Pseudoalteromonas byunsanensis sp. nov., isolated from tidal flat sediment in Korea

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A Gram-negative, motile, strictly aerobic, violet-pigment-producing bacterium, designated strain FR1199^T, was isolated from tidal flat sediment of Byunsan, South Korea. Phylogenetic analysis of the 16S rRNA gene sequence revealed that strain FR1199^T represents a distinct line of descent within the genus *Pseudoalteromonas*. The phenotypic features of strain FR1199^T were similar to those of *Pseudoalteromonas phenolica* and *Pseudoalteromonas luteoviolacea*, but several physiological and chemotaxonomical properties readily distinguished strain FR1199^T from these species. Major fatty acids were straight-chain saturated (C_{16:0}) and monounsaturated C_{18:1ω7c} fatty acids. The DNA G + C content was 39 mol%. On the basis of polyphasic evidence, it is concluded that the isolate represents a novel species within the genus *Pseudoalteromonas*, for which the name *Pseudoalteromonas byunsanensis* sp. nov. is proposed. The type strain is FR1199^T (=JCM 12483^T =KCTC 12274^T).

The genus *Alteromonas*, originally described by Baumann *et al.* (1972) for marine aerobic, Gram-negative, non-fermentative, polarly flagellated bacteria, was later divided into two genera, *Alteromonas* and *Pseudoalteromonas*, on the basis of phylogenetic analysis (Gauthier *et al.*, 1995). The genus *Pseudoalteromonas* currently comprises 33 species (Gauthier, 1976, 1977, 1982; Gauthier & Breittmayer, 1979; Novick & Tyler, 1985; Romanenko *et al.*, 1995, 2003a; Ivanova *et al.*, 1996, 1998, 2000, 2001, 2002a, b, c, d, 2004; Bozal *et al.*, 1997; Bowman, 1998; Holmström *et al.*, 1998; Sawabe *et al.*, 1998, 2000; Venkateswaran & Dohmoto, 2000; Egan *et al.*, 2001; Isnansetyo & Kamei, 2003; Kobayashi *et al.*, 2003). In the course of our study on marine microbial diversity, a pseudoalteromonad, designated strain FR1199^T, was isolated from a tidal flat sediment sample and was the subject of a polyphasic taxonomic investigation. On the basis of our evidence, strain FR1199^T represents a novel species in the genus *Pseudoalteromonas*.

A marine sediment sample was collected from the Korean tidal flat of Byunsan in South Korea (35° 34' 52.3" N 126° 30' 51.3" E) in August 2002. The sample was diluted with sterilized artificial sea water (ASW; Lyman & Fleming, 1940), spread onto a plate containing marine agar 2216 (MA; Difco) and incubated at 25 °C for 3 weeks. The isolate was routinely cultured on MA and maintained as a glycerol suspension (20 % v/v) at –80 °C.

Bacterial DNA preparation, PCR amplification and sequencing of the 16S rRNA gene were carried out as described previously (Chun & Goodfellow, 1995). The resultant sequence of strain FR1199^T was aligned manually against sequences obtained from GenBank. Phylogenetic trees were inferred from the regions available for all sequences (positions 43–1438; *Escherichia coli* numbering system) using the Fitch–Margoliash (Fitch & Margoliash, 1967), maximum-parsimony (Fitch, 1971) and neighbour-joining (Saitou & Nei, 1987) methods. Evolutionary distance matrices were generated according to Jukes & Cantor (1969). The resultant neighbour-joining tree topology was evaluated by bootstrap analyses (Felsenstein, 1985) based on 1000 resamplings. Alignment and phylogenetic analyses were carried out using the jPHYDIT program (<http://chunlab.snu.ac.kr/jphydit/>; Jeon *et al.*, 2005) and PAUP 4.0 (Swofford, 1998) as described previously (Chun *et al.*, 2000).

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Abbreviation: ASW, artificial sea water.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of *Pseudoalteromonas byunsanensis* sp. nov. FR1199^T is DQ011289.

Preliminary sequence comparison with 16S rRNA gene sequences held in GenBank indicated that our isolate was closely related to the genus *Pseudoalteromonas*. The newly determined sequence was then aligned manually against representatives of the genus *Pseudoalteromonas* using information on bacterial 16S rRNA secondary structures. Strain FR1199^T showed low levels of 16S rRNA gene sequence similarity to other pseudoalteromonads. The highest similarity was found with *Pseudoalteromonas rubra* ATCC 29570^T (97.4%), followed by *Pseudoalteromonas mariniglutinosa* NCIMB 1770^T (97.2%), *Pseudoalteromonas luteoviolacea* NCIMB 1893^T (96.7%) and *Pseudoalteromonas piscicida* ATCC 15057^T (96.6%). Our isolate formed an independent phyletic line in the *Pseudoalteromonas* clade in the comprehensive phylogenetic analysis (Fig. 1), to which two species (*P. mariniglutinosa* and *P. luteoviolacea*) showing >97% 16S rRNA similarities were not phylogenetically related. It is clear from the phylogenetic analysis that the tidal flat isolate FR1199^T represents a novel species in the genus *Pseudoalteromonas*.

Morphological characteristics were observed by differential interference microscopy (Nikon) and scanning electron

microscopy (JEOL) using cells grown at 25 °C for 3 days. Motility was examined using wet mounts. The pH range (pH 3–12) for growth was determined using MA. Na⁺ requirement and tolerance of 0–11% (w/v) NaCl were determined using synthetic ZoBell medium (ZoBell, 1941; 15 g Bacto agar, 5 g Bacto peptone, 1 g yeast extract, 0.1 g ferric citrate l⁻¹ distilled water) prepared on an ASW base, supplemented with appropriate amounts of NaCl.

Growth at various temperatures was examined on MA at 4–50 °C. Growth under anaerobic conditions was checked in an anaerobic chamber [1% (v/v) CO₂, 10% (v/v) H₂, 80% (v/v) N₂; Sheldon Manufacturing] using anaerobically prepared MA. Catalase and oxidase activities were determined using 3% (v/v) hydrogen peroxide and Kovacs reagent (Kovacs, 1956), respectively. Other biochemical tests were performed using API 20NE and API 20E kits (bioMérieux). Enzyme activities were tested using an API ZYM kit (bioMérieux) following the manufacturer's instructions. Strips were inoculated with a heavy bacterial suspension in ASW or AUX medium (bioMérieux) supplemented with 2% (w/v) sea salts. The results of biochemical and physiological tests are given in Table 1

Fig. 1. Neighbour-joining tree based on nearly complete 16S rRNA gene sequences showing relationships between strain FR1199^T and other species of the genus *Pseudoalteromonas*. Percentage bootstrap values (>50%, 1000 resamplings) are given at branch points and solid circles indicate that the corresponding nodes (groupings) are also recovered in Fitch–Margoliash and maximum-parsimony trees. *Vibrio cholerae* ATCC 14035^T was used as an out-group (not shown). Bar, 0.01 nucleotide substitutions per position.

Table 1. Characteristics that differentiate strain FR1199^T from related *Pseudoalteromonas* species

Strains: 1, strain FR1199^T; 2, *P. phenolica* O-BC30^T; 3, *P. luteoviolacea* NCIMB 1893^T; 4, *P. piscicida* ATCC 15057^T; 5, *P. rubra* ATCC 29570^T; 6, *P. peptidolytica* MBIC 1416^T; 7, *P. flavipulchra* NCIMB 2033^T; 8, *P. maricaloris* LMG 19692^T; 9, *P. citrea* NCIMB 1889^T; 10, *P. aurantia* DSM 6057^T; 11, *P. rutenica* KMM 300^T; 12, *P. mariniglutinosa* NCIMB 1770^T. Data from this and earlier studies (Gauthier, 1976; Novick & Tyler, 1985; Gauthier *et al.*, 1995; Ivanova *et al.*, 1998, 2002a, 2002d; Venkateswaran & Dohmoto, 2000; Isnansetyo & Kamei, 2003; Romanenko *et al.*, 2003b). +, Positive; –, negative; ND, no data available.

Characteristic	1	2	3	4	5	6	7	8	9	10	11	12
Pigmentation	Violet	Brown	Purple	–	Red	Yellow	Orange	Yellow	Lemon-yellow	Yellow	Orange	–
Growth at:												
4 °C	–	–	–	–	–	–	–	–	–	+	–	–
37 °C	+	+	–	+	+	+	+	+	+	–	+	+
Growth at:												
8 % (w/v) NaCl	–	–	+	+	–	+	+	+	ND	–	+	+
10 % (w/v) NaCl	–	–	–	+	–	–	+	+	ND	–	–	+
Utilization of:												
Acetate	–	+	–	–	–	–	ND	–	–	ND	ND	+
N-Acetylglucosamine	+	+	+	–	+	+	+	ND	ND	ND	ND	+
D-Arabinose	–	–	–	–	ND	ND	–	+	–	–	–	+
Citrate	–	–	–	+	–	–	+	ND	–	–	–	–
Maltose	+	+	+	+	–	+	+	–	–	–	–	+
D-Mannitol	–	–	–	–	–	–	–	+	–	–	–	+
D-Mannose	+	+	+	+	+	–	+	+	+	+	ND	–
Melibiose	–	–	–	–	ND	ND	–	+	ND	–	–	–
D-Sorbitol	–	–	–	–	ND	–	–	+	–	–	–	ND
Sucrose	–	+	–	–	–	–	+	–	–	–	–	+
Catalase	+	–	–	–	+	+	+	+	+	ND	+	+
Lipase	–	+	+	+	+	+	ND	+	+	+	+	–
DNA G + C content (mol%)	39	40–41	40–43	43–46	46–48	41–42	42	39	39–40	44	48	40

and the species description. Our isolate can be readily differentiated from other phylogenetically related species by several phenotypic properties as shown in Table 1.

Cellular fatty acids of strain FR1199^T were analysed as methyl esters by GLC using the Microbial Identification System (MIDI). Fatty acid methyl esters were prepared from biomass grown on MA at 30 °C for 2 days. The G + C content of the DNA was determined by using the thermal denaturation method of Marmur & Doty (1962). The major cellular fatty acids of the strain FR1199^T were C_{16:0} (27.6 ± 0.4 %), C_{16:1ω7c} and/or iso-C_{15:0} 2-OH (21.7 ± 1.2 %) (summed feature 3) and C_{18:1ω7c} (23.3 ± 0.5 %). In addition, C_{12:0} (1.1 ± 0.1 %), C_{10:0} 3-OH (4.0 ± 0.3 %), C_{12:0} 3-OH (3.4 ± 0.2 %), iso-C_{16:0} 3-OH (2.8 ± 0.6 %), C_{18:0ω6c} (2.2 ± 0.2 %), C_{17:0} (1.6 ± 0.2 %), C_{17:1ω8c} (1.0 ± 0.1 %) and C_{18:1ω6c} (2.9 ± 0.1 %) were also detected. The DNA G + C content of strain FR1199^T was 39 mol%.

The formation of a distinctive phyletic line within the genus *Pseudoalteromonas* indicates that strain FR1199^T can be assigned as a novel species in this genus. In addition, a number of physiological and chemotaxonomic characters clearly distinguished our isolate from other phylogenetically related species (Table 1). Therefore, strain FR1199^T should be classified as a member of a novel species within the genus

Pseudoalteromonas, for which the name *Pseudoalteromonas byunsanensis* sp. nov. is proposed.

Description of *Pseudoalteromonas byunsanensis* sp. nov.

Pseudoalteromonas byunsanensis (by.un.san.en' sis. N.L. fem. adj. *byunsanensis* named after Byunsan, South Korea, the geographical origin of the type strain).

Cells are rod-shaped, 0.5–0.8 µm in diameter and 1.5–2.0 µm in length, Gram-negative and motile. Strictly aerobic. Cells do not form endospores. Oxidase- and catalase-positive. Requires sea water for growth. Growth occurs in media with 0.5–5 % (w/v) NaCl, with the optimum at 1.5–2 %. Temperature for growth ranges from 10 to 40 °C, with the optimum at 25–30 °C. The pH for growth ranges from 5.0 to 10.0, with the optimum at pH 8.0. Colonies are colourless at pH 5.0 but violet-coloured at pH 6–10. Colonies are usually 2–3 mm in diameter within 3 days at 25 °C. Does not reduce nitrate to nitrite. Produces gelatinase, cytochrome oxidase and aesculin dihydrolase, but not arginine dihydrolase, β-galactosidase, lysine decarboxylase, ornithine decarboxylase, urease, H₂S, tryptophan deaminase, indole or acetone. Produces alkaline phosphatase, esterase (C4), esterase lipase (C8), leucine arylamidase, trypsin,

acid phosphatase, naphthol-AS-BI-phosphohydrolase, α -glucosidase and acid phosphatase, but not lipase (C14), cystine arylamide, valine arylamidase, α -chymotrypsin, α -galactosidase, β -galactosidase, β -glucuronidase, β -glucosidase, *N*-acetyl- β -glucosaminidase, α -mannosidase, α -fucosidase, lysine decarboxylase, ornithine decarboxylase or tryptophan deaminase. Utilizes the following substrates as sole carbon and energy sources: glucose, arabinose, mannose, mannitol, *N*-acetylglucosamine, maltose and tetramethyl-*p*-phenylenediamine dichloride. Does not utilize the following substrates: gluconate, caprate, malate, malonate, citrate, phenylacetate and *p*-nitrophenyl β -galactopyranoside. Other phenotypic characteristics are given in Table 1. The major cellular fatty acids are C_{16:0} (27.6 $\pm$ 0.4 %), C_{16:1} ω 7c and/or iso-C_{15:0} 2-OH (21.7 $\pm$ 1.2 %) and C_{18:1} ω 7c (23.3 $\pm$ 0.5 %). The DNA G + C content is 39 mol%.

The type strain, FR1199^T (= JCM 12483^T = KCTC 12274^T), was isolated from Korean tidal flat sediment.

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