Erythrobacter gangjinensis sp. nov., a marine bacterium isolated from seawater

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A novel Gram-negative, aerobic, orange-pigmented bacterial strain, designated K7-2^T, was isolated from seawater of Gangjin Bay, Korea, and subjected to a polyphasic taxonomic study. Strain K7-2^T contained ubiquinone-10 (Q-10) as the predominant respiratory lipoquinone and did not produce bacteriochlorophyll *a*. Major fatty acids were C_{18:1}ω7c (51.4 %), iso-C_{15:0} 2-OH and/or C_{16:1}ω7c (15.0 %) and C_{17:1}ω6c (8.8 %). Major polar lipids were phosphatidylethanolamine and phosphatidylcholine. The DNA G + C content was 61.6 mol%. Phylogenetic analyses based on 16S rRNA gene sequences revealed that strain K7-2^T formed a distinct phylogenetic lineage within the cluster comprising *Erythrobacter* strains. Similarities between the 16S rRNA gene sequences of strain K7-2^T and the type strains of *Erythrobacter* species ranged from 95.0 % (*Erythrobacter litoralis* DSM 8509^T) to 96.8 % (*Erythrobacter citreus* RE35F/1^T). On the basis of polyphasic taxonomic data, strain K7-2^T (=KCTC 22330^T=JCM 15420^T) is classified in a novel species within the genus *Erythrobacter*, for which the name *Erythrobacter gangjinensis* sp. nov. is proposed.

The genus *Erythrobacter*, proposed by Shiba & Simidu (1982), belongs to the α -subclass of the *Proteobacteria* and the family *Erythrobacteraceae*. This family contains the genera *Altererythrobacter* (Kwon *et al.*, 2007), *Erythrobacter*, *Porphyrobacter* and *Erythromicrobium* (Lee *et al.*, 2005), which previously belonged to the family *Sphingomonadaceae*. At the time of writing, the genus *Erythrobacter* contains eight species: *E. longus* (Shiba & Simidu, 1982), *E. litoralis* (Yurkov *et al.*, 1994), *E. citreus* (Denner *et al.*, 2002), *E. flavus* (Yoon *et al.*, 2003), *E. aquimaris* (Yoon *et al.*, 2004), *E. vulgaris* (Ivanova *et al.*, 2005), *E. seohaensis* and *E. gaetbuli* (Yoon *et al.*, 2005). During bacteriological testing of seawater from shellfish culture, to determine the safety of shellfish for human consumption, a novel Gram-negative marine bacterium producing orange pigments, designated strain K7-2^T, was isolated. On the basis of polyphasic analysis of phenotypic and phylogenetic data, we propose that strain K7-2^T should be assigned to a novel species of the genus *Erythrobacter*.

Abbreviation: BChl *a*, bacteriochlorophyll *a*.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain K7-2^T is EU428782.

A scanning electron micrograph of cells of strain K7-2^T is available with the online version of this paper.

Strain K7-2^T was isolated from seawater collected from Gangjin Bay (34° 27' N 126° 47' E), Korea, by using a standard dilution-plating technique on marine agar 2216 (MA; Difco) at 28 °C for 5 days. Subcultivation was routinely performed on MA at 30 °C for 3 days under aerobic conditions and the strain was stored at –80 °C in marine broth (MB; Difco) supplemented with 20 % (v/v) glycerol.

Bacterial genomic DNA was extracted using a commercial genomic DNA extraction kit (Bioneer). The 16S rRNA gene was amplified by using the universal bacterial primers 27f (5'-AGAGTTTGATCCTGGCTCAG-3') and 1525r (5'-AAAGGAGGTGATCCAGCC-3') (Lane, 1991) and the purified PCR product was sequenced. The almost-complete 16S rRNA gene sequence of strain K7-2^T (1435 nt) was aligned manually with those of type strains of *Erythrobacter* species obtained from GenBank. Secondary-structural information implemented in the jPHYDIT program (Jeon *et al.*, 2005) was used for accurate alignment. Phylogenetic trees were inferred by using three tree-making algorithms, neighbour joining (Saitou & Nei, 1987), maximum likelihood (Felsenstein, 1981) and maximum parsimony (Fitch, 1971), in the jPHYDIT program and PAUP 4.0 (Swofford, 1998). Evolutionary distance matrices were generated according to Jukes & Cantor (1969). The tree topologies obtained were evaluated by bootstrap analyses

(Felsenstein, 1981) of the neighbour-joining method based on 1000 replications.

The initial similarity analyses of 16S rRNA gene sequences indicated that strain K7-2^T was closely related to the genus *Erythrobacter*. Similarities between the 16S rRNA gene sequence of strain K7-2^T and those of the type strains of recognized *Erythrobacter* species ranged from 96.8 to 95.0%. The closest relative of strain K7-2^T was *E. citreus* RE35F/1^T (96.8% 16S rRNA gene sequence similarity), followed by *E. seohaensis* SW-135^T (96.3%), *E. aquimaris* SW-110^T (96.1%), *E. vulgaris* 022-2-10^T (96.0%), *E. gaetbuli* SW-161^T (95.6%), *E. flavus* SW-46^T (95.5%), *E. longus* DSM 6997^T (95.3%) and *E. litoralis* DSM 8509^T (95.0%). Also, strain K7-2^T occupied a distinct position in the neighbour-joining tree (Fig. 1).

The phenotypic properties of strain K7-2^T were tested using standard procedures. Cell morphology was examined with a scanning electron microscope (S-4800; Hitachi) using cells grown for 18 h at 30 °C on MB (Supplementary Fig. S1, available in IJSEM Online). The optimal temperature and temperature range for growth were tested on MA at 4, 10, 15, 20, 25, 30, 35, 37, 40, 42, 45 and 50 °C. Tolerance to sea salts and growth with NaCl as the sole salt were determined on ZoBell agar (ZoBell, 1946; 5 g Bacto peptone, 1 g yeast extract, 0.1 g ferric citrate, 15 g Bacto agar, 1 l distilled water) containing 0–10% (w/v) sea salts (Sigma) and 0–10% NaCl at intervals of 1%, respectively. Tolerance to NaCl was determined in modified ZoBell medium (5 g Bacto peptone, 1 g Bacto yeast extract, 7 g

MgCl₂·6H₂O, 3 g MgSO₄·7H₂O, 1 g CaCl₂·2H₂O, 1 g KCl, 1 l distilled water) supplemented with 0–10% NaCl at intervals of 1%. The pH range for growth was assessed on ZoBell medium containing 2% sea salts adjusted to pH 3.0–11.0 at intervals of 1 pH unit with HCl or NaOH after sterilization. Gliding motility was tested by the hanging-drop method as described by Suzuki *et al.* (2001). Anaerobic growth was tested on MA in a jar containing the AnaeroPack-Anaero (Mitsubishi Gas Chemical), which works as oxygen absorber and CO₂ generator, for up to 10 days. Catalase and oxidase activities were determined using standard methods (Tindall *et al.*, 2007). Enzymic hydrolysis of casein, chitin, starch and Tween 80 was examined on MA amended with 1% substrates as described by Hansen & Sørheim (1991). Antibiotic resistance was determined with the disc-diffusion method using commercial antibiotic-impregnated discs (BBL Becton Dickinson). Other phenotypic and enzymic characterizations of strain K7-2^T were conducted using API 20E, API 20NE and API ZYM kits (bioMérieux). The utilization of different carbon sources was tested with a GN2 MicroPlate (Biolog) according to the manufacturer's instructions. Bacterial suspensions were prepared in artificial seawater or 2% sea salts. Detailed results of morphological, physiological and biochemical tests are given in the species description and in Table 1.

Analysis of the *in vitro* pigment-absorption spectrum was performed as described by Yoon *et al.* (2005). In brief, cells cultivated aerobically in the dark at 30 °C in MB were washed twice using a 20 mM MOPS buffer (pH 7.0) and disrupted

Fig. 1. Neighbour-joining tree based on 16S rRNA gene sequences showing relationships between strain K7-2^T and related strains belonging to the family *Sphingomonadaceae*. Bootstrap values (>50%) based on 1000 replications are given at branch nodes. Filled circles indicate that the corresponding nodes were also recovered in maximum-parsimony and maximum-likelihood trees. *Rhodospirillum rubrum* ATCC 11170^T was used as an outgroup. Bar, 0.02 substitutions per nucleotide position.

Table 1. Characteristics that differentiate strain K7-2^T from related *Erythrobacter* strains

Strains: 1, *Erythrobacter gangjinensis* K7-2^T; 2, *E. flavus* KCCM 41642^T; 3, *E. seohaensis* KCTC 12228^T; 4, *E. aquimaris* KCCM 41818^T; 5, *E. citreus* KCTC 12214^T; 6, *E. longus* KCCM 12180^T. All data are from this study. All strains were positive for alkaline phosphatase, esterase (C4), leucine arylamidase, valine arylamidase, trypsin and acid phosphatase activities, hydrolysis of Tween 80 and susceptibility to (µg per disc) kanamycin (30), chloramphenicol (30), erythromycin (15), vancomycin (30), gentamicin (10), novobiocin (30) and rifampicin (5). All strains were negative for arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase, citrate utilization, H₂S production, urease, indole production, fermentation/oxidation of D-glucose, D-mannitol, inositol, D-sorbitol, L-rhamnose, sucrose, melibiose, amygdalin, L-arabinose, lipase (C14), α-galactosidase, β-glucuronidase, β-glucosidase, N-acetyl-β-glucosaminidase, α-mannosidase and α-fucosidase activities, hydrolysis of agar and casein and susceptibility to polymyxin B (300 U) and (µg per disc) streptomycin (10) and nalidixic acid (30).

Characteristic	1	2	3	4	5	6
Colour of colonies	Orange	Yellow	Orange–yellow	Orange	Yellow	Orange
Motility	–	+	–	–	–	+
Presence of BChl <i>a</i>	–	–	–	–	–	+
Hydrolysis of:						
Gelatin	–	–	–	–	–	+
Starch	+	+	–	–	–	–
API 20E/API ZYM tests						
β-Galactosidase	–	–	+	+	–	+
Tryptophan deaminase	–	+	+	+	–	–
Voges–Proskauer	–	+	–	–	–	–
Esterase lipase (C8)	–	+	+	+	+	+
Cystine arylamidase	–	+	+	–	+	–
α-Chymotrypsin	+	–	–	–	–	+
Naphthol-AS-BI-phosphohydrolase	–	+	–	–	+	+
β-Galactosidase	–	–	+	+	–	–
α-Glucosidase	+	+	–	–	–	–
Susceptibility to:						
Amikacin (30 µg)	+	+	+	+	+	–
Penicillin (10 U)	+	–	–	–	–	–
Ampicillin (10 µg)	+	–	–	–	–	+
Tetracycline (30 µg)	+	–	–	–	–	–

by sonication with a Cole-Parmer ultrasonic homogenizer 4710. After removal of cell debris, the absorption spectrum of the supernatant was examined on a Shimadzu UV-1601 spectrophotometer. Bacteriochlorophyll *a* (BChl *a*) was not detected *in vitro* in strain K7-2^T. *E. longus* KCCM 12180^T was used as a positive control for spectrum analysis. Although the presence of BChl *a* was one of the characteristics of the genus *Erythrobacter*, only the two first-described species, *E. longus* and *E. litoralis*, contain this photopigment (Shiba & Simidu, 1982; Yurkov *et al.*, 1994). Therefore, it has been proposed that this trait be removed from the genus description (Denner *et al.*, 2002). Respiratory lipoquinones were analysed as described elsewhere (Collins & Jones, 1980; Komagata & Suzuki, 1987). Ubiquinones were extracted from 200 mg dry cell mass with chloroform and methanol (2:1, v/v). After drying in a rotary evaporator, the residue was dissolved in 500 µl acetone. The extract was applied to the TLC plate (20 × 20, silica gel 60 F₂₅₄; Merck) and developed using petroleum ether and acetone (95:5, v/v). Purified ubiquinones were dissolved in acetone and loaded on a reversed-phase TLC plate (10 × 10, HPTLC silica gel 60 RP-18 F₂₅₄; Merck) and developed with acetone/acetonitrile (80:20, v/v). Reference compounds were obtained from

Sigma. The predominant respiratory lipoquinone was ubiquinone-10 (Q-10), which has been found in other *Erythrobacter* species (Denner *et al.*, 2002; Yoon *et al.*, 2003, 2004, 2005). Polar lipids were extracted according to the procedures described by Minnikin *et al.* (1984) and separated by two-dimensional TLC using silica gel 60 F₂₅₄ plates. Individual phospholipids were identified by spraying with appropriate detection reagents and co-migration with authentic standards (Sigma) (Komagata & Suzuki, 1987). Phosphatidylethanolamine and phosphatidylcholine were identified as the predominant phospholipids.

The total cellular fatty acid compositions of strain K7-2^T and related strains were analysed according to the instructions of the Microbial Identification System (MIDI) using cells grown on MA at 30 °C for 2 days. The cellular fatty acid composition of strain K7-2^T is shown in Table 2, together with those of the type strains of *Erythrobacter* species. Major cellular fatty acids of strain K7-2^T were C_{18:1}ω7c (51.4%), summed feature 3 (consisting of iso-C_{15:0} 2-OH and/or C_{16:1}ω7c; 15.0%) and C_{17:1}ω6c (8.8%). The G + C content of the DNA was determined by thermal denaturation method (Marmur & Doty, 1962) using Ultrospec 2100

Table 2. Cellular fatty acid compositions of strain K7-2^T and the type strains of related *Erythrobacter* species

Strains: 1, *Erythrobacter gangjinensis* K7-2^T; 2, *E. flavus* KCCM 41642^T; 3, *E. seohaensis* KCTC 12228^T; 4, *E. aquimaris* KCCM 41818^T; 5, *E. citreus* KCTC 12214^T; 6, *E. longus* KCCM 12180^T. All data are from this study. tr, Trace amount (<0.5 % of total); –, not detected.

Fatty acid (%)	1	2	3	4	5	6
Saturated straight-chain						
C _{14:0}	0.5	—	0.5	0.8	—	—
C _{16:0}	6.4	5.2	11.8	14.3	4.6	11.9
C _{17:0}	—	2.4	tr	tr	—	7.8
C _{18:0}	1.0	—	1.2	—	1.9	1.2
Unsaturated						
C _{16:1} ω5c	0.8	—	1.5	1.2	—	—
C _{16:1} ω11c	—	—	—	—	—	0.5
C _{17:1} ω6c	8.8	5.8	7.3	7.9	13.9	3.6
C _{17:1} ω8c	—	8.8	1.1	—	—	5.1
C _{18:1} ω5c	—	—	1.3	0.5	1.5	—
C _{18:1} ω7c	51.4	56.3	38.2	42.8	45.0	52.3
C _{18:1} ω9c	—	—	0.5	—	—	—
11-Methyl-C _{18:1} ω7c	3.6	4.6	4.0	4.1	8.1	—
Hydroxy						
C _{14:0} 2-OH	5.1	1.6	11.5	8.9	3.5	6.5
C _{15:0} 2-OH	1.3	6.1	2.7	1.9	2.8	9.7
C _{16:0} 2-OH	4.7	1.6	2.6	1.6	5.7	1.4
iso-C _{16:0} 3-OH	—	—	0.9	—	1.5	—
C _{16:1} 2-OH	—	—	0.8	—	1.8	—
C _{18:1} 2-OH	1.5	—	0.9	—	4.1	—
Summed feature 3*	15.0	7.7	12.8	15.7	5.6	—

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

spectrophotometer (Pharmacia Biotech). DNA from *Escherichia coli* K-12 was used as a control. The DNA G + C content of strain K7-2^T was 61.6 mol%.

On the basis of the analysis presented above, strain K7-2^T is a member of the genus *Erythrobacter* and distinguishable from described *Erythrobacter* species. Therefore, a novel species is proposed, with the name *Erythrobacter gangjinensis* sp. nov.

Description of *Erythrobacter gangjinensis* sp. nov.

Erythrobacter gangjinensis (gang.jin.en'sis. N.L. masc. adj. *gangjinensis* referring to Gangjin, the name of the bay in Korea from which the type strain was isolated).

Cells are Gram-negative, aerobic rods, approximately 0.3–0.4 × 0.6–0.8 µm in size. Colonies are smooth, circular with entire margin, convex, opaque and orange on MA. After growth on MA at 30 °C for 7 days, colonies are 1.0–1.2 mm in diameter. No growth occurs with NaCl as the sole salt. Optimal growth occurs with 2–3 % (w/v) NaCl;

no growth occurs without NaCl or with >5 % NaCl. Growth occurs with 1–7 % (w/v) sea salt. Growth occurs at 15–37 °C (optimum 30 °C; no growth above 40 °C) and pH 6.0–10.0 (optimum pH 7–8). Bacteriochlorophyll *a* is not detected. Sensitive to (µg per disc unless otherwise indicated) ampicillin (10), chloramphenicol (30), erythromycin (15), penicillin (10 U), tetracycline (30), kanamycin (30), amikacin (30), gentamicin (10), vancomycin (30), novobiocin (30) and rifampicin (5), but resistant to polymyxin B (300 U), streptomycin (10) and nalidixic acid (30). Positive for catalase and oxidase activities. Starch and Tween 80 are hydrolysed, but chitin and casein are not. According to API ZYM tests, activities for alkaline phosphatase, esterase (C4), leucine arylamidase, valine arylamidase, trypsin, α-chymotrypsin, acid phosphatase and α-glucosidase are present, but activities for esterase lipase (C8), lipase (C14), cystine arylamidase, naphthol-AS-BI-phosphohydrolase, α- and β-galactosidase, β-glucuronidase, β-glucosidase, N-acetyl-β-glucosaminidase, α-mannosidase and α-fucosidase are absent. According to API 20NE and API 20E tests, nitrate is not reduced, Voges-Proskauer test is negative, H₂S and indole are not produced and activities for glucose fermentation, aesculin hydrolysis, urease and arginine dihydrolase are absent. With Biolog GN2, utilizes α-cyclodextrin, glycogen, Tweens 40 and 80, turanose, pyruvic acid methyl ester, succinic acid monomethyl ester, β-hydroxybutyric acid, α-ketoglutaric acid, succinic acid, succinamic acid, L-alanine, L-alanyl glycine, L-glutamic acid, glycyl L-glutamic acid and L-proline. The predominant respiratory lipoquinone is Q-10. The major cellular fatty acids of strain K7-2^T were C_{18:1}ω7c, iso-C_{15:0} 2-OH and/or C_{16:1}ω7c and C_{17:1}ω6c. The DNA G + C content of the type strain is 61.6 mol%.

The type strain, K7-2^T (=KCTC 22330^T=JCM 15420^T), was isolated from seawater of Gangjin Bay, Korea.

References

- Collins, M. D. & Jones, D. (1980). Lipids in the classification and identification of coryneform bacteria containing peptidoglycans based on 2,4-diaminobutyric acid. *J Appl Bacteriol* **48**, 459–470.
- Denner, E. B. M., Vybiral, D., Kobližek, M., Kämpfer, P., Busse, H.-J. & Velimirov, B. (2002). *Erythrobacter citreus* sp. nov., a yellow-pigmented bacterium that lacks bacteriochlorophyll *a*, isolated from the western Mediterranean Sea. *Int J Syst Evol Microbiol* **52**, 1655–1661.
- Felsenstein, J. (1981). Evolutionary trees from DNA sequences: a maximum likelihood approach. *J Mol Evol* **17**, 368–376.
- Fitch, W. M. (1971). Toward defining the course of evolution: minimum change for a specific tree topology. *Syst Zool* **20**, 406–416.
- Hansen, G. H. & Sørheim, R. (1991). Improved method for phenotypical characterization of marine bacteria. *J Microbiol Methods* **13**, 231–241.
- Ivanova, E. P., Bowman, J. P., Lysenko, A. M., Zhukova, N. V., Gorshkova, N. M., Kuznetsova, T. A., Kalinovskaya, N. I., Shevchenko, L. S. & Mikhailov, V. V. (2005). *Erythrobacter vulgaris* sp. nov., a novel organism isolated from the marine invertebrates. *Syst Appl Microbiol* **28**, 123–130.

- Jeon, Y. S., Chung, H., Park, S., Hur, I., Lee, J. H. & Chun, J. (2005). jPHYDIT: a JAVA-based integrated environment for molecular phylogeny of ribosomal RNA sequences. *Bioinformatics* **21**, 3171–3173.
- Jukes, T. H. & Cantor, C. R. (1969). Evolution of protein molecules. In *Mammalian Protein Metabolism*, vol. 3, pp. 21–132. Edited by H. N. Munro. New York: Academic Press.
- Komagata, K. & Suzuki, K. (1987). Lipid and cell-wall analysis in bacterial systematics. *Methods Microbiol* **19**, 161–207.
- Kwon, K. K., Woo, J.-H., Yang, S.-H., Kang, J.-H., Kang, S. G., Kim, S.-J., Sato, T. & Kato, C. (2007). *Altererythrobacter epoxidivorans* gen. nov., sp. nov., an epoxide hydrolase-active, mesophilic marine bacterium isolated from cold-seep sediment, and reclassification of *Erythrobacter luteolus* Yoon et al. 2005 as *Altererythrobacter luteolus* comb. nov. *Int J Syst Evol Microbiol* **57**, 2207–2211.
- Lane, D. J. (1991). 16S/23S rRNA sequencing. In *Nucleic Acid Techniques in Bacterial Systematics*, pp. 115–175. Edited by E. Stackebrandt & M. Goodfellow. Chichester, UK: Wiley.
- Lee, K.-B., Liu, C.-T., Kim, H., Aono, T. & Oyaizu, H. (2005). The hierarchical system of the 'Alphaproteobacteria': description of *Hyphomonadaceae* fam. nov., *Xanthobacteraceae* fam. nov. and *Erythrobacteraceae* fam. nov. *Int J Syst Evol Microbiol* **55**, 1907–1919.
- Marmur, J. & Doty, P. (1962). Determination of the base composition of deoxyribonucleic acid from its thermal denaturation temperature. *J Mol Biol* **5**, 109–118.
- 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.
- Saitou, N. & Nei, M. (1987). The neighbor-joining method: a new method for reconstructing phylogenetic trees. *Mol Biol Evol* **4**, 406–425.
- Shiba, T. & Simidu, U. (1982). *Erythrobacter longus* gen. nov., sp. nov., an aerobic bacterium which contains bacteriochlorophyll *a*. *Int J Syst Bacteriol* **32**, 211–217.
- Suzuki, M., Nakagawa, Y., Harayama, S. & Yamamoto, S. (2001). Phylogenetic analysis and taxonomic study of marine *Cytophaga*-like bacteria: proposal for *Tenacibaculum* gen. nov., with *Tenacibaculum maritimum* comb. nov. and *Tenacibaculum ovolyticum* comb. nov., and description of *Tenacibaculum mesophilum* sp. nov. and *Tenacibaculum amylolyticum* sp. nov. *Int J Syst Evol Microbiol* **51**, 1639–1652.
- Swofford, D. L. (1998). Phylogenetic analysis using parsimony (PAUP), version 4. Sunderland, MA: Sinauer Associates.
- Tindall, B. J., Sikorski, J., Smibert, R. A. & Krieg, N. R. (2007). Phenotypic characterization and principles of comparative systematics. In *Methods for General and Molecular Microbiology*, 3rd edn, pp. 330–393. Edited by C. A. Reddy, T. J. Beveridge, J. A. Breznak, G. A. Marzluf, T. M. Schmidt & L. R. Snyder. Washington, DC: American Society for Microbiology.
- Yoon, J.-H., Kim, H., Kim, I.-G., Kang, K. H. & Park, Y.-H. (2003). *Erythrobacter flavus* sp. nov., a slight halophile from the East Sea in Korea. *Int J Syst Evol Microbiol* **53**, 1169–1174.
- Yoon, J.-H., Kang, K. H., Oh, T.-K. & Park, Y.-H. (2004). *Erythrobacter aquimaris* sp. nov., isolated from sea water of a tidal flat of the Yellow Sea in Korea. *Int J Syst Evol Microbiol* **54**, 1981–1985.
- Yoon, J.-H., Oh, T.-K. & Park, Y.-H. (2005). *Erythrobacter seohaensis* sp. nov. and *Erythrobacter gaetbuli* sp. nov., isolated from a tidal flat of the Yellow Sea in Korea. *Int J Syst Evol Microbiol* **55**, 71–75.
- Yurkov, V., Stackebrandt, E., Holmes, A., Fuerst, J. A., Hugenholz, P., Golecki, J., Gad'on, N., Gorlenko, V. M., Kompantseva, E. I. & Drews, G. (1994). Phylogenetic positions of novel aerobic, bacteriochlorophyll *a*-containing bacteria and description of *Roseococcus thiosulfatophilus* gen. nov., sp. nov., *Erythromicrobium ramosum* gen. nov., sp. nov., and *Erythrobacter litoralis* sp. nov. *Int J Syst Bacteriol* **44**, 427–434.
- ZoBell, C. E. (1946). *Marine Microbiology: a Monograph on Hydrobacteriology*. Waltham, MA: Chronica Botanica.