Jannaschia donghaensis sp. nov., isolated from seawater of the East Sea, Korea

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A Gram-negative, non-motile and rod-, oval- or coccoid-shaped strain, DSW-17^T, was isolated from seawater of the East Sea, Korea, and subjected to a polyphasic taxonomic study. Strain DSW-17^T grew optimally at pH 7.0–8.0 and 25 °C. It contained Q-10 as the predominant ubiquinone and C_{18:1ω7c} as the major fatty acid. Major polar lipids were phosphatidylcholine, phosphatidylglycerol, phosphatidylethanolamine and an unidentified glycolipid. The DNA G + C content was 65.2 mol%. Phylogenetic analysis based on 16S rRNA gene sequences showed that strain DSW-17^T was phylogenetically most closely affiliated to the genus *Jannaschia*. Strain DSW-17^T exhibited 16S rRNA gene sequence similarity values of 96.5 % with the type strains of three recognized species of the genus *Jannaschia*. DNA–DNA relatedness data and differential phenotypic properties, together with the phylogenetic distinctiveness, demonstrated that strain DSW-17^T is distinguishable from the recognized species of the genus *Jannaschia*. On the basis of phenotypic, phylogenetic and genetic data, strain DSW-17^T was classified in the genus *Jannaschia* as a member of a novel species, for which the name *Jannaschia donghaensis* sp. nov. is proposed. The type strain is DSW-17^T (=KCTC 12862^T=JCM 14563^T).

The genus *Jannaschia* was created by Wagner-Döbler *et al.* (2003) with the description of a single species, *Jannaschia helgolandensis*. Three further species of the genus have been described subsequently, *Jannaschia cystaugens* (Adachi *et al.*, 2004), *Jannaschia rubra* (Macián *et al.*, 2005) and *Jannaschia seosinensis* (Choi *et al.*, 2006). However, *Jannaschia cystaugens* was reclassified as a synonym of *Thalassobacter stenotrophicus* by Pujalte *et al.* (2005). Phylogenetic analyses based on 16S rRNA gene sequences have shown that the genus *Jannaschia* falls within the class *Alphaproteobacteria* (Wagner-Döbler *et al.*, 2003; Choi *et al.*, 2006). In this study, we report the taxonomic characterization of a *Jannaschia*-like bacterial strain, DSW-17^T, which was isolated from seawater off Dokdo in the East Sea, Korea.

Seawater collected from the coast of Dokdo in the East Sea, Korea, was used as the source for the isolation of novel bacterial strains. Strain DSW-17^T was isolated by means of the standard dilution plating technique at 25 °C on marine agar 2216 (MA; Difco). The type strains of three species of the genus *Jannaschia* were used as reference strains for DNA–DNA hybridization. Cultures of *J. helgolandensis* DSM 14858^T and *J. rubra* DSM 16279^T were obtained from the Deutsche Sammlung von Mikroorganismen und Zellkulturen (DSMZ), Braunschweig, Germany. *J. seosinensis*

KCCM 42114^T was obtained from the Korean Culture Center of Microorganisms (KCCM), Seoul, Korea. The morphological, physiological and biochemical characteristics of strain DSW-17^T were investigated using routine cultivation on MA at 25 °C.

Cell morphology was examined by light microscopy (E600; Nikon) and transmission electron microscopy (TEM). Flagellation was determined by TEM (CM-20; Philips) with cells from exponentially growing cultures. Cells were negatively stained with 1 % (w/v) phosphotungstic acid and the grids were examined after being air-dried.

Growth under anaerobic conditions was determined after incubation in a Forma anaerobic chamber on MA and MA supplemented with nitrate, both of which had been prepared anaerobically using nitrogen. Growth in the absence of NaCl was investigated using trypticase soy broth prepared according to the formula of the Difco medium except that NaCl was excluded. Growth at various NaCl concentrations was investigated in marine broth 2216 (MB; Difco) or trypticase soy broth (Difco). Growth at various temperatures (4, 10, 15, 20, 22, 25, 28, 30, 31, 32, 33, 34, 35 and 40 °C) was measured on MA. Growth on trypticase soy agar (TSA; Difco), nutrient agar (NA; Difco) and MacConkey agar (Difco) was tested at 25 °C. Catalase and oxidase activities and hydrolysis of casein, starch and Tweens 20, 40, 60 and 80 were determined as described by Cowan & Steel (1965). Hydrolysis of hypoxanthine, tyrosine and xanthine was tested on MA using the substrate

Abbreviation: TEM, transmission electron microscopy.

The GenBank/EMBL/DBJ accession number for the 16S rRNA gene sequence of strain DSW-17^T is EF202612.

concentrations described by Cowan & Steel (1965). Hydrolysis of aesculin, gelatin and urea and nitrate reduction were investigated as described previously (Lanyi, 1987) with the modification that artificial seawater was used for the preparation of media. 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 previously (Bruns *et al.*, 2001).

Susceptibility to antibiotics was investigated on MA plates by using discs containing the following concentrations of antibiotic; 100 U polymyxin B, 50 μ g streptomycin, 20 U penicillin G, 100 μ g chloramphenicol, 10 μ g ampicillin, 30 μ g cephalothin, 30 μ g gentamicin, 5 μ g novobiocin, 30 μ g kanamycin, 30 μ g neomycin, 15 μ g oleandomycin, 100 μ g carbenicillin and 30 μ g tetracycline. Acid production from carbohydrates was tested as described by Leifson (1963) with the modification that artificial seawater was used. Utilization of various substrates for growth was determined as described by Baumann & Baumann (1981), using supplementation with 2% (v/v) Hutner's mineral salts solution (Cohen-Bazire *et al.*, 1957) and 1% (v/v) vitamin solution (Staley, 1968), and by Yurkov *et al.* (1994). Other physiological and biochemical tests were performed with the API 20E and API ZYM systems (bioMérieux). For *in vivo* pigment-absorption spectrum analysis, strain DSW-18^T was cultivated aerobically in the dark at 25 °C in MB. The culture was washed twice by centrifugation using a MOPS buffer (MOPS, 0.01 M NaOH, 0.1 M KCl, 0.001 M $MgCl_2$; pH 7.5) and disrupted by sonication (Sonifier 450; Branson). After removal of cell debris by centrifugation, the absorption spectrum of the supernatant was examined on a spectrophotometer (DU800; Beckman Coulter).

Cell biomass for DNA extraction and for isoprenoid quinone and polar lipid analyses was obtained from cultivation in MB at 25 °C. Chromosomal DNA was isolated and purified according to the method described by Yoon *et al.* (1996), with the exception that RNase T1 was used in combination with RNase A to minimize the contamination of RNA. The 16S rRNA gene was amplified by PCR using two universal primers, 5'-GAGTTTGA-TTCCTGGCTCAG-3' and 5'-AGAAAGGAGGTGATCCAG-CC-3', as described previously (Yoon *et al.*, 1998). Sequencing of the amplified 16S rRNA gene and phylogenetic analysis were performed as described by Yoon *et al.* (2003).

Isoprenoid quinones were analysed according to Komagata & Suzuki (1987) using reversed-phase HPLC. Polar lipids were extracted using the procedures described by Minnikin *et al.* (1984) and were identified by two-dimensional TLC followed by spraying with appropriate detection reagents (Minnikin *et al.*, 1984; Komagata & Suzuki, 1987). The presence of phosphatidylcholine was confirmed by spraying with Dragendorff's reagent (Sigma). For cellular fatty acid analysis, cell mass of strain DSW-17^T was harvested

from MA plates after cultivation for 7 days at 25 °C. The fatty acids were extracted and fatty acid methyl esters were 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 a modification that DNA was hydrolysed using nuclease P1 (Boehringer Mannheim) 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 DNA probes and 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.

The morphological, cultural, physiological and biochemical characteristics of strain DSW-17^T are given in the species description (see below) or are shown in Table 1. Strain DSW-17^T did not produce bacteriochlorophyll *a* aerobically in the dark. The sonicated *in vivo* cell extracts of strain DSW-17^T showed no absorption maximum between 400 and 1000 nm. The almost complete 16S rRNA gene sequence of strain DSW-17^T determined in this study comprised 1422 nucleotides, representing approximately 96% of the *Escherichia coli* 16S rRNA gene sequence. Comparative 16S rRNA gene sequence analysis revealed that strain DSW-17^T was most closely related to the genus *Jannaschia*. In the phylogenetic tree based on the neighbour-joining algorithm, strain DSW-17^T joined the clade comprising species of the genus *Jannaschia* with a bootstrap resampling value of 95.4% (Fig. 1). The same tree topology was also found in the trees based on the maximum-likelihood and maximum-parsimony algorithms (Fig. 1). Strain DSW-17^T exhibited 16S rRNA gene sequence similarity values of 96.5% to all of three recognized species of the genus *Jannaschia* and of less than 95.3% to other species used in the phylogenetic analysis.

The predominant isoprenoid quinone detected in strain DSW-17^T was ubiquinone-10 (Q-10) at a peak area ratio of approximately 95%. Major polar lipids found in strain DSW-17^T were phosphatidylcholine, phosphatidylglycerol, phosphatidylethanolamine and an unidentified glycolipid. The polar lipid profile of DSW-17^T was distinguishable from that of *J. helgolandensis* in that diphosphatidylglycerol was absent (Wagner-Döbler *et al.*, 2003). The fatty acid profile of strain DSW-17^T contained large amounts of unsaturated and straight-chain fatty acids; the major component (>10% of total fatty acids) was $C_{18:1\omega7c}$ (Table 2). This fatty acid profile was similar to those of recognized species of the genus *Jannaschia*, although there were differences in the proportions of some fatty acids, particularly $C_{19:0}$ and cyclo $C_{19:0\omega8c}$. These differences may result from variations in cultivation conditions and

Table 1. Differential phenotypic characteristics of *Jannaschia donghaensis* sp. nov. and other species of the genus *Jannaschia*

Species: 1, *J. donghaensis* sp. nov.; 2, *J. helgolandensis* (data from Wagner-Döbler *et al.*, 2003; Choi *et al.*, 2006); 3, *J. rubra* (Macián *et al.*, 2005; Choi *et al.*, 2006); 4, *J. seosinensis* (Choi *et al.*, 2006). +, Positive; –, negative; w, weakly positive; ND, not determined. Data in parentheses are for the type strain. All species are positive for catalase (not determined for *J. rubra*). All species are negative for Gram-staining and hydrolysis of urea (not determined for *J. rubra*).

Characteristic	1	2	3	4
Cell shape	Pleomorphic	Irregular rods	Rods	Rods
Cell length (µm)	0.6–5.0	1.9–3.2	1.0–2.0	1.1–2.3
Cell diameter (µm)	0.5–2.5	0.7–1.1	0.5	0.7–1.2
Motility	–	–	+	+
Colony colour	Strong orange	White	Red	Dark red
Maximum growth temperature (°C)	32	30	25	35
Optimum temperature for growth (°C)	25	25–30	20–25	30–35
Oxidase	+	w	+	–
Nitrate reduction to nitrite	–	–	–	+
Hydrolysis of:				
Aesculin	–	–	ND	+
Gelatin	–	–	–	+
Starch	–	–	–	+
Tween 80	w	–	–	–
Utilization of:				
Cellobiose	–	+	–	–
Citrate	–	+	w	–
D-Fructose	–	+	+	–
Galactose	–	+	+	ND
D-Glucose	–	+	+	+
Malate	–	+	+	ND
Mannose	–	+	+	–
Succinate	–	+	+	+
D-Xylose	–	+	+	–
Enzyme activity (by API ZYM)				
α-Glucosidase	–	(–)	+	+
Acid phosphatase	+	(w)	+	–
Esterase lipase (C8)	+	(w)	w	+
Naphthol-AS-BI-phosphohydrolase	–	(–)	+	–
Valine arylamidase	–	(–)	+	+
DNA G + C (mol%)	65.2	63.0–63.1	64.6	63

extraction procedures (Table 2). The DNA G + C content of strain DSW-17^T was 65.2 mol%.

There were no distinct phenotypic, particularly chemotaxonomic, properties which differentiated strain DSW-17^T from members of the genus *Jannaschia* (Wagner-Döbler *et al.*, 2003; Macián *et al.*, 2005; Choi *et al.*, 2006). Accordingly, it was concluded that strain DSW-17^T is a member of the genus *Jannaschia*. Strain DSW-17^T was distinguishable from recognized species of this genus by means of several phenotypic characteristics as listed in Table 1. Mean DNA–DNA relatedness values between strain DSW-17^T and the type strains of the three recognized species of the genus *Jannaschia* were 7–13%, when their DNAs were used individually as labelled DNA probes for cross-hybridization, indicating that strain DSW-17^T represents a separate species (Wayne *et al.*, 1987). This phylogenetic distinctiveness, together with the genetic distinctiveness and differential phenotypic properties, are

sufficient to designate strain DSW-17^T as a representative of the genus *Jannaschia* (Stackebrandt & Goebel, 1994). Therefore, on the basis of the data presented, strain DSW-17^T should be placed in the genus *Jannaschia* as representing a novel species, for which the name *Jannaschia donghaensis* sp. nov. is proposed.

Description of *Jannaschia donghaensis* sp. nov.

Jannaschia donghaensis (dong.ha.en'sis. N.L. fem. adj. *donghaensis* of Donghae, the Korean name for the East Sea of Korea, from where the organism was isolated).

Cells are Gram-negative and rod-, oval- or coccoid-shaped (0.5–2.5 × 0.6–5.0 µm). Colonies on MA are circular, raised, strong orange in colour and 1.0–1.5 mm in diameter after 7 days incubation at 25 °C. Growth does not occur on TSA, NA or MacConkey agar. Growth occurs at 4 and 32 °C, but not at 33 °C. Optimal pH for growth is

Fig. 1. Neighbour-joining phylogenetic tree based on 16S rRNA gene sequences showing the positions of *Jannaschia donghaensis* sp. nov. DSW-17^T, other species of the genus *Jannaschia* and other related taxa. Bootstrap values (expressed as percentages of 1000 replications) of >50% are shown at branch points. Filled circles indicate that the corresponding nodes were also recovered in the trees generated with the maximum-likelihood and maximum-parsimony algorithms. GenBank accession numbers are given in parentheses. *Stappia stellulata* IAM 12621^T was used as an outgroup. Bar, 0.01 substitutions per nucleotide position.

between 7.0 and 8.0; growth occurs at pH 6.0, but not at pH 5.5. Growth occurs in the presence of 7% (w/v) NaCl, but not in the absence of NaCl or in the presence of more than 8% (w/v) NaCl. Anaerobic growth does not occur

Table 2. Cellular fatty acid content (% of total) of *Jannaschia donghaensis* sp. nov. and other species of the genus *Jannaschia*

Strains, 1, *J. donghaensis* DSW-17^T; 2, *J. helgolandensis* Hel 10^T (data from Wagner-Döbler *et al.*, 2003); 3, *J. rubra* CECT 5088^T (Macián *et al.*, 2005); 4, *J. seosinensis* CL-SP26^T (Choi *et al.*, 2006). Fatty acids that represented <1.0% in all strains were omitted. —, Not detected.

Fatty acid	1	2	3	4
Straight-chain fatty acids				
C _{17:0}	1.8	1.0	—	—
C _{18:0}	5.2	10.8	8.1	12.0
C _{19:0}	5.9	—	—	—
Unsaturated fatty acids				
C _{12:1}	—	4.9	—	—
C _{18:1} ω7c	69.2	45.1	79.4	64.0
C _{18:3} ω6c	—	—	—	2.2
C _{20:1} ω7c	2.8	—	—	—
Hydroxy fatty acids				
C _{10:0} 3-OH	1.5	5.6	2.3	4.6
11-Methyl C _{18:1} ω7c	6.9	5.7	—	—
10-Methyl C _{19:0}	—	—	—	1.9
Cyclo C _{19:0} ω8c	—	25.1	5.7	—
C _{14:0} 3-OH/iso C _{16:1}	—	—	—	3.6
Summed feature 7*	2.9	—	—	—
Unknown fatty acids				
ECL 11.799	2.1	—	2.2	4.7
ECL 15.273	—	—	1.7	—

*Summed features represent groups of two or three fatty acids which could not be separated by GLC with the MIDI system. Summed feature 7 contained one or more of C_{19:1}ω6c, cyclo C_{19:0}ω10c and/or unknown fatty acid (ECL 18.846).

on MA or on MA supplemented with nitrate. Bacteriochlorophyll *a* is not produced. Hypoxanthine and Tweens 20, 40 and 60 are hydrolysed, but casein, L-tyrosine and xanthine are not. H₂S and indole are not produced. Arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase and tryptophan deaminase are absent. In assays with the API ZYM system, alkaline phosphatase, esterase (C4) and leucine arylamidase are present, but lipase (C14), cystine arylamidase, trypsin, α-chymotrypsin, α-galactosidase, β-galactosidase, β-glucuronidase, β-glucosidase, N-acetyl-β-glucosaminidase, α-mannosidase and α-fucosidase are absent. L-Arabinose, maltose, sucrose, trehalose, acetate, benzoate, pyruvate, salicin, formate and L-glutamate are not utilized. Acid is not produced from L-arabinose, D-cellobiose, D-fructose, D-galactose, D-glucose, lactose, maltose, D-mannose, D-melezitose, melibiose, D-raffinose, L-rhamnose, D-ribose, sucrose, trehalose, D-xylose, D-mannitol, D-sorbitol or *myo*-inositol. Susceptible to ampicillin, carbenicillin, cephalothin, chloramphenicol, gentamicin, kanamycin, neomycin, novobiocin, penicillin G, polymyxin B, streptomycin and tetracycline, but not to lincomycin or oleandomycin. The predominant ubiquinone is Q-10. The major fatty acid (>10% of total fatty acids) is C_{18:1}ω7c. Major polar lipids are phosphatidylcholine, phosphatidylglycerol, phosphatidylethanolamine and an unidentified glycolipid. The DNA G+C content is 65.2 mol% (determined by HPLC). Other phenotypic characteristics are given in Table 1.

The type strain, DSW-17^T (=KCTC 12862^T=JCM 14563^T), was isolated from seawater off Dokdo in the East Sea, Korea.

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References

- Adachi, M., Kanno, T., Okamoto, R., Shinozaki, A., Fujikawa-Adachi, K. & Nishijima, T. (2004). *Jannaschia cystaugens* sp. nov., an *Alexandrium* (Dinophyceae) cyst formation-promoting bacterium from Hiroshima Bay, Japan. *Int J Syst Evol Microbiol* **54**, 1687–1692.
- 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. G. Trüper, A. Balows & H. G. Schlegel. Berlin: Springer-Verlag.
- 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.
- Choi, D. H., Yi, H., Chun, J. & Cho, B. C. (2006). *Jannaschia seosinensis* sp. nov., isolated from hypersaline water of a solar saltern in Korea. *Int J Syst Evol Microbiol* **56**, 45–49.
- Cohen-Bazire, G., Sistrom, W. R. & Stanier, R. Y. (1957). Kinetic studies of pigment synthesis by non-sulfur purple bacteria. *J Cell Physiol* **49**, 25–68.
- 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 microdilution 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). Lipids and cell-wall analysis in bacterial systematics. *Methods Microbiol* **19**, 161–207.
- Lanyi, 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.
- Macián, M. C., Arahál, D. R., Garay, E., Ludwig, W., Schleifer, K. H. & Pujalte, M. J. (2005). *Jannaschia rubra* sp. nov., a red-pigmented bacterium isolated from sea water. *Int J Syst Evol Microbiol* **55**, 649–653.
- Minnikin, D. E., O'Donnell, A. G., Goodfellow, M., Alderson, G., Athalye, M., Schaál, A. & Parlett, J. H. (1984). An integrated procedure for the extraction of bacterial isoprenoid quinones and polar lipids. *J Microbiol Methods* **2**, 233–241.
- Pujalte, M. J., Macián, M. C., Arahál, D. R. & Garay, E. (2005). *Thalassobacter stenotrophicus* Macián et al. 2005 is a later synonym of *Jannaschia cystaugens* Adachi et al. 2004, with emended description of the genus *Thalassobacter*. *Int J Syst Evol Microbiol* **55**, 1959–1963.
- Sasser, M. (1990). *Identification of bacteria by gas chromatography of cellular fatty acids*, MIDI Technical Note 101. 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.
- Wagner-Döbler, I., Rheims, H., Felske, A., Pukall, R. & Tindall, B. J. (2003). *Jannaschia helgolandensis* gen. nov., sp. nov., a novel abundant member of the marine *Roseobacter* clade from the North Sea. *Int J Syst Evol Microbiol* **53**, 731–738.
- 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.
- 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., Kang, K. H. & Park, Y.-H. (2003). *Psychrobacter jeotgali* sp. nov., isolated from jeotgal, a traditional Korean fermented seafood. *Int J Syst Evol Microbiol* **53**, 449–454.
- Yurkov, V., Stackebrandt, E., Holmes, A., Fuerst, J. A., Hugenholtz, 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.