Pseudidiomarina donghaiensis sp. nov. and
Pseudidiomarina maritima sp. nov., isolated from
the East China Sea

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Two Gram-negative, aerobic, motile, rod-shaped bacteria, designated strains 908033T and
908087T, were isolated from a seawater sample collected from the East China Sea. Chemotaxonomic
characteristics of the two isolates included the presence of iso-C15:0, iso-
C17:0 and iso-C17:1ω9c as the major cellular fatty acids and Q-8 as the predominant ubiquinone. The
genomic DNA G+C contents of strains 908033T and 908087T were 45.5 and 45.2 mol%,
respectively. Phylogenetic analyses based on 16S rRNA gene sequences revealed that the new
isolates were related to members of the genus Pseudidiomarina, showing levels of similarity of
95.8–96.6 % with the type strains of recognized species of the genus. The results of DNA–DNA
hybridization experiments among these two isolates and Pseudidiomarina sediminum CICC
10319T, in combination with chemotaxonomic and phenotypic data, demonstrated that the new
isolates represent two novel species of the genus Pseudidiomarina, for which the names
Pseudidiomarina donghaiensis sp. nov. (type strain 908033T =CGMCC 1.7284T =JCM 15533T)
and Pseudidiomarina maritima sp. nov. (type strain 908087T =CGMCC 1.7285T =JCM 15534T)
are proposed.

The family Idiomarinaceae, belonging to the class Gammaproteobacteria, was proposed by Ivanova et al.
(2004) based on a comprehensive phylogenetic analysis, and the family comprises two recognized genera: Idiomarina (Ivanova et al., 2000) and Pseudidiomarina (Jean et al., 2006). At the time of writing, the genus Pseudidiomarina comprised two recognized species, namely Pseudidiomarina taiwanensis (Jean et al., 2006) and Pseudidiomarina sediminun (Hu & Li, 2007). Members of the genus contain iso-branched fatty acids with 15 and
17 carbons as the predominant components. In this study, we present a polyphasic study describing two motile
bacteria isolated from a seawater sample. The resultant phylogenetic and phenotypic data showed that the new
isolates represent two novel species of the genus Pseudidiomarina.

A seawater sample was collected from the East China Sea (125°59’24” E 30°58’16” N) at a depth of 70 m
(temperature 16.7 °C; salinity 33.95 ‰). Approximately 150 μl seawater was plated on marine agar 2216 (MA;
Difco). After 3 days aerobic incubation at 25 °C, two non-pigmented colonies, designated strains 908033T
and 908087T, were picked. The isolates were purified by repeated restreaking; purity was confirmed based on
uniformity of cell morphology. Unless stated otherwise, strains 908033T and 908087T were maintained on halo-
philic medium (HM) containing 3 % NaCl (w/v) at 37 °C. HM contained (per litre distilled water): NaCl as indicated, 2.0 g KCl, 1.0 g MgSO4 .7H2O, 0.36 g CaCl2 .2H2O, 0.23 g NaBr, 0.06 g NaHCO3, trace FeCl3, 10.0 g yeast extract (Difco), 5.0 g peptone (Difco) and 1.0 g glucose (pH 7.5) (Ventosa et al., 1982).

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene
sequences of strains 908033T and 908087T are EU600204 and EU600203, respectively.

Transmission electron micrographs of cells of strains 908033T and
908087T, maximum-parsimony and maximum-likelihood phylogenetic
trees based on 16S rRNA gene sequences, and a table giving the
cellular fatty acid contents of strains 908033T and 908087T and related
Pseudidiomarina species are available as supplementary material with
the online version of this paper.
Optimal conditions for growth were determined in MYP medium with various NaCl concentrations (0, 0.5, 1, 3, 5, 7.5, 10, 15, 20 and 25, w/v). MYP medium contained (per litre distilled water): 1.0 g MgSO4·7H2O, 10.0 g yeast extract (Difco), 5.0 g peptone (Difco) and 1.0 g glucose (pH 7.5). The pH range for growth (from pH 5.0 to 10.0, at intervals of 0.5 pH units) was determined in HM with the addition of MES (50 mM; pH 5.0–6.5), PIPES (50 mM; pH 6.5–7.5), Tris (50 mM; pH 7.5–9.0) or Na2CO3/NaHCO3 (pH 9.0–10.0). The temperature range for growth was determined by incubating at 4, 10, 15, 20, 25, 30, 35, 37, 40, 42, 45 and 50 °C. Cell morphology and motility were examined by using optical microscopy (BX40; Olympus) and electron microscopy (JEM-1200EX; JEOL).

Single-carbon assimilation tests were performed by using a basal medium (Kämpfer et al., 1991) containing (per litre distilled water): 30.0 g NaCl, 0.5 g MgSO4·7H2O, 0.1 g CaCl2·2H2O, 1.74 g K2HPO4, 1.36 g KH2PO4, 5 g (NH4)2SO4, 0.02 g yeast extract (Difco), 0.02 g peptone (Difco), 1 ml vitamin mixture solution (Wolin et al., 1963), 5 ml mineral mixture solution (Balch et al., 1979) and 25 mM PIPES (pH 7.2). The corresponding filter-sterilized sugar (0.2 %), alcohol (0.1 %), organic acid (0.1 %) or amino acid (0.1 %) was added to the liquid medium. Acid production was tested by using modified MOF medium supplemented with 1 % sugars (Leifson, 1963; Xu et al., 2008). Biochemical and nutritional tests were performed in HM according to Xu et al. (2007) as described by Mata et al. (2002). Additional enzyme activities and biochemical characteristics were determined by using API 20E, API 20NE and API ZYM kits at 37 °C as recommended by the manufacturer (bioMérieux). P. sediminum CICC 10319T was used as a control in these tests.

Genomic DNA was obtained by using the method described by Marmur (1961). The 16S rRNA gene was amplified and analysed as described by Xu et al. (2007). PCR products were cloned into pMD19-T vector (TaKaRa) and were then sequenced to determine the almost-complete sequence of the 16S rRNA gene. The sequence was compared with those of closely related reference organisms from the FASTA and EzTaxon services (Chun et al., 2007). Sequence data were aligned with CLUSTAL W 1.8 (Thompson et al., 1994). Phylogenetic trees were constructed according to the neighbour-joining method (Saitou & Nei, 1987) and maximum-parsimony (Fitch, 1971) methods with the MEGA 3.1 program package (Kumar et al., 2004), and according to the maximum-likelihood method (Felsenstein, 1981) with the TreePuzzle 5.2 program. Evolutionary distances were calculated based on the algorithm of the Kimura two-parameter model (Kimura, 1980) for the neighbour-joining method.

Cellular fatty acid methyl esters were prepared from cells grown on MA for 2 days at 30 °C and were analysed by using GC/MS (Kuykendall et al., 1988), according to the instructions of the Microbial Identification System (MIDI Inc.). Isoprenoid quinones were extracted from freeze-dried cells (200 mg) with chloroform/methanol (2:1, by vol.) and were analysed by using reversed-phase HPLC. The purified DNA was hydrolysed with P1 nuclease and the nucleotides were dephosphorylated with calf intestine alkaline phosphatase (Mesbah & Whitman, 1989). The G+C contents of the resulting deoxyribonucleosides were determined by reversed-phase HPLC and were calculated from the ratio of deoxyguanosine (dG) and thymidine (dT) (Mesbah & Whitman, 1989). DNA–DNA hybridizations were performed by using the thermal denaturation and renaturation method of De Ley et al. (1970) as modified by Huß et al. (1983), with a Beckman DU 800 spectrophotometer.

Cells of strains 908033T and 908087T were Gram-negative, slightly curved rods that were motile by means of peritrichous flagella (see Supplementary Fig. S1, in IJSEM Online). The NaCl concentration and temperature ranges for growth of strain 908033T were 0.5–10.0 % (w/v) and 15–45 °C, whereas those of strain 908087T were 0.5–15.0 % (w/v) and 10–45 °C. Strain 908033T could be distinguished from strain 908087T based on H2S formation, selenite reduction, lecithinase production and tyrosine hydrolysis (Table 1). Physiological and chemotaxonomic characteristics of the two strains are summarized in the species descriptions below.

Almost-complete 16S rRNA gene sequences of strains 908033T (1507 nt) and 908087T (1507 nt) were obtained. The two strains were found to be phylogenetically closely related, showing 97.5 % 16S rRNA gene sequence similarity (Fig. 1). 16S rRNA gene sequence comparisons with representative bacteria with validly published names indicated that strains 908033T and 908087T were related most closely to members of the genera Pseudidiomarina (95.8–96.6 % similarity) and Idiomarina (93.7–97.5 %). Phylogenetic analysis based on 16S rRNA gene sequences showed that the novel isolates formed a coherent cluster with the type strains of P. taiwanensis and P. sediminum with a moderately high bootstrap resampling value (71 % based on the neighbour-joining method) (Fig. 1). The topologies of the phylogenetic trees constructed by using the maximum-likelihood and maximum-parsimony algorithms also supported the suggestion that strains 908033T and 908087T represent novel species of the genus Pseudidiomarina (Supplementary Fig. S2, in IJSEM Online). The major cellular fatty acids of strains 908033T and 908087T were iso-C15 : 0 (22.9 and 26.8 % of the total, respectively), iso-C17 : 0 (12.5 and 11.6 %) (Supplementary Table S1, available in IJSEM Online). This profile was similar to that of recognized species of the genus Pseudidiomarina (Jean et al., 2006; Hu & Li., 2007).

Strains 908033T and 908087T showed less than 97.0 % 16S rRNA gene sequence similarity to the type strains of the two recognized species of the genus Pseudidiomarina. Levels of DNA–DNA relatedness between strains 908033T and 908087T were less than 70 %, which was in accordance with DNA–DNA hybridization values.
and 908087T with respect to P. sediminum CICC 10319T were 39.1 and 37.5 %, respectively. A low level of DNA–DNA relatedness (41.3 %) was found between strains 908033T and 908087T, suggesting that the two strains represent two species of the genus Pseudidiomarina (Stackebrandt & Goebel, 1994). Comparison of phenotypic properties (Table 1 and Supplementary Table S1) indicated differences between strains 908033T and 908087T and the type strains of P. taiwanensis and P. sediminum, such as motility, salt or temperature range for growth, nitrate reduction, H₂S formation, hydrolysis of substrates, susceptibility to antimicrobial compounds and DNA G+C content.

Based on 16S rRNA gene sequence analysis, as well as the DNA–DNA hybridization data and differential phenotypic properties, we suggest that strains 908033T and 908087T represent two novel species of the genus Pseudidiomarina, for which the names Pseudidiomarina donghaiensis sp. nov. and Pseudidiomarina maritima sp. nov. are proposed, respectively.

**Description of Pseudidiomarina donghaiensis** sp. nov.

*Pseudidiomarina donghaiensis* (dong.ha.i.en'sis. N.L. fem. adj. donghaiensis pertaining to Donghai, the Chinese name for the East China Sea).

Cells are Gram-negative, slightly curved rods, approximately 0.4–0.6 μm in width and 1.0–1.4 μm in length. Cells are motile by means of peritrichous flagella. No endospores are formed. Colonies on MA plates are 1–2 mm in diameter, non-pigmented, circular and smooth after 48 h at 37°C. Growth occurs at NaCl concentrations of 0.5–10.0 % (w/v) with optimum growth at 3.0 %. pH and temperature ranges for growth are pH 6.5–10.0 and 15–45°C (optimum growth at pH 8.0–9.0 and 37°C). No growth is detected at 10 or 50°C. Positive for oxidase and catalase. No growth occurs on MacConkey agar or cetrimide agar. Casein, gelatin, DNA, Tweens 20 and 80 and tyrosine are hydrolysed. Aesculin and starch are not.

**Table 1.** Differential taxonomic characteristics between strains 908033T (P. donghaiensis sp. nov.) and 908087T (P. maritima sp. nov.) and other related Pseudidiomarina and Idiomarina species

<table>
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<td>–</td>
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<td>45.2</td>
<td>50.0*</td>
<td>49.3</td>
<td>53.9</td>
</tr>
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</table>

*Data from Hu & Li (2007).

![Fig. 1. Neighbour-joining tree based on 16S rRNA gene sequences, showing the phylogenetic relationships among strains 908033T and 908087T and related taxa. Bootstrap values are based on 1000 replicates; only values >50% are shown. Bar, 0.02 substitutions per nucleotide position. Filled circles indicate nodes that were also recovered with bootstrap values >50% in both the maximum-likelihood and the maximum-parsimony trees](http://ijs.sgmjournals.org)
Description of Pseudidiomarina maritima sp. nov.

Pseudidiomarina maritima (ma.ri.ti’ma. L. fem. adj. maritima inhabiting marine environments).

Cells are Gram-negative, slightly curved rods, approximately 0.4–0.6 µm wide and 1.4–2.0 µm long. Cells are motile by means of peritrichous flagella. Colonies on MA plates are 1–2 mm in diameter, non-pigmented, circular and smooth after 48 h at 37 °C. Growth occurs at NaCl concentrations of 0.5–15.0 % (w/v) with optimum growth at 3.0 %. The pH and temperature ranges for growth are pH 6.5–10.0 and 10–45 °C (optimum growth at pH 8.0–9.0 and 37 °C). No growth is detected at 4 or 50 °C. Positive for oxidase and catalase. No growth occurs on MacConkey agar or cetrimide agar. Casein, DNA, gelatin and Tween 20 and 80 are hydrolysed. Aesculin, starch and tyrosine are not hydrolysed. Positive for selenite reduction. Negative for arginine dihydrolase, gluconate oxidation, indole production, lecithinase, lysine decarboxylase, methyl red, o-nitrophenyl β-D-galactopyranosidase, ornithine decarboxylase, selenite reduction and urease. H₂S is not formed from thiosulfate. No nitrate or nitrite reduction. The following substrates are not utilized as sole carbon and energy sources: acetate, adonitol, L-alanine, L-arabinose, L-arginine, L-aspartate, D-cellobiose, citrate, L-cysteine, ethanol, formate, D-fructose, fumarate, D-galactose, glucose, L-glutamate, glycerol, glycine, gluconate, L-glutamine, L-histidine, inositol, isoleucine, lactate, lactose, lysine, malate, malonate, maltose, mannitol, D-mannose, melibiose, L-methionine, L-proline, propionate, pyruvate, D-raffinose, rhamnose, ribose, salicin, L-serine, L-sorbitol, sorbose, succinate, succrose, trehalose, L-valine, xylitol and xylose. Acid is not produced from adonitol, L-arabinose, D-cellobiose, D-fructose, D-galactose, glucose, inositol, lactose, malate, mannitol, D-mannose, melibiose, D-raffinose, rhamnose, ribose, L-sorbitol, sorbose, succrose, trehalose, xylitol or xylose. The following constitutive enzyme activities are detected in API ZYM tests: alkaline phosphatase, esterase (C4), esterase lipase (C8), lipase (C14), leucine arylamidase, valine arylamidase, cystine arylamidase, trypsin, z-chymotrypsin, acid phosphatase and naphthol-AS-BI-phosphohydrolase. In API 20NE tests, negative for use of any of the substrates provided with the kit except gelatin. In API 20E tests, produces gelatinase, but cannot ferment glucose or other carbohydrates as substrates. Susceptible to amoxicillin (10 µg), ampicillin (10 µg), carbenicillin (100 µg), cefotaxime (30 µg), cefoxitin (30 µg), chloramphenicol (30 µg), erythromycin (10 µg), minocycline (30 µg), nitrofurantoin (300 µg), novobiocin (30 µg), penicillin (10 IU), polymyxin B (300 IU), rifampicin (5 µg) and tetracycline (30 µg), but resistant to bacitracin (0.04 IU), kanamycin (30 µg), neomycin (30 µg), nystatin (100 µg) and tobramycin (10 µg). The predominant ubiquinone is Q-8. Major fatty acids are iso-C₁₅:₀, iso-C₁₇:₀ and iso-C₁₇:₁ω9c. The DNA G+C content of the type strain is 45.5 mol% (determined by HPLC).

The type strain, 908033T (=CGMCC 1.7284T=JCM 15533T), was isolated from a coastal seawater sample collected from the East China Sea, China.


