Both strains are positive for oxidase and catalase activities and oxidation of β-hydroxybutyrate, monomethyl succinate and DL-lactate. Both strains are negative for nitrate reduction, phototrophic growth, indole production, urease activity and hydrolysis of gelatin and arginine. In the API ZYM system, both strains are positive for esterase, esterase lipase, leucine arylamidase and acid phosphatase and negative for lipase, cystine arylamidase, trypsin, chymotrypsin, α-galactosidase, β-glucuronidase, N-acetyl-β-glucosaminidase, α-mannosidase and α-fucosidase. +, Positive; w, weakly positive; –, negative.

Characteristic	A1-9 ^T	<i>C. nectarophilum</i> JCM 11959 ^T
Requirement for diffusible compounds from other bacterial cultures for vigorous growth	–	+*
Motility	+	–*
NaCl tolerance (% w/v)	1.0	2.5
Temperature for growth (°C)		
Range	10–40	20–37
Optimum	25–30	30
pH for growth		
Range	5.5–9.0	6.0–8.0
Optimum	6.0–6.5	6.5–7.5
Utilization of:		
L-Arabinose, L-alanyl glycine	+	–
Glycogen, Tween 80, methyl pyruvate, α-ketoglutarate	–	+
Succinate, succinamate, alaninamide, L-glutamate, L-serine	–	+
API ZYM results		
Alkaline phosphatase	–	+
Valine arylamidase, naphthol-AS-BI-phosphohydrolase	–	w
β-Galactosidase, α-glucosidase, β-glucosidase	+	–
DNA G + C content (mol%)	64.4	64.5*

*Data taken from Tanaka *et al.* (2004).

grew at 10–40 °C (optimum, 25–30 °C) and pH 5.5–9.0 (optimum, pH 6.0–6.5). NaCl was not required for growth; strain A1-9^T tolerated up to 1.0 % (w/v) NaCl.

Phototrophic growth under microaerobic and anaerobic conditions was determined after incubation in an Oxoid AnaeroGen system using the medium of Pfennig & Trüper (1974) and as detailed by Imhoff & Caumette (2004), mainly including the detection of an internal membrane system and photosynthetic pigments and utilization of some carbon sources. *In vivo* pigment-absorption spectrum analysis was examined as described by Yoon *et al.* (2004) using a Unico UV-2802H spectrophotometer (Shanghai Optical Company). Detection of *puf* genes was performed by a PCR-amplification method and 13 pairs of primers as described by Nagashima *et al.* (1997); *Rhodobacter capsulatus* JCM 21090^T was used as a positive control. The PCR products were then sequenced to confirm the correct amplification.

Strain A1-9^T was unable to grow photoautotrophically [anaerobically in the light, with thiosulfate (0.1 % w/v) or NaHCO₃ (0.1 %, w/v)] or photoheterotrophically [anaerobically in the light, with methanol (0.1 %, w/v), yeast extract (0.3 %, w/v), tryptone (0.3 %, w/v), sodium acetate (0.3 %, w/v) or sodium pyruvate (0.3 %, w/v)]. An internal membrane system and carotenoids were absent, and no *in vivo* absorption peaks were detected. Furthermore, no *puf* gene products were detected from the PCR amplification of genomic DNA of strain A1-9^T using all the primer pairs described by Nagashima *et al.* (1997); meanwhile, several *puf* gene-specific products were amplified from genomic DNA of *Rba. capsulatus* JCM 21090^T (not shown). All of these results indicated that strain A1-9^T was not a member of the genus *Rhodobacter*.

Genomic DNA extraction, PCR and sequencing of the 16S rRNA gene were carried out according to the procedures given by Kim *et al.* (1998). The sequence of the amplified fragment was determined by direct sequencing and compared with available 16S rRNA gene sequences in GenBank using the BLAST program (Altschul *et al.*, 1990). Multiple alignment with closely related sequences was performed by using the CLUSTAL_X program (Thompson *et al.*, 1994). Ambiguous and unalignable bases were omitted manually and then the phylogenetic tree was reconstructed from an evolutionary distance matrix calculated using the neighbour-joining method in the MEGA program (version 3.1; Kumar *et al.*, 2004). Phylogenetic analyses based on 16S rRNA gene sequences revealed that strain A1-9^T was closely related to species of the genera *Rhodobacter* (95.5–90.7 % sequence similarity), *Catellibacterium* (94.2 %), *Haematobacter* (93.2 %), *Paracoccus* (93.5–91.1 %) and *Rhodovulum* (91.4–90.2 %). It formed a deep phyletic cluster with *C. nectarophilum* AST4^T within the family *Rhodobacteraceae* (Fig. 1).

For fatty acid methyl ester analysis, cell mass of strain A1-9^T was obtained from NPB agar (Tanaka *et al.*, 2004) after cultivation for 3 days at 30 °C. Cellular fatty acids were extracted, methylated and analysed by using the Sherlock

Microbial Identification System (MIDI) according to the manufacturer's instructions. Strain A1-9^T had a fatty acid profile similar to that of *C. nectarophilum* JCM 11959^T (Table 2). The dominant fatty acid was C_{18:1}ω7c for both strains. However, C_{10:0} 3-OH (15.3 %) was another major fatty acid for strain A1-9^T. Furthermore, in the fatty acid composition, A1-9^T differed from *C. nectarophilum* JCM 11959^T in the presence of small amounts of some fatty acids such as 11-methyl C_{18:1}ω7c and 10-methyl C_{19:0} and the absence of some minor fatty acids such as C_{19:0} cyclo ω8c and summed feature 3. Isoprenoid quinones were extracted and analysed as described by Komagata & Suzuki (1987). Strain A1-9^T contained ubiquinone Q-10 as the sole respiratory quinone. The DNA G+C content was determined by the thermal denaturation method (Sly *et al.*, 1986) and DNA from *Escherichia coli* K-12 was used as a control. The DNA G+C content of strain A1-9^T was 64.4 mol%.

Although strain A1-9^T showed the highest 16S rRNA gene sequence similarity to *Rba. changlensis* JA139^T (95.5 %), it could be clearly distinguished from members of the genus *Rhodobacter* by the absence of photosynthetic activity and carotenoids, indicating that it is not a member of the genus *Rhodobacter*. Strain A1-9^T shared several important characteristics with the genus *Catellibacterium*, as shown in Table 1, such as strictly aerobic growth, with no growth under anaerobic conditions by fermentation, nitrate reduction or phototrophy, the presence of oxidase and catalase activities and absence of nitrate reduction, indole production, urease activity and hydrolysis of gelatin and arginine, indicating that it is likely to be a member of the genus *Catellibacterium*. However, several properties, including nutrient requirements for growth, motility, growth temperature and pH ranges, NaCl tolerance, utilization of several carbon sources and activities of some enzymes (Table 1) differentiate strain A1-9^T from *C. nectarophilum* JCM 11959^T.

On the basis of our phenotypic, chemotaxonomic and phylogenetic data, strain A1-9^T is considered to represent a novel species of the genus *Catellibacterium*, for which we propose the name *Catellibacterium aquatile* sp. nov.

Emended description of the genus *Catellibacterium* Tanaka *et al.* 2004

The formal description given by Tanaka *et al.* (2004) remains correct except that some species are motile.

Description of *Catellibacterium aquatile* sp. nov.

Catellibacterium aquatile (a.qua'ti.le. L. neut. adj. *aquatile* living in water).

Exhibits the following properties in addition to those given in the genus description (Tanaka *et al.*, 2004). Cells are 0.5–0.6 µm wide and 1.0–1.6 µm long. Grows at 10–40 °C and pH 5.5–9.0, with optimal growth at 25–30 °C and pH 6.0–6.5. NaCl is not required for growth; tolerates up to 1.0 %

Fig. 1. Neighbour-joining tree based on 16S rRNA gene sequences showing the phylogenetic position of strain A1-9^T and representatives of some other related taxa. Bootstrap values (expressed as percentages of 1000 replications) >50% are shown at branch points. The sequence of *Rhodopseudomonas palustris* ATCC 17001^T was used as an outgroup. Bar, 0.01 substitutions per nucleotide position.

Table 2. Comparison of cellular fatty acid contents (%) of strain A1-9^T and *C. nectarophilum* JCM 11959^T

Data are from this study. Both strains were grown on NPB agar for 3 days at 30 °C. –, <1% or not detected.

Fatty acid	A1-9 ^T	<i>C. nectarophilum</i> JCM 11959 ^T
C _{10:0} 3-OH	15.3	6.0
C _{16:0}	1.1	1.6
C _{18:1} ω7c	70.0	75.7
C _{18:0}	4.7	2.7
11-Methyl C _{18:1} ω7c	2.4	—
10-Methyl C _{19:0}	1.2	—
C _{18:0} 3-OH	1.6	2.8
C _{19:0} cyclo ω8c	—	5.5
Summed feature 3*	—	1.2

*Summed features are groups of two or three fatty acids that cannot be separated by GLC using the MIDI system. Summed feature 3 contained iso-C_{15:0} 2-OH and/or C_{16:1} ω7c.

(w/v) NaCl. Colonies were transparent, non-pigmented, smooth, circular and convex, 1–2 mm in diameter after 2 days of incubation on YP agar. Positive for H₂S production and hydrolysis of aesculin, L-tyrosine and Tweens 20 and 80; negative for nitrate reduction, indole production, arginine dihydrolase and urease activity and hydrolysis of gelatin, casein, starch and Tweens 40 and 60. In the API ZYM system, strongly positive enzyme activity is observed for acid phosphatase and positive activity is observed for esterase (C4), esterase lipase (C8), leucine arylamidase, β-galactosidase, α-glucosidase and β-glucosidase; no activity is observed for alkaline phosphatase, lipase (C14), valine arylamidase, cystine arylamidase, trypsin, chymotrypsin, naphthol-AS-BI-phosphohydrolase, α-galactosidase, β-glucuronidase, N-acetyl-β-glucosaminidase, α-mannosidase or α-fucosidase. Utilizes L-arabinose, monomethyl succinate, β-hydroxybutyrate, DL-lactate and L-alanyl glycine; does not utilize other carbohydrates in the Biolog GN2 test. The DNA G + C content of the type strain is 64.4 mol% (T_m). Sensitive to (μg per disc unless indicated) vancomycin (30), gentamicin (10), carbenicillin

(100), streptomycin (10), tetracycline (30), kanamycin (30), ampicillin (10), erythromycin (15), novobiocin (5), neomycin (30), chloramphenicol (30), ciprofloxacin (5), norfloxacin (10), rifampicin (5) and polymyxin B (300 IU).

The type strain, A1-9^T (=CGMCC 1.7029^T =NBRC 104254^T), was isolated from fresh water of Daqing reservoir, north-east China.

Acknowledgements

This work was supported by grants from the High-Tech Development Program of China (863 program no. 2006AA06Z316) and the Knowledge Innovation Program of the Chinese Academy of Sciences (no. KSCS2-YW-G-055-01).

References

- Altschul, S. F., Gish, W., Miller, W., Myers, E. W. & Lipman, D. J. (1990). Basic local alignment search tool. *J Mol Biol* **215**, 403–410.
- Anil Kumar, P., Aparna, P., Srinivas, T. N. R., Sasikala, Ch. & Ramana, Ch. V. (2008). *Rhodovulum kholense* sp. nov. *Int J Syst Evol Microbiol* **58**, 1723–1726.
- Arunasri, K., Venkata Ramana, V., Spröer, C., Sasikala, Ch. & Ramana, Ch. V. (2008). *Rhodobacter megalophilus* sp. nov., a phototroph from the Indian Himalayas possessing a wide temperature range for growth. *Int J Syst Evol Microbiol* **58**, 1792–1796.
- Boldareva, E. N., Akimov, V. N., Boychenko, V. A., Stadnichuk, I. N., Moskalenko, A. A., Makhneva, Z. K. & Gorlenko, V. M. (2008). *Rhodobaca barguzinensis* sp. nov., a new alkaliphilic purple nonsulfur bacterium isolated from a soda lake of the Barguzin Valley (Buryat Republic, Eastern Siberia). *Mikrobiologiya* **77**, 241–254 (in Russian).
- 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.
- Chakravarthy, S. K., Sucharitha, K., Sasikala, C. & Ramana, C. V. (2009). *Rhodovulum lacipuneice* sp. nov., an obligate sulfide-demanding phototrophic alphaproteobacterium isolated from a purple pond in India. *Int J Syst Evol Microbiol* **59**, 1615–1619.
- Cowan, S. T. & Steel, K. J. (1965). *Manual for the Identification of Medical Bacteria*. London: Cambridge University Press.
- Dong, X.-Z. & Cai, M.-Y. (editors) (2001). Determination of biochemical properties. In *Manual for the Systematic Identification of General Bacteria*, pp. 370–398. Beijing: Science Press (in Chinese).
- Gerhardt, P., Murray, R. G. E., Wood, W. A. & Krieg, N. R. (editors) (1994). *Methods for General and Molecular Bacteriology*. Washington, DC: American Society for Microbiology.
- Imhoff, J. F. & Caumette, P. (2004). Recommended standards for the description of new species of anoxygenic phototrophic bacteria. *Int J Syst Evol Microbiol* **54**, 1415–1421.
- Kim, S. B., Falconer, C., Williams, E. & Goodfellow, M. (1998). *Streptomyces thermocarboxydovrans* sp. nov. and *Streptomyces thermocarboxydus* sp. nov., two moderately thermophilic carboxydophilic species from soil. *Int J Syst Bacteriol* **48**, 59–68.
- Komagata, K. & Suzuki, K. (1987). Lipid and cell-wall analysis in bacterial systematics. *Methods Microbiol* **19**, 161–207.
- Kumar, S., Tamura, K. & Nei, M. (2004). MEGA 3: integrated software for molecular evolutionary genetics analysis and sequence alignment. *Brief Bioinform* **5**, 150–163.
- Liu, Z.-P., Wang, B.-J., Liu, X.-Y., Dai, X., Liu, Y.-H. & Liu, S.-J. (2008). *Paracoccus halophilus* sp. nov., isolated from marine sediment of the South China Sea, China, and emended description of genus *Paracoccus* Davis 1969. *Int J Syst Evol Microbiol* **58**, 257–261.
- Nagashima, K. V. P., Hiraishi, A., Shimada, K. & Matsuura, K. (1997). Horizontal transfer of genes coding for the photosynthetic reaction centers of purple bacteria. *J Mol Evol* **45**, 131–136.
- Pfennig, N. & Trüper, H. G. (1974). The phototrophic bacteria. In *Bergey's Manual of Determinative Bacteriology*, 8th edn, pp. 24–75. Edited by R. E. Buchanan & N. E. Gibbons. Baltimore: Williams & Wilkins.
- Roh, S. W., Nam, Y.-D., Chang, H.-W., Kim, K.-H., Kim, M.-S., Shin, K.-S., Yoon, J.-H., Oh, H.-M. & Bae, J.-W. (2009). *Paracoccus aestuarii* sp. nov., isolated from tidal flat sediment. *Int J Syst Evol Microbiol* **59**, 790–794.
- Sly, L. I., Blackall, L. L., Kraat, P. C., Tian-Shen, T. & Sangkhobol, V. (1986). The use of second derivative plots for the determination of mol% guanine plus cytosine of DNA by the thermal denaturation method. *J Microbiol Methods* **5**, 139–156.
- Srinivas, T. N. R., Anil Kumar, P., Sasikala, Ch., Spröer, C. & Ramana, Ch. V. (2008). *Rhodobacter ovatus* sp. nov., a phototrophic alphaproteobacterium isolated from a polluted pond. *Int J Syst Evol Microbiol* **58**, 1379–1383.
- Tanaka, Y., Hanada, S., Manome, A., Tsuchida, T., Kurane, R., Nakamura, K. & Kamagata, Y. (2004). *Catellibacterium nectariphilum* gen. nov., sp. nov., which requires a diffusible compound from a strain related to the genus *Sphingomonas* for vigorous growth. *Int J Syst Evol Microbiol* **54**, 955–959.
- Thompson, J. D., Higgins, D. G. & Gibson, T. J. (1994). CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. *Nucleic Acids Res* **22**, 4673–4680.
- Venkata Ramana, V., Sasikala, Ch. & Ramana, Ch. V. (2008). *Rhodobacter maris* sp. nov., a phototrophic alphaproteobacterium isolated from a marine habitat of India. *Int J Syst Evol Microbiol* **58**, 1719–1722.
- Venkata Ramana, V., Anil Kumar, P., Srinivas, T. N. R., Sasikala, Ch. & Ramana, Ch. V. (2009). *Rhodobacter aestuarii* sp. nov., a phototrophic alphaproteobacterium isolated from an estuarine environment. *Int J Syst Evol Microbiol* **59**, 1133–1136.
- Wang, Y., Tang, S.-K., Lou, K., Mao, P.-H., Jin, X., Jiang, C.-L., Xu, L.-H. & Li, W.-J. (2009). *Paracoccus saliphilus* sp. nov., a novel halophilic bacterium isolated from a salt lake. *Int J Syst Evol Microbiol* **59**, 1924–1928.
- Yoon, J.-H., Yeo, S.-H. & Oh, T.-K. (2004). *Hongiella marincola* sp. nov., isolated from sea water of the East Sea in Korea. *Int J Syst Evol Microbiol* **54**, 1845–1848.