Erythrobacter marinus sp. nov., isolated from seawater

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A Gram-negative, non-motile, ovoid to rod-shaped bacterium, designated strain HWDM-33^T, was isolated from seawater of the Yellow Sea, Korea, and was subjected to a polyphasic taxonomic study. Strain HWDM-33^T grew optimally at pH 7–8, at 25 °C and in the presence of 2–3 % (w/v) NaCl. Neighbour-joining, maximum-likelihood and maximum-parsimony phylogenetic trees based on 16S rRNA gene sequences showed that strain HWDM-33^T clustered with *Erythrobacter gangjinensis* K7-2^T, with which it shared 96.9 % sequence similarity. Strain HWDM-33^T exhibited 94.2–95.8 % 16S rRNA gene sequence similarity to the type strains of other recognized species of the genus *Erythrobacter*. Strain HWDM-33^T contained Q-10 as the predominant ubiquinone and C_{18:1}ω7c, C_{17:1}ω6c, and C_{16:1}ω7c and/or iso-C_{15:0} 2-OH as the major fatty acids. The major polar lipids were sphingoglycolipid, phosphatidylglycerol, phosphatidylcholine, phosphatidylethanolamine and an unidentified lipid. The DNA G + C content of strain HWDM-33^T was 66.1 mol%. Differential phenotypic properties and phylogenetic distinctiveness demonstrated that strain HWDM-33^T was separate from *E. gangjinensis* and other recognized species of the genus *Erythrobacter*. On the basis of the data presented here, strain HWDM-33^T represents a novel species of the genus *Erythrobacter*, for which the name *Erythrobacter marinus* sp. nov. is proposed. The type strain is HWDM-33^T (=KCTC 23554^T =CCUG 60528^T).

The genus *Erythrobacter*, a member of the class *Alpha-proteobacteria*, was first proposed by Shiba & Simidu (1982) with the description of a single species, *Erythrobacter longus*. Ten further species of the genus *Erythrobacter*, namely *Erythrobacter litoralis* (Yurkov *et al.*, 1994), *E. citreus* (Denner *et al.*, 2002), *E. flavus* (Yoon *et al.*, 2003b), *E. aquimaris* (Yoon *et al.*, 2004), *E. gaetbuli* and *E. seohaensis* (Yoon *et al.*, 2005a), *E. luteolus* (Yoon *et al.*, 2005b), *E. vulgaris* (Ivanova *et al.*, 2005), *E. gangjinensis* (Lee *et al.*, 2010) and *E. nanhaiediminis* (Xu *et al.*, 2010), have since been described. However, *E. luteolus* has been reclassified as *Altererythrobacter luteolus* (Kwon *et al.*, 2007). In this study, we describe a bacterial strain, designated HWDM-33^T, which was isolated from seawater of the Yellow Sea, Korea. Comparative 16S rRNA gene sequence analysis indicated that this strain was phylogenetically most closely related to members of the genus *Erythrobacter*. The aim of the present work was to determine the exact taxonomic

position of strain HWDM-33^T by using a polyphasic approach that included the determination of phenotypic properties and a detailed phylogenetic investigation based on 16S rRNA gene sequences.

Strain HWDM-33^T was isolated by using the standard dilution plating technique at 25 °C on marine agar 2216 (MA; Difco) and cultivated routinely on MA at 25 °C. *E. gangjinensis* KCTC 22330^T and *E. longus* DSM 6997^T (the type species of the genus *Erythrobacter*) were used as reference strains for fatty acid and polar lipid analyses and other phenotypic tests. Cell morphology was examined by light microscopy (DP70; Olympus) and transmission electron microscopy (CM-20; Philips). The latter technique was also used to assess the presence of flagella on cells from an exponentially growing culture on MA. For this, cells were negatively stained with 1 % (w/v) phosphotungstic acid and the grids were examined after being air-dried. The Gram reaction was determined by using the bioMérieux Gram stain kit according to the manufacturer's instructions. Growth under anaerobic conditions was determined

The GenBank/EMBL/DBJ accession number for the 16S rRNA gene sequence of strain HWDM-33^T is HQ117934.

after incubation in an anaerobic chamber (1029; Forma, N₂/CO₂/H₂, 86:7:7%) on MA that had been prepared anaerobically in a nitrogen atmosphere. Growth at 4, 10, 20, 25, 30, 34, 35 and 37 °C was measured on MA. The pH range for growth was investigated in marine broth 2216 (MB; Difco) adjusted to pH 4.5–9.5 (increments of 0.5 pH units) by using sodium acetate/acetic acid and Na₂CO₃ buffers. pH was verified after autoclaving. 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 in trypticase soy broth prepared according to the formula of the Difco medium except that NaCl was excluded and that 0.45 % (w/v) MgCl₂·6H₂O was added. Growth in the presence of 2.0–6.0 % (w/v) NaCl (increments of 1.0 %) was investigated in

MB. Catalase and oxidase activities were determined as described by Cowan & Steel (1965). Hydrolysis of casein, starch, hypoxanthine, tyrosine and xanthine was tested on MA by 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 the preparation of media. The artificial seawater contained (l⁻¹ distilled water) 23.6 g NaCl, 0.64 g KCl, 4.53 g MgCl₂·6H₂O, 5.94 g MgSO₄·7H₂O and 1.3 g CaCl₂·2H₂O (Bruns *et al.*, 2001). H₂S production was tested as described by Bruns *et al.* (2001). Acid production from carbohydrates was tested as described by Leifson (1963). Utilization of various substrates

Table 1. Differential phenotypic characteristics between strain HWDM-33^T and the type strains of *Erythrobacter gangjinensis* and *Erythrobacter longus*

Strains: 1, HWDM-33^T; 2, *E. gangjinensis* KCTC 22330^T; 3, *E. longus* DSM 6997^T. All data are from this study unless indicated otherwise. +, Positive; –, negative; w, weakly positive. All strains were positive for: oxidase and catalase activity*; hydrolysis of Tweens 40, 60 and 80, and activity of alkaline phosphatase, esterase lipase (C8) and leucine arylamidase. All strains were susceptible to carbenicillin, cephalothin (*E. longus* DSM 6997^T was weakly susceptible), novobiocin and oleandomycin. All strains were negative for Gram reaction*, hydrolysis of gelatin*, hypoxanthine, urea and xanthine, utilization of L-arabinose, D-fructose, D-galactose, D-mannose, salicin, sucrose, trehalose, benzoate, citrate, formate and L-glutamate, and activity of lipase (C14), α-galactosidase, β-galactosidase, β-glucuronidase, α-glucosidase, β-glucosidase, N-acetyl-β-glucosaminidase, α-mannosidase and α-fucosidase. All strains were resistant to neomycin.

Characteristic	1	2	3
Optimal growth temperature (°C)	25	30*	25–30*
Motility	–	–*	+*
Presence of bacteriochlorophyll <i>a</i>	–	–*	+*
Nitrate reduction	–	–*	+*
Hydrolysis of:			
Aesculin	+	–	+
Casein	+	–*	+
Starch	–	+*	–
Tween 20, L-tyrosine	–	+	+
Utilization of:			
Cellobiose, D-glucose	+	+	–
Maltose, acetate, L-malate, succinate	–	+	–
D-Xylose, pyruvate	+	–	–
Susceptibility to:			
Ampicillin	+	–†	–†
Chloramphenicol	–	+	+
Gentamicin, kanamycin	–	+	–
Lincomycin, polymyxin B, streptomycin	+	–	–
Penicillin G	+	+	–
Tetracycline	+	+	w
Enzyme activity (API ZYM)			
Esterase (C4)	w	w	+
Valine arylamidase, trypsin	–	–	+
Cystine arylamidase, naphthol-AS-BI-phosphohydrolase	–	–	w
α-Chymotrypsin	w	+	+
Acid phosphatase	–	+	–
DNA G + C content (mol%)	66.1	61.6*	60.7*

*Data for reference strains from Shiba & Simidu (1982) and Lee *et al.* (2010).

†Opposite to result obtained by Lee *et al.* (2010).

for growth was determined according to Baumann & Baumann (1981), in medium supplemented with 2% (v/v) Hutner's mineral salts solution (Cohen-Bazire *et al.*, 1957) and 1% (v/v) vitamin solution (Staley, 1968). Carbon sources were added at a concentration of 0.2% (w/v) after sterilization by filtration. Susceptibility to antibiotics was tested on MA plates by using antibiotic discs (Advantec) containing the following compounds (μg per disc, unless stated otherwise): ampicillin (10), carbenicillin (100), cephalothin (30), chloramphenicol (100), gentamicin (30), kanamycin (30), lincomycin (15), neomycin (30), novobiocin (5), oleandomycin (15), penicillin G (20 U), polymyxin B (100 U), streptomycin (50) and tetracycline (30). The API ZYM system (bioMérieux), with incubation at 25 °C for 8 h, was used to investigate enzyme activities. For spectral analysis of *in vivo* pigment absorption, strain HWDM-33^T was cultivated aerobically in the dark at 25 °C in MB. The culture was washed twice by using centrifugation with a 3-(*N*-morpholino)propanesulfonic acid (MOPS) buffer (MOPS/NaOH, 0.01 M; KCl, 0.1 M; MgCl₂, 0.001 M; pH 7.5) and disrupted by means of sonication (450 sonifier; Branson). After removal of cell debris by centrifugation, the absorption spectrum of the supernatant was examined on a Beckman Coulter DU800 spectrophotometer.

Strain HWDM-33^T was cultivated in MB at 25 °C to obtain the cell biomass required for DNA extraction and for analyses of isoprenoid quinones and polar lipids. Cell mass of *E. gangjinensis* KCTC 22330^T and *E. longus* DSM 6997^T for polar lipid analysis was obtained from cultures grown at 25 °C in MB. 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 contamination by RNA. The 16S rRNA gene was amplified by PCR with two universal primers (5'-GAGTTTGATCCTGGCTCAG-3' and 5'-AG-AAAGGAGGTGATCCAGCC-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.* (2003a). Isoprenoid quinones were extracted according to the method of Komagata & Suzuki (1987) and analysed by using reversed-phase HPLC with a YMC ODS-A (250 × 4.6 mm) column. For cellular fatty acid analysis, cell mass of strains HWDM-33^T, *E. gangjinensis* KCTC 22330^T and *E. longus* DSM 6997^T was harvested from MA plates after cultivation for 5 days at 25 °C. Fatty acids were saponified, methylated and extracted by using the standard protocol of the MIDI system (Sherlock Microbial Identification System, version 4.0). The fatty acids were analysed by GC (Hewlett Packard 6890) and identified with reference to the TSBA40 database of the Microbial Identification System (Sasser, 1990). Polar lipids were extracted according to the procedures described by Minnikin *et al.* (1984) and identified by two-dimensional TLC followed by spraying with molybdophosphoric acid, molybdenum blue, ninhydrin and α -naphthol reagents (Minnikin *et al.*, 1984; Komagata & Suzuki, 1987). The presence of phosphatidylcholine was identified by spraying with Dragendorff's reagent (Sigma). The DNA G + C content was determined by using the method of Tamaoka & Komagata (1984) with the modification that DNA was hydrolysed and the resultant nucleotides were analysed by reversed-phase HPLC with a YMC ODS-A (250 × 4.6 mm) column. The nucleotides were eluted by a mixture of 0.55 M

Fig. 1. Neighbour-joining tree based on 16S rRNA gene sequences showing the phylogenetic positions of strain HWDM-33^T, the type strains of recognized species of the genus *Erythrobacter* and representatives of some other related taxa. Bootstrap values >50% (expressed as percentages of 1000 replications) 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. *Rhodospirillum rubrum* ATCC 11170^T (GenBank accession no. D30778) was used as an outgroup (not shown). Bar, 0.01 substitutions per nucleotide position.

NH₄H₂PO₄ (pH 4.0) and acetonitrile (40:1, v/v), by using a flow rate of 1 ml min⁻¹ at room temperature, and detected by measuring A₂₇₀.

The morphological, cultural, physiological and biochemical characteristics of strain HWDM-33^T are given in the species description below and in Table 1. Sonicated cell extracts of strain HWDM-33^T showed an absorption maximum at 450 nm, indicating the presence of carotenoids. The almost-complete 16S rRNA gene sequence of strain HWDM-33^T comprised 1442 nt. In the phylogenetic tree reconstructed with the neighbour-joining algorithm, strain HWDM-33^T joined the type strain of *E. gangjinensis* with a bootstrap resampling value of 100 % (Fig. 1). The relationship between strain HWDM-33^T and *E. gangjinensis* K7-2^T was also found in the trees reconstructed with the maximum-likelihood and maximum-parsimony algorithms (Fig. 1). Strain HWDM-33^T shared 96.9 % 16S rRNA gene sequence similarity with *E. gangjinensis* K7-2^T and 94.2–95.8 % sequence similarity with the type strains of other recognized species of the genus *Erythrobacter*. The predominant isoprenoid quinone detected in strain HWDM-33^T was ubiquinone-10 (Q-10), which is in line with previous data for the genus *Erythrobacter* (Yoon *et al.*, 2003b, 2005a; Lee *et al.*, 2010; Xu *et al.*, 2010). The complete fatty acid profiles of strain HWDM-33^T and the type strains of *E. gangjinensis* and *E. longus*, grown and analysed under identical conditions in this study, are given in Table 2. The major fatty acids (>10 % of the total) found in strain HWDM-33^T were C_{18:1}ω7c (39.6 %), C_{17:1}ω6c (13.2 %), and C_{16:1}ω7c and/or iso-C_{15:0} 2-OH (12.4 %). Strain HWDM-33^T contained significant amounts of 2-hydroxy fatty acids, similar to other recognized species of the genus *Erythrobacter* (Table 2; Xu *et al.*, 2010). The fatty acid profiles of the three strains were similar, even though there were differences in the respective proportions of some components (Table 2). The polar lipid profiles of strains HWDM-33^T, *E. gangjinensis* KCTC 22330^T and *E. longus* DSM 6997^T analysed in this study are given in Fig. 2. The major polar lipids detected in strain HWDM-33^T were sphingoglycolipid, phosphatidylcholine, phosphatidylglycerol, phosphatidylethanolamine and an unidentified lipid (Fig. 2). The polar lipid profile of strain HWDM-33^T was similar to those of *E. gangjinensis* KCTC 22330^T and *E. longus* DSM 6997^T in that sphingoglycolipid, phosphatidylglycerol, phosphatidylcholine and phosphatidylethanolamine are major components. However, unidentified lipids, which are major components in *E. gangjinensis* KCTC 22330^T and *E. longus* DSM 6997^T, were not found in strain HWDM-33^T. In this study, the three strains showed the presence of sphingoglycolipid, which is characteristic of all taxa of the family *Sphingomonadaceae*; *E. citreus* has also been found to contain sphingoglycolipid (Kosako *et al.*, 2000; Denner *et al.*, 2002). However, in the study of Xu *et al.* (2010), several *Erythrobacter* strains, including the type strains of *E. longus* and *E. citreus*, were found not to have sphingoglycolipid. The DNA G + C content of strain HWDM-33^T was 66.1 mol%. The phylogenetic and chemotaxonomic

Table 2. Cellular fatty acid compositions (%) of strain HWDM-33^T and the type strains of *Erythrobacter gangjinensis* and *Erythrobacter longus*

Strains: 1, HWDM-33^T; 2, *E. gangjinensis* KCTC 22330^T; 3, *E. longus* DSM 6997^T. All data are from this study. Fatty acids that represented <0.5 % in all strains were omitted. —, Not detected.

Fatty acid	1	2	3
Straight-chain			
C _{15:0}	1.0	—	2.1
C _{16:0}	4.8	3.8	7.6
C _{17:0}	0.8	—	6.8
Unsaturated			
C _{16:1} ω5c	0.7	1.1	—
C _{17:1} ω6c	13.2	4.3	4.5
C _{17:1} ω8c	1.4	—	6.5
C _{18:1} ω5c	0.6	0.6	—
C _{18:1} ω7c	39.6	54.9	47.2
Hydroxy			
C _{13:0} 2-OH	—	—	0.6
C _{14:0} 2-OH	5.3	8.7	5.0
C _{15:0} 2-OH	4.0	1.4	10.8
C _{16:0} 2-OH	6.5	—	0.8
C _{16:1} 2-OH	1.1	5.4	—
iso-C _{16:0} 3-OH	1.2	0.7	—
Branched			
iso-C _{17:0}	—	—	1.8
11-methyl C _{18:1} ω7c	7.1	3.8	—
Summed feature 3*	12.4	14.9	0.9
Unknown ECL 18.814†	—	—	3.6

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

†ECL, equivalent chain-length.

data presented here suggest that strain HWDM-33^T is a member of the genus *Erythrobacter*.

Strain HWDM-33^T was clearly distinguishable from *E. gangjinensis* based on differences in several phenotypic characteristics, most of which were determined by using the same methods in this study (Table 1). The phylogenetic distinctiveness and differential phenotypic properties of strain HWDM-33^T are sufficient to categorize it as a member of a novel species that is separate from recognized species of the genus *Erythrobacter* (Stackebrandt & Goebel, 1994). On the basis of the data presented here, strain HWDM-33^T represents a novel species of the genus *Erythrobacter*, for which the name *Erythrobacter marinus* sp. nov. is proposed.

Description of *Erythrobacter marinus* sp. nov.

Erythrobacter marinus (ma.ri'nus. L. masc. adj. *marinus* of the sea, marine).

Cells are Gram-negative, non-motile, 0.3–0.5 × 0.5–1.0 μm and ovoid to rod-shaped. Colonies on MA are circular,

Fig. 2. Thin-layer chromatograms of polar lipids of strain HWDM-33^T (a), *Erythrobacter gangjinensis* KCTC 22330^T (b) and *Erythrobacter longus* DSM 6997^T (c). SGL, sphingoglycolipid; PC, phosphatidylcholine; PG, phosphatidylglycerol; PE, phosphatidylethanolamine; L1–L4, unidentified lipids.

convex, smooth, glistening, yellowish-orange and 0.5–0.8 mm long after incubation for 5 days at 25 °C. Optimal growth occurs at 25 °C; growth occurs at 4 and 34 °C but not at 35 °C. Optimal pH for growth is between pH 7.0 and 8.0; growth occurs at pH 5.5 but not at pH 5.0. Optimal growth occurs in the presence of 2–3% (w/v) NaCl; growth occurs in the presence of 5.0% (w/v) NaCl, but not in the absence of NaCl or in the presence of more than 6.0% (w/v) NaCl. Mg²⁺ ions are required for growth. Anaerobic growth does not occur on MA. Acid is produced from cellobiose, L-rhamnose and D-xylose but not from L-arabinose, D-fructose, D-galactose, D-glucose, lactose,

maltose, D-mannose, melezitose, melibiose, raffinose, D-ribose, sucrose, trehalose, *myo*-inositol, D-mannitol or D-sorbitol. H₂S is not produced. Carotenoid pigments are produced but bacteriochlorophyll *a* is not. The predominant ubiquinone is Q-10. The major fatty acids (>10% of the total) are C_{18:1}ω7c, C_{17:1}ω6c, and C_{16:1}ω7c and/or iso-C_{15:0} 2-OH. The major polar lipids are sphingoglycolipid, phosphatidylglycerol, phosphatidylcholine, phosphatidylethanolamine and an unidentified lipid. Other phenotypic characteristics are given in Table 1.

The type strain, HWDM-33^T (=KCTC 23554^T =CCUG 60528^T), was isolated from seawater of Hwang-do, an island of the Yellow Sea, Korea. The DNA G + C content of the type strain is 66.1 mol% (determined by HPLC).

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