Porphyrobacter dokdonensis sp. nov., isolated from sea water

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A Gram-negative, non-motile, non-spore-forming, slightly halophilic bacterial strain, DSW-74^T, was isolated from sea water off the island of Dokdo, Korea, and its taxonomic position was investigated by a polyphasic study. Strain DSW-74^T grew optimally at 37 °C and in the presence of 2% (w/v) NaCl. It contained Q-10 as the predominant ubiquinone and C_{17:1}ω6c and C_{18:1}ω7c as the major fatty acids. Its DNA G + C content was 65.8 mol%. Phylogenetic analyses based on 16S rRNA gene sequences revealed that strain DSW-74^T was most closely related to *Porphyrobacter* species. Similarity values between the 16S rRNA gene sequence of strain DSW-74^T and those of the type strains of recognized *Porphyrobacter* species and of *Erythromicrobium ramosum* were in the range 97.4–98.7%. Strain DSW-74^T exhibited 16S rRNA gene sequence similarity values of <97.5% to recognized *Erythrobacter* species and the other species used in the phylogenetic analysis. DNA–DNA relatedness levels and differential phenotypic properties made it possible to categorize strain DSW-74^T as representing a novel *Porphyrobacter* species. On the basis of the taxonomic data presented, it is proposed that DSW-74^T (=KCTC 12395^T = DSM 17193^T) should be classified in the genus *Porphyrobacter* as the type strain of a novel species, *Porphyrobacter dokdonensis* sp. nov.

The genus *Porphyrobacter* was proposed by Fuerst *et al.* (1993) and, at the time of writing, the genus comprises five recognized species: *Porphyrobacter neustonensis* (Fuerst *et al.*, 1993), *Porphyrobacter tepidarius* (Hanada *et al.*, 1997), *Porphyrobacter sanguineus* (Hiraishi *et al.*, 2002), *Porphyrobacter cryptus* (Rainey *et al.*, 2003) and *Porphyrobacter donghaensis* (Yoon *et al.*, 2004). Phylogenetic analyses based on 16S rRNA gene sequences have shown that the genus *Porphyrobacter* belongs within the *Alphaproteobacteria* (Anzai *et al.*, 2000; Hiraishi *et al.*, 2002; Rainey *et al.*, 2003; Yoon *et al.*, 2004). Here we report on the detailed taxonomic characterization of a *Porphyrobacter*-like bacterial strain, designated DSW-74^T.

Sea water collected from off the island of Dokdo, Korea, was used as the source for isolation of bacterial strains. Strain DSW-74^T was isolated by the standard dilution plating

technique on marine agar 2216 (MA; Difco) at 30 °C. The type strains of the five recognized *Porphyrobacter* species were used as reference strains for DNA–DNA hybridization and phenotypic characterization: *P. neustonensis* DSM 9434^T, *P. tepidarius* DSM 10594^T, *P. sanguineus* DSM 11032^T and *P. cryptus* DSM 12079^T were obtained from the Deutsche Sammlung von Mikroorganismen und Zellkulturen (DSMZ), Braunschweig, Germany, and *P. donghaensis* SW-132^T was obtained from the study of Yoon *et al.* (2004). To investigate its morphological and some physiological characteristics, strain DSW-74^T was routinely cultivated on MA at 30 °C. Cell morphology was examined by light microscopy (Nikon E600) and transmission electron microscopy. Transmission electron microscopy was also used to determine whether flagella were present in cells from exponentially growing cultures; cells were negatively stained with 1% (w/v) phosphotungstic acid and the grids were examined after air-drying with a Philips CM-20 transmission electron microscope. The Gram reaction was determined by using the bioMérieux Gram stain kit according to the manufacturer's instructions. The pH range for growth was determined in marine broth 2216 (MB; Difco) that was adjusted to various pH values (initial pH 4.5–10.5 at intervals of 0.5 pH units). The pH was adjusted prior to sterilization to various levels by the addition of HCl or Na₂CO₃. Growth in the absence of NaCl was investigated in

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Abbreviation: BChl, bacteriochlorophyll.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain DSW-74^T is DQ011529.

A figure showing the absorption spectra of sonicated cell extract and acetone–methanol cell extract of strain DSW-74^T is available as supplementary material in IJSEM Online.

trypticase soy broth lacking NaCl. Growth at various NaCl concentrations [0.5 % (w/v) and 1.0–10.0 % (w/v) at intervals of 1.0 % units] was investigated in MB and trypticase soy broth (Difco). Growth at various temperatures (4–50 °C) was measured on MA. Growth under anaerobic conditions was determined after incubation in an anaerobic chamber on MA and on MA supplemented with nitrate, both of which had been prepared anaerobically using nitrogen. Catalase and oxidase activities and hydrolysis of casein and starch were determined as described by Cowan & Steel (1965). Hydrolysis of Tweens 20, 40, 60 and 80 was determined as described by Cowan & Steel (1965) with a modification that artificial sea water was used instead of distilled water. Hydrolysis of aesculin, gelatin and urea and reduction of nitrate were determined as described by Lanyi (1987) with a modification that artificial sea water was used instead of distilled water. The artificial sea water contained (per litre of 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). Hydrolysis of hypoxanthine, tyrosine and xanthine was investigated on MA with the substrate concentrations given by Cowan & Steel (1965). Production of H₂S was tested as described by Bruns *et al.* (2001). Acid production from carbohydrates was determined using the method of Leifson (1963). Utilization of substrates as sole carbon and energy sources was tested as described by Baumann & Baumann (1981) using supplementation with 2 % (v/v) Hutner's mineral base (Cohen-Bazire *et al.*, 1957) and 1 % (v/v) vitamin solution (Staley, 1968). For *in vivo* pigment-absorption spectrum analysis, two test strains were cultivated aerobically in the dark at 37 °C in liquid *Erythromicrobium*/*Roseococcus* medium (Yurkov *et al.*, 1994; DSMZ medium no. 767) with a modification that D-glucose was used instead of acetate. The cultures were washed twice by centrifugation using a MOPS buffer (MOPS/NaOH, 0.01 M; KCl, 0.1 M; MgCl₂, 0.001 M; pH 7.5) and disrupted by sonication with a Branson Sonifier 450. After removal of cell debris by centrifugation, the absorption spectrum of the supernatant was examined on a Beckman Coulter DU800 spectrophotometer. Susceptibility to antibiotics was tested on MA plates using antibiotic discs containing the following: 100 U polymyxin B, 50 µg streptomycin, 20 U penicillin G, 100 µg chloramphenicol, 10 µg ampicillin, 30 µg cephalothin, 30 µg gentamicin, 5 µg novobiocin, 30 µg tetracycline, 30 µg kanamycin, 15 µg lincomycin, 15 µg oleandomycin, 30 µg neomycin or 100 µg carbenicillin. Other physiological and biochemical tests were performed with the API 20E system (bioMérieux).

Cell biomass of strain DSW-74^T for DNA extraction and for isoprenoid quinone analysis was obtained by cultivation for 6 days in MB at 37 °C. Chromosomal DNA was isolated and purified according to the method described previously (Yoon *et al.*, 1996), with the exception that RNase T1 was used in combination with RNase A to minimize contamination with RNA. The 16S rRNA gene was amplified by PCR using two universal primers (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 extracted according to the method of Komagata & Suzuki (1987) and analysed using reversed-phase HPLC and a YMC ODS-A (250 × 4.6 mm) column. For fatty acid methyl ester analysis, cell mass of strain DSW-74^T was harvested from agar plates after incubation for 7 days on MA at 37 °C. The fatty acid methyl esters were extracted and 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 and the resultant nucleotides were analysed by reversed-phase HPLC. DNA–DNA hybridization was performed fluorometrically according to the method of Ezaki *et al.* (1989) by 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.

Morphological, cultural, physiological and biochemical characteristics of strain DSW-74^T are given in the species description (see later) or are shown in Table 1, together with those of the five recognized *Porphyrobacter* species. Strain DSW-74^T produced bacteriochlorophyll (BChl) *a* aerobically in the dark. The sonicated cell extract showed absorption maxima at approximately 457, 481, 583, 800, 835 and 862 nm, which indicated the presence of carotenoids and BChl *a* (see Supplementary Fig. S1 in IJSEM Online). The *in vivo* absorption spectrum of strain DSW-74^T was distinguishable from those of the other *Porphyrobacter* species, with the exception of *P. sanguineus*, in that three absorption maxima existed between 799 and 870 nm (Table 1). The acetone–methanol extract had *in vitro* absorption peak maxima at 454, 477 and 769 nm, confirming the presence of carotenoids and BChl *a* (Supplementary Fig. S1).

The almost complete 16S rRNA gene sequence of strain DSW-74^T, comprising 1440 nt (approximately 96 % of the *Escherichia coli* 16S rRNA sequence), was determined in this study. The 16S rRNA gene sequence analyses revealed that strain DSW-74^T was most closely affiliated to the genus *Porphyrobacter*. In the neighbour-joining tree based on 16S rRNA gene sequences, strain DSW-74^T fell within the radiation of the cluster comprising *Porphyrobacter* species, and joined the type strain of *P. cryptus* at a bootstrap confidence level of 91.1 %. Similar topologies were found in the tree generated with the maximum-parsimony algorithm (data not shown). The 16S rRNA gene sequence of strain DSW-74^T exhibited similarity values of 97.4–98.7 % to those of the type strains of the five recognized *Porphyrobacter* species and *Erythromicrobium ramosum*. Strain DSW-74^T exhibited 16S rRNA gene sequence similarity levels of 93.8–97.5 % to *Erythrobacter* species and of <93.6 % to all other species used in the phylogenetic analysis (Fig. 1).

Table 1. Differential phenotypic characteristics of *Porphyrobacter* species

Species: 1, *P. dokdonensis* sp. nov.; 2, *P. neustonensis*, data from Fuerst *et al.* (1993) and this study; 3, *P. tepidarius*, data from Hanada *et al.* (1997) and this study; 4, *P. sanguineus*, data from Hiraishi *et al.* (2002) and this study; 5, *P. cryptus*, data from Rainey *et al.* (2003) and this study; 6, *P. donghaensis*, data from Yoon *et al.* (2004). *n*, Number of strains; +, positive reaction; –, negative reaction; w, weakly positive; v, variable reaction; data in parentheses are for the type strain. All species are aerobic, Gram-negative and non-sporulating. All species are positive for the presence of BChl *a* and utilization of D-glucose. All species are negative for utilization of citrate.

Characteristic	1 (<i>n</i> =1)	2 (<i>n</i> =4)	3 (<i>n</i> =1)	4 (<i>n</i> =2)	5 (<i>n</i> =2)	6 (<i>n</i> =2)
Cell morphology	Pleomorphic	Pleomorphic	Ovoid or short rods	Pleomorphic	Short rods	Pleomorphic
Catalase	+	+	+	+	+	+
Oxidase	+	–	–	+	+	+
Motility	–	+	–	+	+	–
Growth at 0% (w/v) NaCl	w	+	+	–	+	+
Hydrolysis of:						
Aesculin	+	v (+)	+	+	+	+
Casein	–	v (–)	–	–	–	–
Gelatin	–	–	–	–	+	–
Starch	+	–	+	–	+	+
Tween 80	+	+	+	–	+	+
Utilization of:						
D-Fructose	–	v (–)	–	–	–	–
D-Galactose	–	+	–	–	–	–
D-Cellobiose	+	v (–)	+	+	+	+
D-Mannose	–	+	–	–	–	–
D-Trehalose	–	v (+)	–	+	–	–
D-Xylose	–	+	–	–	+	v (+)
L-Arabinose	–	–	–	–	–	–
Sucrose	–	+	–	+	+	v (–)
Acetate	–	–	+	+	–	v (–)
Succinate	+	v (+)	–	–	–	+
L-Malate	+	–	–	–	–	+
Pyruvate	+	v (+)	–	+	+	+
L-Glutamate	–	–	+	+	+	–
Maximum growth temperature (°C)	43	37	52	37	<60	<50
Optimum growth temperature (°C)	35–37	30	40–48	30	50	30–37
Absorption maxima (nm) of sonicated cell extracts	457, 481, 583, 800, 835, 862	799–806, 868–871	460, 494, 596, 800, 870	463, 799, 814, 861	800, 870	467, 590, 808, 867
DNA G+C content (mol%)	65.8	65.7–66.4	65.0	63.8–64.0	66.2	65.9–66.8

*Data taken from this study for the type strain.

The predominant respiratory lipoquinone detected in strain DSW-74^T was ubiquinone-10 (Q-10) at a peak area ratio of approximately 82%. Strain DSW-74^T had a cellular fatty acid profile that contained large amounts of unsaturated, straight-chain and hydroxy fatty acids; the major components (>1% of total fatty acids) were C_{17:1}ω6c (30.6%), C_{18:1}ω7c (28.5%), C_{16:0} (8.7%), C_{15:0} 2-OH (6.4%), C_{18:0} (5.0%), C_{14:0} 2-OH (4.5%), C_{18:1}ω5c (3.0%), C_{17:1}ω8c (2.8%), C_{17:0} (2.0%), C_{13:0} 2-OH (1.9%), C_{16:0} 2-OH (1.7%), C_{15:0} (1.7%) and C_{16:1}ω7c and/or iso-C_{15:0} 2-OH (1.2%). Branched fatty acids were found as minor components in strain DSW-74^T, which was also characteristic for the five recognized *Porphyrobacter* species (Hiraishi *et al.*, 2002; Rainey *et al.*, 2003; Yoon *et al.*, 2004). This fatty

acid profile was similar to those of *Porphyrobacter* species analysed previously, although there were differences in the proportions of some fatty acids, perhaps owing to differences in the cultivation conditions used, e.g. temperature and cultivation medium (Hiraishi *et al.*, 2002; Rainey *et al.*, 2003; Yoon *et al.*, 2004). The DNA G+C content of strain DSW-74^T was 65.8 mol%.

There were no distinct phenotypic, particularly chemotaxonomic, properties for differentiating strain DSW-74^T and the genus *Porphyrobacter* from the genera *Erythrobacter* and *Erythromicrobium* (Rainey *et al.*, 2003). The relationship between the clade comprising strain DSW-74^T and the genera *Porphyrobacter* and *Erythromicrobium* and the clade

Fig. 1. Neighbour-joining tree based on 16S rRNA gene sequences showing the phylogenetic positions of strain DSW-74^T and representatives of some other related taxa. *Rhodospirillum rubrum* ATCC 11170^T was used as an outgroup. Bar, 0.01 substitutions per nucleotide position.

comprising *Erythrobacter* species was supported by a bootstrap resampling value of 98.9% (Fig. 1). The genera *Porphyrobacter* and *Erythromicrobium* could not be clearly distinguished because they are not well defined chemotaxonomically and are intermixed phylogenetically (Rainey *et al.*, 2003). Indeed, Rainey *et al.* (2003) considered the possibility of combining the genera *Erythrobacter*, *Porphyrobacter* and *Erythromicrobium* into a single genus. However, it is currently necessary to place strain DSW-74^T into one of the three genera. Based on its highest 16S rRNA gene sequence similarity values to *Porphyrobacter* species, strain DSW-74^T should be placed within the genus *Porphyrobacter* before taxonomic criteria regarding the above three genera are proposed. There are several differential phenotypic properties between strain DSW-74^T and recognized *Porphyrobacter* species, including motility, the abilities to hydrolyse and to utilize some substrates, maximum and optimal temperatures for growth, and absorption spectrum pattern of *in vivo* cell extracts (Table 1). The genetic distinctiveness was sufficient to assign strain DSW-74^T to a novel species within the genus *Porphyrobacter* (Wayne *et al.*, 1987). Levels of DNA–DNA relatedness between strain DSW-74^T and the type strains of the five recognized *Porphyrobacter* species were in the range 9–25%. Therefore, on the basis of the data presented, strain DSW-74^T should be classified in the genus *Porphyrobacter* as the type strain of a novel species, for which the name *Porphyrobacter dokdonensis* sp. nov. is proposed.

Description of *Porphyrobacter dokdonensis* sp. nov.

Porphyrobacter dokdonensis (dok.do.nen'sis. N.L. masc. adj. *dokdonensis* of Dokdo, from where the strain was isolated).

Cells are pleomorphic: cocci, ovals and rods (0.4–0.6 × 0.5–2.5 µm) are present. Cells are Gram-negative, non-spore-forming and non-motile. Colonies on MA are circular, smooth, slightly convex, reddish orange in colour and 0.5–1.0 mm in diameter after incubation for 7 days at 37 °C. Optimal growth occurs at 35–37 °C; growth occurs at 10 and 43 °C, but not at 4 or 44 °C. Optimal pH for growth is 7.0–8.0; growth occurs at pH 5.5, but not at pH 5.0. Optimal growth occurs in the presence of 2% (w/v) NaCl; growth occurs weakly in the absence of NaCl and in the presence of 7% (w/v) NaCl, but not in the presence of >8% (w/v) NaCl. Growth does not occur under anaerobic conditions on MA or on MA supplemented with nitrate. Urease-negative. L-Tyrosine and Tweens 20, 40 and 60 are hydrolysed, but hypoxanthine and xanthine are not. H₂S and indole are not produced. Arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase and tryptophan deaminase are absent. Maltose is utilized as the sole carbon and energy source, but benzoate, salicin and formate are not. Acid is not produced from the following substrates: L-arabinose, D-cellobiose, D-fructose, D-galactose, D-glucose, lactose, maltose, D-mannitol, D-mannose, D-melezitose, melibiose, D-raffinose, L-rhamnose, D-ribose, sucrose, D-trehalose, D-xylose, *myo*-inositol or D-sorbitol. Sensitive to penicillin G, chloramphenicol, cephalothin, novobiocin and carbenicillin, but not to polymyxin B, streptomycin, ampicillin, gentamicin, tetracycline, kanamycin, lincomycin, oleandomycin or neomycin. The predominant ubiquinone is Q-10. The major fatty acids are C_{17:1ω6c} (30.6%) and C_{18:1ω7c} (28.5%). The DNA G+C content is 65.8 mol% (HPLC). Other phenotypic properties are given in Table 1.

The type strain, DSW-74^T (=KCTC 12395^T=DSM 17193^T), was isolated from sea water.

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