Psychrobacter aquimaris sp. nov. and *Psychrobacter namhaensis* sp. nov., isolated from sea water of the South Sea in Korea

Jung-Hoon Yoon,¹ Choong-Hwan Lee,¹ Soo-Hwan Yeo² and Tae-Kwang Oh¹

Correspondence

Jung-Hoon Yoon
jhyoon@kribb.re.kr

¹Korea Research Institute of Bioscience and Biotechnology (KRIBB), PO Box 115, Yusong, Taejeon, Korea

²The Center for Traditional Microorganism Resources, Keimyung University, Shindang-Dong, Dalseo-gu, Daegu, Korea

Two Gram-negative, non-motile, non-spore-forming, slightly halophilic bacterial strains, SW-210^T and SW-242^T, were isolated from sea water of the South Sea in Korea, and were characterized taxonomically by means of a polyphasic approach. The two isolates grew optimally at 25–30 °C and in the presence of 2–3 % (w/v) NaCl. Strains SW-210^T and SW-242^T contained Q-8 as the predominant respiratory lipoquinone and C_{18:1}ω₉c as the major fatty acid. The DNA G+C contents of strains SW-210^T and SW-242^T were 43.2 and 45.3 mol%, respectively. The 16S rRNA gene sequences of strains SW-210^T and SW-242^T were 98.9 % similar, and the mean DNA–DNA relatedness value between them was 24 %. Phylogenetic analysis based on 16S rRNA gene sequences showed that strains SW-210^T and SW-242^T form distinct phylogenetic lineages within the radiation of the cluster comprising *Psychrobacter* species, having 16S rRNA gene sequence similarity levels of 95.9–99.2 % with respect to the type strains of *Psychrobacter* species. The levels of DNA–DNA relatedness between the two isolates and the type strains of 15 phylogenetically related *Psychrobacter* species were well below 70 %. On the basis of phenotypic and phylogenetic data and genomic distinctiveness, strains SW-210^T and SW-242^T were classified in the genus *Psychrobacter* as representing two distinct novel species, for which the names *Psychrobacter aquimaris* sp. nov. (type strain, SW-210^T=KCTC 12254^T=DSM 16329^T) and *Psychrobacter namhaensis* sp. nov. (type strain, SW-242^T=KCTC 12255^T=DSM 16330^T) are proposed, respectively.

The genus *Psychrobacter* was proposed by Juni & Heym (1986), and, at the time of writing, the genus comprises at least 18 species with validly published names: *Psychrobacter immobilis* (Juni & Heym, 1986), *Psychrobacter frigidicola*, *Psychrobacter urativorans* and *Psychrobacter phenylpyruvicus* (Bowman *et al.*, 1996), *Psychrobacter glacincola* (Bowman *et al.*, 1997), *Psychrobacter pacificensis* (Maruyama *et al.*, 2000), *Psychrobacter proteolyticus* (Denner *et al.*, 2001), *Psychrobacter submarinus* and *Psychrobacter marincola* (Romanenko *et al.*, 2002), *Psychrobacter faecalis* (Kämpfer *et al.*, 2002), *Psychrobacter pulmonis* (Vela *et al.*, 2003), *Psychrobacter jeotgali* (Yoon *et al.*, 2003), *Psychrobacter luti* and *Psychrobacter fozii* (Bozal *et al.*, 2003), *Psychrobacter okhotskensis* (Yumoto *et al.*, 2003), *Psychrobacter maritimus*

and *Psychrobacter arenosus* (Romanenko *et al.*, 2004) and *Psychrobacter alimentarius* (Yoon *et al.*, 2005). In this study, we report on the detailed taxonomic characterization of two *Psychrobacter*-like bacterial strains, SW-210^T and SW-242^T, which were isolated from sea water of the South Sea in Korea.

Sea water collected from the South Sea in Korea was used as source for the isolation of bacterial strains. Strains SW-210^T and SW-242^T were isolated by using the usual dilution plating technique on marine agar 2216 (MA; Difco) at 30 °C. The type strains of 15 *Psychrobacter* species were used as reference strains for DNA–DNA hybridization. *P. faecalis* DSM 14664^T, *P. frigidicola* DSM 12411^T, *P. glacincola* DSM 12194^T, *P. immobilis* DSM 7229^T, *P. marincola* DSM 14160^T, *P. proteolyticus* DSM 13887^T, *P. submarinus* DSM 14161^T and *P. urativorans* DSM 14009^T were obtained from the Deutsche Sammlung von Mikroorganismen und Zellkulturen, Braunschweig, Germany. *P. okhotskensis* JCM 11840^T was obtained from the Japan

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The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of strains SW-210^T and SW-242^T are AY722804 and AY722805, respectively.

Table 1. Differential phenotypic characteristics of *Psychrobacter* species

1, *P. aquimaris* ($n=1$); 2, *P. namhaensis* ($n=1$); 3, *P. immobilis* ($n=20$), data from Juni & Heym (1986), Bowman *et al.* (1996) and Romanenko *et al.* (2002); 4, *P. frigidicola* ($n=4$), Bowman *et al.* (1996) and Romanenko *et al.* (2002); 5, *P. urativorans*, Bowman *et al.* (1996) and Romanenko *et al.* (2002); 6, *P. glacincola* ($n=4$), Bowman *et al.* (1997) and Romanenko *et al.* (2002); 7, *P. proteolyticus* ($n=1$), Denner *et al.* (2001) and Bozal *et al.* (2003); 8, *P. submarinus* ($n=1$), Romanenko *et al.* (2002); 9, *P. marincola* ($n=1$), Romanenko *et al.* (2002); 10, *P. faecalis* ($n=1$), Kämpfer *et al.* (2002); 11, *P. jeotgali* ($n=2$), Yoon *et al.* (2003); 12, *P. pulmonis* ($n=2$), Vela *et al.* (2003); 13, *P. okhotskensis* ($n=1$), Yumoto *et al.* (2003); 14, *P. luti* ($n=1$), Bozal *et al.* (2003); 15, *P. fozii* ($n=2$), Bozal *et al.* (2003); 16, *P. alimentarius* ($n=2$), Yoon *et al.* (2005); 17, *P. maritimus* ($n=3$), Romanenko *et al.* (2004); 18, *P. phenylpyruvicus* ($n=1$), Bowman *et al.* (1996) and Romanenko *et al.* (2002); 19, *P. pacificensis* ($n=6$), Maruyama *et al.* (2000). +, Positive reaction; –, negative reaction; ND, not determined; W, weakly positive reaction; V, variable reaction. Data in parentheses relate to the type strain; n , number of strains. All species are positive for catalase and oxidase. All species are negative for Gram stain, spore formation, motility, hydrolysis of aesculin, acid production from D-mannitol, utilization of D-glucose, arginine dihydrolase, lysine decarboxylase and ornithine decarboxylase.

Characteristic	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
Cell morphology*	C or SR	C or SR	CB	C	C	C	CB	O	C	R	C	C	R	CB	CB	C	O	SR	CB
Anaerobic growth	+	+	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
Urease	–	–	V(+)	–	V(+)	V(–)	+	–	–	–	+	–	–	–	+	–	ND	+	+
Tryptophan deaminase	–	–	V(–)	+	–	–	–	–	–	ND	–	–	ND	–	–	–	ND	–	–
Nitrate reduction	–	–	V(–)	–	V(–)	V(+)	–	–	–	ND	+	+	+	+	–	–	+	–	–
Hydrolysis of:																			
Casein	–	–	–	–	–	–	+	–	–	ND	–	ND	–	+	–	–	–	–	ND
Gelatin	–	–	–	–	–	–	+	–	–	ND	–	–	–	–	–	–	–	–	–
Starch	–	–	–	–	–	–	–	–	–	ND	–	ND	ND	–	–	–	–	–	ND
Tween 40	+	+	+	–	–	+	ND	+	–	ND	ND	ND	+	ND	ND	+	+	–	ND
Tween 80	+	+	+	–	–	+	W	+	+	ND	+	ND	+	+	–	+	+	+	ND
Xanthine	–	–	ND	ND	ND	V	ND	ND	ND	ND	–	ND	ND	ND	ND	–	ND	–	ND
Growth in:																			
0% (w/v) NaCl	+	+	+	+	+	+	ND	–	–	ND	+	ND	+	+	V(+)	+	+	+	–
10% (w/v) NaCl	+	+	V(+)	–	–	+	+	+	+	+	+	ND	+	–	+	+	+	–	–
15% (w/v) NaCl	–	–	–	–	–	–	ND	+	+	ND	–	ND	–	–	–	–	–	–	–
Growth temp. (max., °C)	34	37	(<35–37)	19–22	25–27	19–22	<35	35	35	36	36	<42	35	30	30	35	39–40	<40	38
Optimum growth temp. (°C)	25–30	25–30	(20)	14–16	18–20	13–15	19–25	25–28	25–28	15–30	25–30	ND	25	15	15	30	25–28	33–37	25
Acid production from:																			
D-Glucose	+	+	+	–	–	–	+	–	–	–	–	–	–	–	–	+	–	–	+
D-Xylose	+	+	+	–	–	–	ND	–	–	–	–	ND	–	–	–	+	–	–	+
L-Arabinose	+	+	+	–	–	–	+	+	–	–	–	–	–	–	–	+	–	–	+
D-Fructose	–	–	–	–	–	–	ND	+	–	ND	–	ND	–	–	–	–	–	–	ND
L-Rhamnose	+	+	+	–	–	–	+	–	–	–	–	–	ND	–	–	+	–	–	ND
D-Galactose	+	+	+	–	–	–	ND	–	–	ND	–	ND	–	–	–	+	–	–	ND
Maltose	–	–	–	–	–	–	ND	–	–	–	–	ND	–	–	–	–	–	–	ND
Lactose	+	+	V(–)	–	–	–	ND	–	–	–	–	ND	–	–	–	+	–	–	ND
Utilization of:																			
Acetate	+	+	+	+	V(+)	+	+	–	–	+	+	ND	ND	+	V(+)	+	+	+	V(–)
Pyruvate	+	+	+	–	+	+	ND	ND	ND	+	+	ND	+	ND	+	+	–	+	ND
Citrate	–	–	V(–)	–	–	V	+	–	–	+	–	–	ND	+	–	+	–	+	–
Malate	+	+	+	+	V(+)	–	–	–	–	+	V(–)	–	+	+	+	+	V(–)	+	+
Succinate	+	+	+	–	–	–	ND	ND	ND	ND	+	ND	ND	+	+	+	–	–	ND

Table 1. cont.

Characteristic	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
Enzymic activities (by API ZYM)																			
Acid phosphatase	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Alkaline phosphatase	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Esterase (C4)	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Lipase (C14)	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Cystine arylamidase	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Valine arylamidase	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Naphthol-AS-BI-phosphohydrolase	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Sensitivity to antibiotics (per disc)																			
Ampicillin (10 µg)	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Gentamicin (10 µg)	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Polymyxin B (300 U)	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Streptomycin (30 µg)	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Tetracycline (30 µg)	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Major fatty acid(s)	C _{18:1} ω9c	C _{18:1} ω9c	C _{18:1} ω9c	C _{18:1} ω9c	C _{16:1} ω7c	C _{18:1} ω9c	C _{18:1} ω9c	C _{18:1} ω9c	C _{18:1} ω9c	C _{18:1} ω9c	C _{18:1} ω9c	C _{18:1} ω9c	C _{18:1} ω9c	C _{18:1} ω9c	C _{18:1} ω9c	C _{18:1} ω9c	C _{18:1} ω9c	C _{18:1} ω9c	C _{18:1} ω9c
DNA G+C content (mol%)	43.2	45.3	44.47	41.42	44.46	43.44	43.6	46.8	50.7	ND	43.44	ND	46.7	45	44.46	43.8-44.2	44.6-44.9	43	43.44

*Abbreviations: C, cocci; CB, coccobacilli; O, ovoid; R, rods; SR, short rods.

Collection of Microorganisms, Saitama, Japan. *P. fozii* CECT 5889^T, *P. luti* CECT 5885^T and *P. pulmonis* CECT 5989^T were obtained from the Colección Española de Cultivos Tipo, Valencia, Spain. *P. jeotgali* KCCM 41559^T and *P. alimentarius* JG-100^T were obtained and described in the studies of Yoon *et al.* (2003, 2005). *P. maritimus* KMM 3646^T was obtained from Dr O. I. Nedashkovskaya and Dr L. A. Romanenko, Pacific Institute of Bioorganic Chemistry, Vladivostok, Russia. Cell morphology was examined by light microscopy (E600 microscope; Nikon) and transmission electron microscopy (CM-20 apparatus; Philips). Transmission electron microscopy was also used to determine if flagella were present in cells from exponentially growing cultures. 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 (pH 4.5–9.5 at intervals of 0.5 pH units). Growth in the absence of NaCl was investigated in trypticase/soy broth (Difco) lacking NaCl. Growth at various NaCl concentrations was investigated in MB or trypticase/soy broth. Growth at various temperatures (4–45 °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, starch and Tweens 20, 40, 60 and 80 were determined as described by Cowan & Steel (1965). Hydrolysis of aesculin and nitrate reduction were determined as described previously (Lanyi, 1987). Hydrolysis of gelatin and urea was determined as described by Lanyi (1987), with the 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 described previously (Cowan & Steel, 1965). H₂S production was tested as described previously (Bruns *et al.*, 2001). Acid production from carbohydrates was determined as described by Leifson (1963). Enzyme activity was determined by using the API ZYM system (bioMérieux). Utilization of substrates as sole carbon and energy sources was tested according to the method of 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). Requirements for yeast extract and vitamins for growth were investigated in liquid medium (Yurkov *et al.*, 1994), omitting yeast extract and vitamin B₁₂ but supplementing with 0.1 % (w/v) acetate as the sole carbon and energy source. Yeast extract and vitamins were added to the medium at the following concentrations (1⁻¹): yeast extract, 0.005 g; *p*-aminobenzoic acid, 1 mg; biotin, 10 µg; thiamine hydrochloride, 1 mg; and vitamin B₁₂, 1 mg. Susceptibility to antibiotics was detected on MA plates using antibiotic discs with the following concentrations:

polymyxin B, 100 U; streptomycin, 50 µg; penicillin G, 20 U; chloramphenicol, 100 µg; ampicillin, 10 µg; cephalothin, 30 µg; gentamicin, 30 µg; novobiocin, 5 µg; erythromycin, 15 µg; and tetracycline, 30 µg. Other physiological tests were performed with the API 20E system (bioMérieux).

Cell biomass for respiratory lipoquinone analysis and for DNA extraction was obtained from cultivation in MB at 30 °C. Respiratory lipoquinones were analysed as described by Komagata & Suzuki (1987), using reversed-phase HPLC. Chromosomal DNA was isolated and purified according to the method described previously (Yoon *et al.*, 1996), with the exception that ribonuclease T1 was used together with ribonuclease A to minimize the contamination of RNA. For fatty acid methyl ester analysis, cell mass of strains SW-210^T and SW-242^T was harvested from agar plates after incubation for 3 days at 30 °C on MA. 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 the modification that DNA was hydrolysed and the resultant nucleotides were analysed by reversed-phase HPLC. 16S rRNA genes were amplified by the PCR method, using two universal primers as described previously (Yoon *et al.*, 1998). Sequencing of the amplified 16S rRNA genes and phylogenetic analysis were performed as described by Yoon *et al.* (2003). DNA–DNA hybridization was performed fluorometrically according to 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 remaining three values were used to calculate similarity values. The DNA relatedness values quoted are the means of the three values.

Cells of strains SW-210^T and SW-242^T were cocci or short rods on MA. Strains SW-210^T and SW-242^T did not require yeast extract or vitamins for growth in minimal salts medium (Yurkov *et al.*, 1994). However, both strains grew better when yeast extract was added to the medium. Benzoate was utilized by strain SW-242^T but not by strain SW-210^T. Strain SW-210^T was sensitive to penicillin G but strain SW-242^T was not. Other morphological, cultural, physiological and biochemical characteristics of strains SW-210^T and SW-242^T are given in the species description (see below) and are shown in Table 1 together with those of some *Psychrobacter* species. The predominant respiratory lipoquinone found in strains SW-210^T and SW-242^T was Q-8, at a peak area ratio of approximately 84–86%. The major components of the fatty acids detected in strains SW-210^T and SW-242^T were C_{18:1}ω9c and C_{17:1}ω8c (Table 2). These fatty acid profiles were similar to those determined previously for other *Psychrobacter* species, although there were differences in the proportions of some fatty acids, perhaps because of differences in cultivation

Table 2. Cellular fatty acid composition (%) of strain SW-210^T and strain SW-242^T on MA

Fatty acids representing less than 0.5% in each of the two strains were omitted. —, Not detected.

Fatty acid*	SW-210 ^T	SW-242 ^T
Straight-chain fatty acids		
C _{9:0}	1.0	1.2
C _{10:0}	3.1	2.9
C _{11:0}	0.4	0.7
C _{16:0}	1.3	0.8
C _{18:0}	1.8	0.9
Branched fatty acid		
iso-C _{17:0}	1.1	0.9
Unsaturated fatty acids		
C _{17:1} ω8c	12.6	18.1
C _{18:1} ω7c	2.0	1.5
C _{18:1} ω9c	64.9	58.7
Hydroxy fatty acids		
C _{12:0} 3-OH	2.6	2.9
C _{16:0} 2-OH	—	0.9
Summed features*		
1	0.9	1.1
2	0.9	1.0
3	5.7	6.5
6	0.8	0.8

*Summed features represent groups of two or three fatty acids that could not be separated by GLC with the MIDI system. Summed feature 1 contained one or more of C_{13:0} 3-OH and/or iso-C_{15:1}. Summed feature 2 contained one or more of iso-C_{16:1} 1 and/or C_{14:0} 3-OH. Summed feature 3 contained one or more of C_{16:1}ω7c and/or iso-C_{15:0} 2-OH. Summed feature 6 contained one or more of C_{19:1}ω9c and/or C_{19:1}ω11c.

conditions, e.g. cultivation media (Maruyama *et al.*, 2000; Romanenko *et al.*, 2002, 2004; Bozal *et al.*, 2003; Yumoto *et al.*, 2003; Yoon *et al.*, 2005). The DNA G+C contents of strains SW-210^T and SW-242^T were 43.2 and 45.3 mol%, respectively.

The almost-complete 16S rRNA gene sequences of strains SW-210^T and SW-242^T determined in this study each comprised 1494 nt, representing approximately 96% of the *Escherichia coli* 16S rRNA sequence. There were 17 bp sequence differences (i.e. 98.9% identity) between the 16S rRNA gene sequence of strain SW-210^T and that of strain SW-242^T. Comparative analysis revealed that strains SW-210^T and SW-242^T had the highest 16S rRNA gene sequence similarities to members of the genus *Psychrobacter*. Phylogenetic trees based on 16S rRNA gene sequences showed that the two isolates fall within the evolutionary radiation encompassed by the genus *Psychrobacter* (Fig. 1). Strains SW-210^T and SW-242^T exhibited 16S rRNA gene sequence similarity levels of 96.0–99.2% and 95.9–98.9%, respectively, with respect to the type strains of *Psychrobacter*

Fig. 1. Neighbour-joining tree, based on 16S rRNA gene sequences, showing the phylogenetic positions of strains SW-210^T and SW-242^T and representatives of some other related taxa. Bootstrap values (expressed as percentages of 1000 replications) greater than 50% are shown at the branch points. *Pseudomonas aeruginosa* DSM 50071^T was used as the outgroup. Scale bar represents 0.01 substitution per nucleotide position.

species with validly published names. The 16S rRNA gene sequence similarities of the two isolates with respect to other species included in the phylogenetic analysis were below 92.5% (Fig. 1). DNA–DNA hybridization was performed to determine the level of genetic relatedness between strain SW-210^T and strain SW-242^T and also those between each of the two strains and the type strains of some *Psychrobacter* species that exhibited 16S rRNA gene sequence similarity values above 97% with respect to the two novel isolates. Strains SW-210^T and SW-242^T exhibited a mean level of DNA–DNA relatedness of 24% when their DNAs were used individually as labelled DNA probes for cross-hybridization. Levels of DNA–DNA relatedness between two strains and the type strains of 15 *Psychrobacter* species were in the range 6–35%.

In the neighbour-joining tree, inferred from comparison of 16S rRNA gene sequences, the cluster comprising the two isolates and *Psychrobacter* species was distinguishable from the genus *Moraxella* at a bootstrap confidence level of 100% (Fig. 1). The thermal tolerance and chemotaxonomic data (the predominant respiratory lipoquinone, the cellular fatty acid profile and the DNA G+C content) for strains SW-210^T and SW-242^T are similar to those for *Psychrobacter* species (Bøvre, 1984; Kodjo *et al.*, 1995, 1997;

Bowman *et al.*, 1997; Maruyama *et al.*, 2000; Yoon *et al.*, 2003; Bozal *et al.*, 2003; Yumoto *et al.*, 2003). Strains SW-210^T and SW-242^T are similar to each other in terms of most phenotypic characteristics (Table 1). However, the two strains differ from each other phylogenetically and genetically. Strains SW-210^T and SW-242^T are distinguishable from phylogenetically related *Psychrobacter* species by differences in physiological and biochemical characteristics (Table 1). The level of DNA relatedness, together with differential phenotypic properties and 16S rRNA gene sequence similarity data, justifies the taxonomic discrimination of strains SW-210^T and SW-242^T from all *Psychrobacter* species (Wayne *et al.*, 1987; Stackebrandt & Goebel, 1994). Therefore, on the basis of the data presented, strains SW-210^T and SW-242^T should be placed in the genus *Psychrobacter* as representing two distinct novel species, for which the names *Psychrobacter aquimaris* sp. nov. and *Psychrobacter namhaensis* sp. nov., respectively, are proposed.

Description of *Psychrobacter aquimaris* sp. nov.

Psychrobacter aquimaris (a.qui.ma'ris. L. n. *aqua* water; L. gen. n. *maris* of the sea; N.L. gen. n. *aquimaris* of the water of the sea).

Cells are cocci or short rods ($1.0\text{--}1.2 \times 1.4\text{--}2.5\ \mu\text{m}$). On MA, colonies are smooth, glistening, raised, circular to slightly irregular, cream in colour and $1.5\text{--}2.5\ \text{mm}$ in diameter after incubation for 3 days at 30°C . Growth occurs at 4 and 34°C but not at 35°C . Optimal pH for growth is $6.5\text{--}7.5$; growth occurs at pH 5.0 but not at 4.5. Growth occurs in the presence of 0–12% (w/v) NaCl, with an optimum of 2–3% (w/v). Yeast extract, biotin, *p*-aminobenzoic acid, thiamine hydrochloride and vitamin B₁₂ are not required for growth. Tyrosine is hydrolysed, but hypoxanthine is not. Indole and H₂S are not produced. In assays with the API ZYM system, lipase (C8) and leucine arylamidase are present, but trypsin, α -chymotrypsin, α -galactosidase, β -galactosidase, β -glucuronidase, α -glucosidase, β -glucosidase, *N*-acetyl- β -glucosaminidase, α -mannosidase and α -fucosidase are absent. L-Arabinose, D-cellobiose, D-fructose, D-galactose, lactose, maltose, D-mannose, sucrose, D-trehalose, D-xylose, benzoate, formate and L-glutamate are not utilized. Acid is produced from D-cellobiose, D-mannose, melibiose and D-ribose. Acid is not produced from D-melezitose, D-raffinose, sucrose, D-trehalose, adonitol, *myo*-inositol or D-sorbitol. Sensitive to cephalothin (30 μg), chloramphenicol (100 μg) and penicillin G (20 U) but not to novobiocin (5 μg). The predominant respiratory lipoquinone is Q-8. The major fatty acid is C_{18:1 ω 9c}. The DNA G + C content is 43.2 mol% (HPLC). Other characteristics are shown in Table 1.

The type strain, SW-210^T (=KCTC 12254^T=DSM 16329^T), was isolated from sea water of the South Sea in Korea.

Description of *Psychrobacter namhaensis* sp. nov.

Psychrobacter namhaensis (nam.ha.en'sis. N.L. masc. adj. *namhaensis* of Namhae, the Korean name for the South Sea in Korea, where the organism was isolated).

Cells are cocci or short rods ($1.0\text{--}1.2 \times 1.4\text{--}2.5\ \mu\text{m}$). On MA, colonies are smooth, glistening, raised, circular to slightly irregular, cream in colour and $1.5\text{--}2.5\ \text{mm}$ in diameter after incubation for 3 days at 30°C . Growth occurs at 4 and 37°C but not at 38°C . Optimal pH for growth is $6.5\text{--}7.5$; growth occurs at pH 5.0 but not at pH 4.5. Growth occurs in the presence of 0–13% (w/v) NaCl, with an optimum of 2–3% (w/v). Yeast extract, biotin, *p*-aminobenzoic acid, thiamine hydrochloride and vitamin B₁₂ are not required for growth. Tyrosine is hydrolysed, but hypoxanthine is not. Indole and H₂S are not produced. In assays with the API ZYM system, lipase (C8) and leucine arylamidase are present, but trypsin, α -chymotrypsin, α -galactosidase, β -galactosidase, β -glucuronidase, α -glucosidase, β -glucosidase, *N*-acetyl- β -glucosaminidase, α -mannosidase and α -fucosidase are absent. Benzoate is utilized. L-Arabinose, D-cellobiose, D-fructose, D-galactose, lactose, maltose, D-mannose, sucrose, D-trehalose, D-xylose, formate and L-glutamate are not utilized. Acid is produced from D-cellobiose,

D-mannose, melibiose and D-ribose. Acid is not produced from D-melezitose, D-raffinose, sucrose, D-trehalose, adonitol, *myo*-inositol or D-sorbitol. Sensitive to cephalothin (30 μg) and chloramphenicol (100 μg) but not to novobiocin (5 μg) or penicillin G (20 U). The predominant respiratory lipoquinone is Q-8. The major fatty acid is C_{18:1 ω 9c}. The DNA G + C content is 45.3 mol% (HPLC). Other characteristics are shown in Table 1.

The type strain, SW-242^T (=KCTC 12255^T=DSM 16330^T), was isolated from sea water of the South Sea in Korea.

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