Marinomonas arenicola sp. nov., isolated from marine sediment

Lyudmila A. Romanenko,¹ Naoto Tanaka² and Galina M. Frolova¹

Correspondence

Lyudmila A. Romanenko

lro@piboc.dvo.ru

¹Pacific Institute of Bioorganic Chemistry, Far-Eastern Branch, Russian Academy of Sciences, Prospect 100 Let Vladivostoku 159, 690022 Vladivostok, Russia

²NODAI Culture Collection Center, Tokyo University of Agriculture, 1-1-1 Sakuragaoka, Setagaya-ku, Tokyo 156-8502, Japan

A *Marinomonas*-like bacterium, strain KMM 3893^T, was isolated from a marine sandy sediment collected close to shore from the Sea of Japan and subjected to a phenotypic and phylogenetic study. Comparative 16S rRNA gene sequence analysis confirmed the novel strain's assignment to the genus *Marinomonas*. Strain KMM 3893^T constituted a separate phyletic line in the genus *Marinomonas*, sharing <97 % sequence similarity with respect to other recognized *Marinomonas* species. Chemotaxonomically, strain KMM 3893^T contained the predominant fatty acids C_{18:1}ω7c, C_{16:1}ω7c and C_{16:0} and had a DNA G + C content of 50.0 mol%. On the basis of the phylogenetic analysis and physiological and biochemical characterization, strain KMM 3893^T represents a novel species of the genus *Marinomonas*, for which the name *Marinomonas arenicola* sp. nov. is proposed. The type strain is KMM 3893^T (=NRIC 0752^T =JCM 15737^T).

The genus *Marinomonas* was created by Van Landschoot & De Ley (1983) as the result of the reclassification of two species, *Alteromonas communis* and *Alteromonas vaga*, as *Marinomonas communis* and *Marinomonas vaga* (Baumann *et al.*, 1972). Subsequently, the genus has been expanded with the addition of *Marinomonas mediterranea* (Solano & Sanchez-Amat, 1999), *M. primoryensis* (Romanenko *et al.*, 2003), *M. aquimarina* (Macián *et al.*, 2005), *M. pontica* (Ivanova *et al.*, 2005), *M. ushuaiensis* (Prabakaran *et al.*, 2005), *M. dokdonensis* (Yoon *et al.*, 2005), *M. polaris* (Gupta *et al.*, 2006), *M. ostreistagni* (Lau *et al.*, 2006) and *M. arctica* (Zhang *et al.*, 2008).

Strain KMM 3893^T was isolated from a marine sandy sediment sample from the Sea of Japan, collected close to shore at a water depth of 1 m, as described previously (Romanenko *et al.*, 2004). The bacterium KMM 3893^T grew aerobically at 25–28 °C on marine 2216 agar (MA) or in marine broth (MB), on TSA and on seawater agar (containing 5 g peptone, 2.5 g yeast extract, 1.0 g glucose, 0.2 g K₂HPO₄, 0.05 g MgSO₄, 750 ml seawater, 250 ml distilled water, 15.0 g agar). The strain was stored at –80 °C in MB supplemented with 30 % (v/v) glycerol. Motility was observed by the hanging-drop method as described by Gerhardt *et al.* (1994). Phenotypic properties were tested according to the standard methods described by Smibert &

Krieg (1994). The oxidation/fermentation medium of Leifson (1963) for marine bacteria was used to test for acid production from carbohydrates with 1 % (w/v) of each compound. Growth at different temperatures and pH and in the presence of various NaCl concentrations and antibiotics was studied as described previously (Romanenko *et al.*, 2003, 2004, 2005). In addition, biochemical tests were carried out using API 20NE, API ID 32GN and API 50CH test kits (bioMérieux), according to the manufacturer's instructions. For comparative fatty acid analysis, strain KMM 3893^T, *M. communis* CIP 74.1^T and *M. primoryensis* KMM 3633^T were cultivated on MA at 28 °C and in MB at 22 °C for 3 days and lipids were extracted using the chloroform/methanol extraction method of Bligh & Dyer (1959). Fatty acid methyl esters were obtained by alkaline methanolysis (15 % NaOH/methanol) and hexane extraction and were analysed using a GLC-MS Hewlett Packard model 6890 gas chromatograph equipped with a HP 5 MS 5 % phenyl methyl siloxane capillary column (30 m × 250 µm × 0.25 µm) and connected to a Hewlett Packard model 5973 mass spectrometer. The DNA base composition was determined as described by Marmur & Doty (1962) and Owen *et al.* (1969). A 16S rRNA gene sequence of 1523 nucleotides was determined for strain KMM 3893^T as described by Shida *et al.* (1997). The sequence obtained was compared with 16S rRNA gene sequences retrieved from the EMBL/GenBank/DDBJ databases with the FASTA program (Pearson & Lipman, 1988). Phylogenetic analysis of 16S rRNA gene sequences was performed using the software package MEGA 4 (Tamura *et al.*, 2007) after alignment using

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain KMM 3893^T is AB467281.

A maximum-parsimony phylogenetic tree based on 16S rRNA gene sequences is available as supplementary material with the online version of this paper.

Fig. 1. Neighbour-joining tree based on 16S rRNA gene sequences showing the phylogenetic relationships between strain KMM 3893^T and *Marinomonas* species. Bootstrap values (>90%) based on 1000 replications are shown at branch nodes. The sequences of *Vibrio cholerae* ATCC 14035^T and *Alteromonas macleodii* IAM 12920^T were used as the outgroup. Bar, 0.01 substitutions per nucleotide position.

CLUSTAL X version 1.83 (Thompson *et al.*, 1997). Trees were constructed using the neighbour-joining and maximum-parsimony methods and distances were calculated according to Kimura's two-parameter model. Bootstrap analysis of 1000 replicates was used to estimate the robustness of the phylogenetic trees.

Comparative 16S rRNA gene sequence analysis showed that strain KMM 3893^T belonged to the genus *Marinomonas* and formed a distinct lineage (Fig. 1). The same relationship was also evident in the 16S rRNA gene sequence dendrogram that was generated using the maximum-parsimony algorithm (Supplementary Fig. S1, available in IJSEM Online). Strain KMM 3893^T shared the highest 16S rRNA gene sequence similarities with *M. pontica* 46-16^T (96.9%) and *M. dokdonensis* DSW10-10^T (96.7%), lower values with *M. ushuaiensis* U1^T (96.1%), *M. vaga* ATCC 27119^T and *M. communis* LMG 2864^T (95.6% each) and less than 95% similarity with the other members of the genus *Marinomonas*. 16S rRNA gene sequence similarity of 97.0% was proposed by Stackebrandt & Goebel (1994) and subsequently re-evaluated to 98.7% by Stackebrandt & Ebers (2006) as a criterion for species discrimination. Taking this into consideration, we concluded that the 16S rRNA gene sequence similarities between strain KMM 3893^T and type strains of *Marinomonas* species are low enough to exclude the assignment of the strain to any of the recognized *Marinomonas* species.

For comparison purposes, the fatty acid profiles of three strains, KMM 3893^T, *M. communis* CIP 74.1^T and *M. primoryensis* KMM 3633^T, grown on MA and in MB at different temperatures, were examined. The profiles are detailed in Table 1. For each strain, no noticeable differences were found that were dependent on culture conditions. *M. communis* CIP 74.1^T, *M. primoryensis* KMM 3633^T and strain KMM 3893^T contained C_{18:1}ω7c, C_{16:1}ω7c and C_{16:0} as the major fatty acids. These results are in accordance with the data reported for *M. communis*, *M. vaga*, *M. mediterranea* (Mikhailov *et al.*, 2006), *M. primoryensis* (Romanenko *et al.*, 2003), *M. dokdonensis* (Yoon *et al.*, 2005), *M. pontica* (Ivanova *et al.*, 2005), *M. ostreistagni* (Lau *et al.*, 2006) and *M. arctica* (Zhang *et al.*,

2008). However, the data obtained disagreed with the results found by Prabakaran *et al.* (2005) and Gupta *et al.* (2006), who reported the presence of significant percentages of iso-C_{16:0} (13.5, 11.3, 16.1 and 18.5%) and minor amounts of C_{16:0} (1.1, 1.1, 2.1 and 6.2%) in the fatty acid profiles of *M. communis*, *M. primoryensis*, *M. ushuaiensis* and *M. polaris*, respectively. In the present study, the fatty acid profiles of strain KMM 3893^T, *M. communis* and *M. primoryensis* appeared to be similar to each other in terms of the presence of C_{18:1}ω7c, C_{16:1}ω7c and C_{16:0} as the predominant fatty acids and the absence of iso-C_{16:0}, independent of the growth conditions. In addition, *M. communis* CIP 74.1^T revealed a slight difference in the absence of C_{12:1} and strain KMM 3893^T differed by possessing a small amount of C_{17:1}.

The DNA G+C content of strain KMM 3893^T was determined to be 50.0 mol%, which is in line with those

Table 1. Cellular fatty acid compositions of strain KMM 3893^T, *M. communis* CIP 74.1^T and *M. primoryensis* KMM 3633^T

Strains: 1, *Marinomonas arenicola* sp. nov. KMM 3893^T; 2, *M. communis* CIP 74.1^T; 3, *M. primoryensis* KMM 3633^T. Data were obtained in this study. Strains were grown on MA at 28 °C (a) and in MB at 22 °C (b). Values are percentages of total fatty acids; major components are highlighted in bold. —, Not detected.

Fatty acid	1		2		3	
	a	b	a	b	a	b
C _{10:0} 3-OH	9.7	8.9	10.4	3.7	4.8	5.0
C _{12:1}	2.1	3.0	—	—	4.4	6.0
C _{12:0}	11.0	10.7	5.6	4.4	0.8	—
C _{13:0}	1.3	—	—	—	—	—
C _{14:0}	1.3	—	2.2	1.9	—	—
C _{16:1} ω7c	10.2	13.0	15.9	22.2	22.1	23.5
C _{16:0}	17.4	16.0	11.4	10.8	11.9	14.4
C _{17:1}	3.2	2.8	—	0.2	—	—
C _{18:1} ω7c	31.0	38.8	44.2	53.2	37.0	38.2
C _{18:1} ω9c	—	—	0.1	0.4	—	—
C _{18:0}	4.2	4.1	2.5	2.6	5.6	5.8

Table 2. Phenotypic characteristics of *M. arenicola* sp. nov. KMM 3893^T and related *Marinomonas* species

Taxa: 1, *M. arenicola* sp. nov. KMM 3893^T (data from this study); 2, *M. ushuaiensis* (Prabakaran *et al.*, 2005); 3, *M. pontica* (Ivanova *et al.*, 2005); 4, *M. dokdonensis* (Yoon *et al.*, 2005); 5, *M. primoryensis* (Romanenko *et al.*, 2003); 6, *M. communis* (Baumann *et al.*, 1972); 7, *M. vaga* (Baumann *et al.*, 1972); 8, *M. mediterranea* (Solano & Sanchez-Amat, 1999). All strains are positive for motility and requirement for sodium ions for growth. All strains are negative for arginine dihydrolase and production of indole and H₂S. +, Positive; w, weak; v, variable between strains; –, negative; ND, no data available.

Characteristic	1	2	3	4	5	6	7	8
Pigmentation	None	None	None	None	Yellowish	None	None	Melanin-like
Oxidase	–	–	+	+	+	+	–	–
Nitrate reduction	–	–	–	–	–	–	–	+
Tolerance of NaCl at:								
8 % (w/v)	+	–	+	+	w*	+	+	ND
10 % (w/v)	+	–	+	+	–	+*	+*	ND
Growth at:								
4 °C	+	+	+	+	+	–	–	–
35 °C	+	–	–	+	–	+	+	–
37 °C	+	–	–	+	–	+	–	–
40 °C	–	–	–	–	–	+	–	–
Hydrolysis of:								
Gelatin	–	–	–	–	–	–	–	+
Tween 80	–	–	–	+	–	–	–	+
Starch	–	+	–	–	–	–	–	–
Utilization of:								
D-Glucose	–	+	+	ND	+†	+	+	+
Maltose	–	w	+	+	+	v	v	–
N-Acetyl-D-glucosamine	–	ND	ND	ND	+	–	+	ND
m-Hydroxybenzoate	–	+	+	–	+	+	+	–
Mannitol	–	–	ND	ND	+	+	+	ND
Malate	–	–	+	+	+†	+	+	+
L-Arginine	–	–	+	ND	v	+	v	ND
L-Lysine	–	–	+	ND	+	+	v	ND
DNA G + C content (mol%)	50.0	43.6	46.5	45.3–45.7	45.3–45.6	46.0–48.0	47.0–49.0	46.3 ± 0.9

*Data for *M. primoryensis* KMM 3633^T, *M. communis* CIP 74.1^T and *M. vaga* CIP 103202^T obtained in this study.

†*M. primoryensis* KMM 3633^T tested weakly positive in this study.

reported for *Marinomonas* (43.6–49.0 mol%) although considerably higher than that for *M. ushuaiensis* U1^T (43.6 mol%) (Table 2). Differential phenotypic features of strain KMM 3893^T and related species of the genus *Marinomonas* are listed in Table 2 and in the species description. It is notable that strain KMM 3893^T was susceptible to 16 of the 20 antibiotics that were tested (µg per disc unless otherwise stated): ampicillin (10), benzylpenicillin (10 U), vancomycin (30), gentamicin (10), kanamycin (30), carbenicillin (100), chloramphenicol (30), neomycin (30), ofloxacin (5), polymyxin (300 U), rifampicin (5), streptomycin (30), erythromycin (15), tetracycline (30), cephalosin (30) and cephalixin (30). Strain KMM 3893^T was resistant to nalidixic acid (30), lincomycin (15), oxacillin (10) and oleandomycin (15). The isolate could be distinguished from recognized *Marinomonas* species in not being able to assimilate most compounds in the API ID 32GN, API 20NE and API 50CH systems. Strain KMM 3893^T was similar to *M. ushuaiensis* (Prabakaran *et al.*, 2005) in terms of their lack of oxidase

and nitrate reduction activities and carbon assimilation pattern, but differed in not being able to degrade starch or to utilize D-glucose or *m*-hydroxybenzoate and by being able to grow at higher temperatures and to tolerate 8–10 % NaCl.

Strain KMM 3893^T could be distinguished from other recognized *Marinomonas* species on the basis of combined differential phenotypic characteristics and phylogenetic distinctiveness. Therefore, it is proposed that strain KMM 3893^T is assigned to the genus *Marinomonas* as representing a novel species, *Marinomonas arenicola* sp. nov.

Description of *Marinomonas arenicola* sp. nov.

Marinomonas arenicola (a.re.ni'co.la. L. n. *arena* sand; L. suff. *-cola* inhabitant, dweller; N.L. n. *arenicola* a sand-dweller).

Cells are aerobic, Gram-negative, oxidase-negative, catalase-positive, motile rods (approx. 2 µm long). Colonies are non-pigmented, semi-transparent, shiny and smooth

with regular edges, 2–3 mm in diameter on MA. Growth occurs at 4–37 °C (optimum 25–28 °C) but not at temperatures above 38 °C. Sodium ions are essential for growth. Growth is observed with 0.5–10 % (w/v) NaCl but not with 12 % NaCl. Grows at pH 5.5–9.5 (optimum pH 6.5–8.0). Negative for hydrolysis of casein, gelatin, Tween 80, starch, chitin and DNA and production of H₂S. On medium containing L-tyrosine, does not produce melanin-like pigments or clearance zones. Acid is formed from D-xylose, but not from D-glucose, D-mannitol, sucrose, lactose, maltose, D-galactose, D-mannose, cellobiose, D-sorbitol, L-arabinose or L-rhamnose. According to API 20NE tests, positive for β -galactosidase activity (*p*-nitrophenyl D-galactopyranoside hydrolysis) and negative for reduction of nitrate, production of indole, urease and arginine dihydrolase, acidification of glucose, hydrolysis of gelatin and aesculin and assimilation of D-glucose, D-mannitol, maltose, L-arabinose, D-mannose, *N*-acetylglucosamine, D-gluconate, caprate, adipate, L-malate, citrate and phenylacetate. According to API 50CH tests, utilizes potassium 5-ketogluconate and potassium 2-ketogluconate weakly, but does not utilize glycerol, erythritol, D- or L-arabinose, D-ribose, D- or L-xylose, D-adonitol, methyl β -D-xylopyranoside, D-galactose, D-glucose, D-fructose, D-mannose, L-sorbose, L-rhamnose, dulcitol, inositol, D-mannitol, D-sorbitol, methyl α -D-mannopyranoside, methyl α -D-glucopyranoside, *N*-acetylglucosamine, amygdalin, arbutin, aesculin, salicin, cellobiose, maltose, lactose, melibiose, sucrose, trehalose, inulin, melezitose, raffinose, starch, glycogen, xylitol, gentiobiose, turanose, D-lyxose, D-tagatose, D- or L-fucose, L- or D-arabitol or gluconate. According to the API ID 32GN tests, does not assimilate itaconic acid, suberic acid, sodium malonate, sodium acetate, lactic acid, propionic acid, capric acid, trisodium citrate, L-alanine, L-proline, 3-hydroxybutyric acid, 3- or 4-hydroxybenzoic acid, potassium 5-ketogluconate, potassium 2-ketogluconate, glycogen, D-mannitol, L-fucose, D-sorbitol, L-rhamnose, inositol, L-arabinose, L-serine, valeric acid or L-histidine. Contains C_{18:1}ω7c, C_{16:0} and C_{16:1}ω7c as the predominant fatty acids. Susceptible to ampicillin, benzylpenicillin, vancomycin, gentamicin, kanamycin, carbenicillin, chloramphenicol, neomycin, ofloxacin, polymyxin, rifampicin, streptomycin, erythromycin, tetracycline, cephalosin and cephalixin. Resistant to nalidixic acid, lincomycin, oxacillin and oleandomycin. The DNA G+C content of the type strain is 50 mol% (thermal denaturation).

The type strain, KMM 3893^T (=NRIC 0752^T =JCM 15737^T), was isolated from a marine sandy sample from the Sea of Japan, Russia.

Acknowledgements

We would like to thank Dr Chantal Bizet (Collection de l'Institut Pasteur) for providing *M. communis* CIP 74.1^T and *M. vaga* CIP 103202^T. This study was supported by a grant from the Presidium of the Far-Eastern Branch of Russian Academy of Sciences for 'Search of

Marine Heterotrophic Bacteria Biodiversity' and by a grant from the Presidium of RAS for 'Molecular and Cell Biology'.

References

- Baumann, L., Baumann, P., Mandel, M. & Allen, R. D. (1972). Taxonomy of aerobic marine eubacteria. *J Bacteriol* **110**, 402–429.
- Bligh, E. G. & Dyer, W. J. (1959). A rapid method of total lipid extraction and purification. *Can J Biochem Physiol* **37**, 911–917.
- 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.
- Gupta, P., Chaturvedi, P., Pradhan, S., Delille, D. & Shivaji, S. (2006). *Marinomonas polaris* sp. nov., a psychrohalotolerant strain isolated from coastal sea water off the subantarctic Kerguelen islands. *Int J Syst Evol Microbiol* **56**, 361–364.
- Ivanova, E. P., Onyshchenko, O. M., Christen, R., Lysenko, A. M., Zhukova, N. V., Shevchenko, L. S. & Kiprianova, E. A. (2005). *Marinomonas pontica* sp. nov., isolated from the Black Sea. *Int J Syst Evol Microbiol* **55**, 275–279.
- Lau, K. W. K., Ren, J., Wai, N. L. M., Lau, S. C. L., Qian, P.-Y., Wong, P.-K. & Wu, M. (2006). *Marinomonas ostreistagni* sp. nov., isolated from a pearl-oyster culture pond in Sanya, Hainan Province, China. *Int J Syst Evol Microbiol* **56**, 2271–2275.
- Leifson, E. (1963). Determination of carbohydrate metabolism of marine bacteria. *J Bacteriol* **85**, 1183–1184.
- Macián, M. C., Arahai, D. R., Garay, E. & Pujalte, M. J. (2005). *Marinomonas aquamarina* sp. nov., isolated from oysters and seawater. *Syst Appl Microbiol* **28**, 145–150.
- Marmur, J. & Doty, P. (1962). Determination of the base composition of deoxyribonucleic acid from its thermal denaturation temperature. *J Mol Biol* **5**, 109–118.
- Mikhailov, V. V., Romanenko, L. A. & Ivanova, E. P. (2006). The genus *Alteromonas* and related proteobacteria. In *The Prokaryotes: a Handbook on the Biology of Bacteria*, 3rd edn, vol. 6, pp. 597–645. Edited by M. Dworkin, S. Falkow, E. Rosenberg, K. H. Schleifer & E. Stackebrandt. New York: Springer.
- Owen, R. J., Hill, L. R. & Lapage, S. P. (1969). Determination of DNA base composition from melting profiles in dilute buffers. *Biopolymers* **7**, 503–516.
- Pearson, W. R. & Lipman, D. J. (1988). Improved tools for biological sequence comparison. *Proc Natl Acad Sci U S A* **85**, 2444–2448.
- Prabakaran, S. R., Suresh, K., Manorama, R., Delille, D. & Shivaji, S. (2005). *Marinomonas ushuaiensis* sp. nov., isolated from coastal sea water in Ushuaia, Argentina, sub-Antarctica. *Int J Syst Evol Microbiol* **55**, 309–313.
- Romanenko, L. A., Uchino, M., Mikhailov, V. V., Zhukova, N. V. & Uchimura, T. (2003). *Marinomonas primoryensis* sp. nov., a novel psychrophile isolated from coastal sea-ice in the Sea of Japan. *Int J Syst Evol Microbiol* **53**, 829–832.
- Romanenko, L. A., Schumann, P., Rohde, M., Mikhailov, V. V. & Stackebrandt, E. (2004). *Reinekea marinisedimentorum* gen. nov., sp. nov., a novel gammaproteobacterium from marine coastal sediments. *Int J Syst Evol Microbiol* **54**, 669–673.
- Romanenko, L. A., Uchino, M., Falsen, E., Frolova, G. M., Zhukova, N. V. & Mikhailov, V. V. (2005). *Pseudomonas pachastrellae* sp. nov. isolated from a marine sponge. *Int J Syst Evol Microbiol* **55**, 919–924.
- Shida, O., Takagi, H., Kadowaki, K., Nakamura, L. K. & Komagata, K. (1997). Transfer of *Bacillus alginolyticus*, *Bacillus chondroitinus*, *Bacillus curdlanolyticus*, *Bacillus glucanolyticus*, *Bacillus kobensis*, and

Bacillus thiaminolyticus to the genus *Paenibacillus* and emended description of the genus *Paenibacillus*. *Int J Syst Bacteriol* **47**, 289–298.

Smibert, R. M. & Krieg, N. R. (1994). Phenotypic characterization. In *Methods for General and Molecular Bacteriology*, pp. 607–655. Edited by P. Gerhardt, R. G. E. Murray, W. A. Wood & N. R. Krieg. Washington, DC: American Society for Microbiology.

Solano, F. & Sanchez-Amat, A. (1999). Studies on the phylogenetic relationships of melanogenic marine bacteria: proposal of *Marinomonas mediterranea* sp. nov. *Int J Syst Bacteriol* **49**, 1241–1246.

Stackebrandt, E. & Ebers, J. (2006). Taxonomic parameters revisited: tarnished gold standards. *Microbiol Today* **33**, 152–155.

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.

Tamura, K., Dudley, J., Nei, M. & Kumar, S. (2007). MEGA 4: molecular evolutionary genetics analysis (MEGA) software version 4.0. *Mol Biol Evol* **24**, 1596–1599.

Thompson, J. D., Gibson, T. J., Plewniak, F., Jeanmougin, F. & Higgins, D. G. (1997). The CLUSTAL_X windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. *Nucleic Acids Res* **25**, 4876–4882.

Van Landschoot, A. & De Ley, J. (1983). Intra- and intergeneric similarities of the rRNA cistrons of *Alteromonas*, *Marinomonas* (gen. nov.) and some other gram-negative bacteria. *J Gen Microbiol* **129**, 3057–3074.

Yoon, J.-H., Kand, S.-J. & Oh, T.-K. (2005). *Marinomonas dokdonensis* sp. nov., isolated from sea water. *Int J Syst Evol Microbiol* **55**, 2303–2307.

Zhang, D. C., Li, H. R., Xin, Y. H., Liu, H. C., Chen, B., Chi, Z. M., Zhou, P. J. & Yu, Y. (2008). *Marinomonas arctica* sp. nov., a psychrotolerant bacterium isolated from the Arctic. *Int J Syst Evol Microbiol* **58**, 1715–1718.