Kordia periserrulae sp. nov., isolated from a marine polychaete *Periserrula leucophryna*, and emended description of the genus *Kordia*

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A Gram-negative, chemoheterotrophic, yellow-pigmented, non-motile, flexirubin-negative, facultatively anaerobic bacterium, designated strain IMCC1412^T, was isolated from a marine polychaete *Periserrula leucophryna* inhabiting a tidal flat of the Yellow Sea, Korea. Phylogenetic analysis based on 16S rRNA gene sequences indicated that strain IMCC1412^T was most closely related to *Kordia algicida*, with a sequence similarity of 96.7 %, but only distantly related to other species in the family *Flavobacteriaceae* (<92 % similarity). The G+C content of the DNA was 37.3 mol%. The strain contained MK-6 as the major respiratory quinone and phosphatidylethanolamine, unidentified aminolipids and unidentified polar lipids as the major polar lipids. On the basis of phylogenetic distinctiveness and differential phenotypic characteristics, strain IMCC1412^T (=KACC 14311^T=KCTC 22801^T=NBRC 106077^T) should be assigned to the genus *Kordia* as the type strain of a novel species, for which the name *Kordia periserrulae* sp. nov. is proposed. An emended description of the genus *Kordia* is also presented.

The genus *Kordia* (Sohn *et al.*, 2004), a member of the family *Flavobacteriaceae* (Bernardet *et al.*, 2002; Bernardet & Nakagawa, 2006), currently comprises only the type species, *Kordia algicida*. The type strain of *Kordia algicida* was isolated from a surface seawater sample from Masan Bay, Korea, and was characterized as being Gram-staining-negative, yellow-pigmented, non-motile, flexirubin-negative and strictly aerobic with rod-shaped cells. Menaquinone 6 (MK-6) was the predominant isoprenoid quinone and the DNA G+C content of the type strain was 34 mol% (Sohn *et al.*, 2004). At the time of publication of the name *Kordia algicida* (Sohn *et al.*, 2004), the type strain, OT-1^T, was deposited in two culture collections in two different countries. However, the strain was deposited in the KCTC (Korean Collection for Type Cultures) as a patent strain, designated KCTC 8814P^T. According to Rule 30 (4) of the Bacteriological Code (Tindall *et al.*, 2008), organisms deposited in such a fashion that access is restricted, such as safe deposits or strains deposited solely for current patent purposes, may not serve as type strains. This ruling meant that the genus name *Kordia* and species name *Kordia algicida* were not regarded as having been validly published. Recently strain OT-1^T was deposited in the KACC (Korean Agricultural Culture Collection) as KACC 15108^T, which now fulfils the criteria for valid publication of the name *Kordia algicida*. In the present study, based on a polyphasic approach, we describe strain IMCC1412^T, which was isolated from a marine polychaete dwelling in a tidal flat. The results of phenotypic and genotypic characterization indicate that strain IMCC1412^T represents a novel species in the genus *Kordia*.

Strain IMCC1412^T was isolated from the digestive tract of a marine polychaete, *Periserrula leucophryna*, collected from a tidal flat on Donggum Island. The marine animal was washed with sterile seawater three times and dissected under a stereoscopic microscope (SZH10; Olympus). The contents of the digestive tract were homogenized and serially diluted samples were spread onto an oligotrophic medium, R2A agar (BD Difco) diluted 1 : 10 (v/v) with aged seawater (1/10 R2A medium), and the plates were incubated aerobically at 20 °C for 1 month. After the optimum growth temperature of the strain had been determined, the strain was routinely grown on marine agar 2216 (MA; BD Difco) at 30 °C. For phenotypic and chemotaxonomic comparisons between strain IMCC1412^T and *K. algicida*, strain KCTC 8814P^T was obtained from the KCTC with the permission of Dr Sang-Jin Kim (the depositor of the strain) and used as a reference strain in the taxonomic study.

Genomic DNA preparation, 16S rRNA gene amplification and sequencing were performed as described previously (Cho & Giovannoni, 2003). The resulting almost-complete 16S rRNA gene sequence (1474 bp) of strain IMCC1412^T was aligned with the nearest neighbours using the ARB software package (Ludwig *et al.*, 2004) and unambiguously aligned nucleotide positions were used for phylogenetic analyses in PAUP* 4.0 beta (Swofford, 2002). The 16S rRNA

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain IMCC1412^T is GU233518.

A supplementary figure is available with the online version of this paper.

gene sequence similarities between strain IMCC1412^T and its phylogenetic relatives were determined using the ARB package and also confirmed by accessing the EzTaxon server (Chun *et al.*, 2007). Phylogenetic trees were generated using neighbour-joining (Saitou & Nei, 1987) with the Jukes–Cantor distance formula (Jukes & Cantor, 1969), maximum-parsimony (Fitch, 1971) and maximum-likelihood (Felsenstein, 1981) methods. The robustness of the neighbour-joining and maximum-parsimony trees was confirmed by bootstrap analyses based on 1000 resamplings of the sequences. Based on 16S rRNA gene sequence comparisons, strain IMCC1412^T was related most closely to *K. algicida* KCTC 8814P^T (96.7 %), followed by *Aquimarina latercula* ATCC 23177^T (91.6 %) and *Psychroserpens mesophilus* KOPRI 13649^T (91.3 %). In all the phylogenetic trees (Fig. 1), strains IMCC1412^T and *K. algicida* KCTC 8814P^T formed a robust monophyletic clade with a high bootstrap value (100 %), indicating the strain belonged to the genus *Kordia*. DNA–DNA hybridization experiments as suggested by Wayne *et al.* (1987) for the determination of bacterial species were not performed because the 16S rRNA gene sequence similarity between strain IMCC1412^T and *K. algicida* was <97 % (Stackebrandt & Goebel, 1994). The phylogenetic results coupled with the 16S rRNA gene sequence analyses suggested that strain IMCC1412^T should be assigned to the genus *Kordia* as representing a novel species.

For phenotypic characterization, strains IMCC1412^T and *K. algicida* KCTC 8814P^T were routinely grown on MA at 30 °C. All the phenotypic tests, except for determination of temperature range and optimum for growth, were performed at 30 °C. Morphology and size of the cells and colonies, Gram reaction, presence of flagellar and gliding motilities, catalase and oxidase activities, presence of flexirubin-type pigments and the absorption spectra of cellular pigments were determined by the methods described by Yang & Cho (2008) and Bernardet *et al.* (2002) except that the bacterial cultures were grown on MA or in marine broth (MB, BD Difco) at 30 °C for 3 days. The temperature range and optimum for growth were determined on MA that was incubated at 4–42 °C (4, 10, 15, 20, 25, 30, 37 and 42 °C). The pH range and optimum for growth were examined from pH 4.0 to 12.0 (at 0.5 pH unit intervals) in MB. The pH was adjusted with 0.1 M HCl or 0.1 M Na_2CO_3. The range and optimum NaCl concentration for growth were determined in NaCl-free artificial seawater medium (ASW, Choo *et al.*, 2007) amended with 5.0 g peptone, 1.0 g yeast extract and various concentrations of NaCl (0–15 %, w/v). Anaerobic growth was tested on MA using the MGC anaerobic system (Mitsubishi Gas Chemical) for 3 weeks. Production of H_2S was investigated using triple-sugar iron agar (BD Difco) in which the salinity was adjusted with 3.0 % (w/v) NaCl. Hydrolysis of casein (10 % skimmed milk, w/v), starch (0.2 %, w/v), elastin (0.5 %, w/v), chitin (0.5 %, w/v), CM-cellulose (0.2 %, w/v), crystalline cellulose (Whatman no. 1 filter paper, 1 %) and Tween 80 (1.0 %, v/v) was tested using MA as the basal medium. Degradation of DNA was tested using DNase test agar (Difco) amended with 1.5 % NaCl. Other biochemical tests and substrate oxidation tests were carried out using API 20NE, API ZYM, API 50CH test strips (bioMérieux) and Biolog GN2 microplates (Biolog) by inoculating the cells into the ASW medium. The following antibiotics were tested using the diffusion plate method: ampicillin (10 μg), chloramphenicol (25 μg), erythromycin (15 μg), gentamicin (10 μg), kanamycin (30 μg), penicillin G (10 μg), rifampicin (50 μg), streptomycin (10 μg), tetracycline (30 μg) and vancomycin (30 μg). The DNA G+C content was determined using the HPLC method (Mesbah *et al.*, 1989).

Cellular fatty acid methyl esters (FAME) of strains IMCC1412^T and *K. algicida* KCTC 8814P^T were extracted

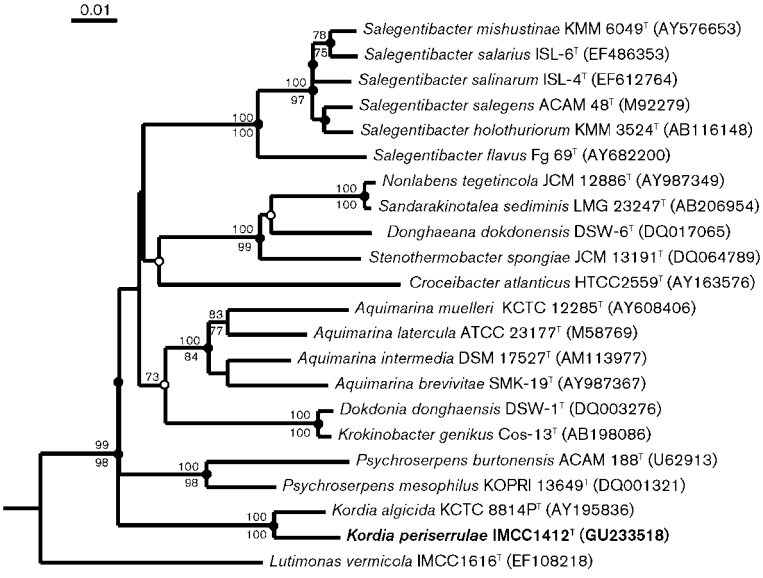

Fig. 1. Neighbour-joining phylogenetic tree, based on 16S rRNA gene sequences, showing the relationship between strain IMCC1412^T and its relatives in the family *Flavobacteriaceae*. Bootstrap values (>70 %) from both neighbour-joining (above nodes) and maximum-parsimony (below nodes) are presented. Nodes recovered reproducibly by neighbour-joining, maximum-parsimony and maximum-likelihood methods (filled circles) or by two of the three treeing methods (open circles) are indicated. *Polaribacter dokdonensis* DSW-5^T (GenBank accession no. DQ004686) was used as an outgroup. Bar, 0.01 substitutions per nucleotide position.

using the Sherlock Rapid Method (MIDI, Inc.) from cultures grown on MA at 30 °C for 4 days. The Sherlock Microbial Identification System (MIDI, Inc.) version 4.5 with the database TBSA40 and version 6.1 with the databases TSBA60 and RTSBA60 were used to assign GC peaks to each fatty acid. Isoprenoid quinones were extracted by TLC according to Minnikin *et al.* (1984) and analysed by using HPLC (Collins, 1985). Polar lipids were extracted by an integrated approach and determined using two-dimensional TLC on silica gel thin layers (Minnikin *et al.*, 1984). The TLC plates were developed in chloroform/methanol/water (65 : 25 : 4, by vol.) in the first direction, followed by chloroform/methanol/acetic acid/water (80 : 12 : 15 : 4, by vol.) in the second direction. Total polar lipids were detected by spraying with 10 % ethanolic molybdophosphoric acid followed by heating at 150 °C for 30 min. Specific functional group-containing lipids were detected with the following spraying reagents: the molybdenum blue reagent for phosphorus-containing lipid; ninhydrin for free amino groups; α-naphthol for sugars; periodate-Schiff for α-glycols and Dragendorff for quaternary nitrogen.

The phenotypic characteristics of strain IMCC1412^T are summarized in the species description and Table 1. In short, cells of strain IMCC1412^T were Gram-staining-negative, chemoheterotrophic, facultatively anaerobic, oxidase- and catalase-positive, non-motile, flexirubin-negative and appeared as yellow-pigmented rods. Table 1 shows the differential phenotypic characteristics between strain IMCC1412^T and the type strain of *K. algicida*. The two strains shared similar characteristics in their patterns of macromolecule degradation and antimicrobial agent susceptibility. However, several phenotypic differences were found between them allowing ready differentiation of strain IMCC1412^T from *K. algicida* KCTC 8814P^T (Table 1).

The DNA G+C content of strain IMCC1412^T was 37.3 mol%. The major respiratory quinone detected was MK-6. The polar lipids of strains IMCC1412^T and KCTC 8814P^T included phosphatidylethanolamine and several unknown lipids (see Supplementary Fig. S1 in IJSEM Online). The polar lipid profiles of both strains were differentiated by the presence of unknown aminolipids and an aminophospholipid. The major cellular fatty acid constituents of strain IMCC1412^T determined using MIDI version 4.5 were iso-$C_{15:0}$ (28.1%), iso-$C_{17:0}$ 3-OH (16.3%), iso-$C_{15:0}$ 3-OH (11.2%) and $C_{16:1}\omega7c$ and/or iso-$C_{15:0}$ 2-OH (12.4%) and were differentiated from those of *K. algicida* in the proportions of iso-$C_{15:0}$ and iso-$C_{15:1}$ F and in the presence/absence of several fatty acids (Table 2). There were huge differences in the fatty acid compositions determined by using different MIDI versions and methods, suggesting more careful consideration should be required for fatty acid profiles generated by different databases and methods. The DNA G+C content, isoprenoid quinone composition, polar lipid profile and predominant cellular fatty acids of strain IMCC1412^T were generally in good agreement with those of *K. algicida*, suggesting the assignment of the novel strain into the genus *Kordia*.

In conclusion, 16S rRNA gene sequence similarity and phylogenetic analyses, together with phenotypic characteristics, indicate that strain IMCC1412^T represents a novel species of the genus *Kordia*, for which the name *Kordia periserrulae* sp. nov. is proposed. Based on differential and additional phenotypic characteristics of strain IMCC1412^T not reported in the description of the genus *Kordia* by Sohn *et al.* (2004), an emended description of the genus *Kordia* is provided.

Emended description of the genus *Kordia* Sohn *et al.* 2004

The description of the genus *Kordia* is as given by Sohn *et al.* (2004) with the following amendments. Cells are obligately aerobic or facultatively anaerobic. Catalase activity is species-dependent. Requires 0.5–7.5 % NaCl for growth. Elastin is hydrolysed but DNA is not. The DNA G+C content is 34–37 mol%. Major polar lipids include phosphatidylethanolamine, unknown aminolipids and polar lipids. The type species is *Kordia algicida*.

Description of *Kordia periserrulae* sp. nov.

Kordia periserrulae (pe.ri.ser.ru′lae. N.L. n. *Periserrula* a scientific generic name, *Periserrula*; N.L. gen. n. *periserrulae* of *Periserrula*, pertaining to a species isolated from the digestive tract of *Periserrula leucophryna*).

Cells are Gram-reaction-negative, chemoheterotophic, oxidase- and catalase-positive, non-motile, non-gliding, flexirubin-negative, yellow-pigmented and facultatively anaerobic. Aerobic growth is better than anaerobic growth. Cells are rod-shaped (1.3–3.7 × 0.4–1.0 μm). After 4 days incubation on MA at 30 °C, colonies are circular, convex, shiny, have an entire margin and are 3.5 mm in diameter. Growth occurs at 4–37 °C (optimum, 30 °C), pH 7.0–9.0 (optimum, pH 7.0–8.0) and 0.5–7.5 % NaCl (optimum, 3.0 % NaCl). Starch, casein and elastin are hydrolysed. Does not hydrolyse DNA, cellulose, CM-cellulose, chitin or Tween 80. H_2S is produced. Absorption spectral peaks of the pigments are observed at 451 nm (major peak) and 478 nm. Positive for aesculin hydrolysis and gelatin liquefaction in API 20NE tests, but negative for nitrate reduction, indole production, glucose fermentation and activities of arginine dihydrolase, urease and PNPG (β-galactosidase). Positive for the following enzyme activities; alkaline phosphatase, esterase (C4), esterase lipase (C8), lipase (C14), leucine arylamidase, valine arylamidase, cystine arylamidase, trypsin, α-chymotrypsin, acid phosphatase, naphthol-AS-BI-phosphohydrolase, α-galactosidase and β-galactosidase in API ZYM tests, but negative for β-glucuronidase, α-glucosidase, β-glucosidase, *N*-acetyl-β-glucosaminidase, α-mannosidase and α-fucosidase. In API 50CH tests, acids are produced from glycerol, D-galactose, D-glucose, D-mannose, L-sorbose, L-rhamnose, *N*-acetylglucosamine, amygdalin, arbutin, aesculin ferric citrate, D-cellobiose, maltose, sucrose, starch, glycogen, gentiobiose, D-tagatose and potassium 2-ketogluconate. In Biolog GN2 microplate tests, oxidizes α-cyclodextrin,

Table 1. Differential characteristics between strain IMCC1412^T and *K. algicida* KCTC 8814P^T

Strains: 1, IMCC1412^T; 2, *K. algicida* KCTC 8814P^T. All data were obtained from the present study except for the temperature and pH range for growth and DNA G+C content of *K. algicida* KCTC 8814P^T (Sohn *et al.*, 2004). +, Positive; –, negative. Both strains were Gram-staining-negative, non-motile, non-gliding, oxidase-positive and flexirubin-negative. Both strains hydrolysed starch, casein and elastin, but did not hydrolyse DNA, cellulose, CM-cellulose, chitin or Tween 80. In API 20NE tests, both strains were positive for gelatin liquefaction, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease and β-galactosidase activities. In API ZYM tests, both strains were positive for alkaline phosphatase, esterase (C4), esterase lipase (C8), lipase (C14), leucine arylamidase, acid phosphatase and naphthol-AS-BI-phosphohydrolase activity, but negative for β-glucuronidase, α-glucosidase, β-glucosidase, *N*-acetyl-β-glucosaminidase, α-mannosidase and α-fucosidase activities. In API 50CH tests, both strains were positive for aesculin ferric citrate, maltose, sucrose, starch, glycogen, D-tagatose and potassium 2-ketogluconate, but negative for erythritol, D-arabinose, L-arabinose, D-ribose, D-xylose, L-xylose, D-adonitol, methyl β-D-xylopyranoside, D-fructose, dulcitol, inositol, D-mannitol, D-sorbitol, methyl α-D-mannopyranoside, methyl α-D-glucopyranoside, salicin, lactose, melibiose, trehalose, inulin, melezitose, raffinose, xylitol, turanose, D-lyxose, D-fucose, L-fucose, D-arabitol, L-arabitol and potassium gluconate. In Biolog GN2 tests, both strains were positive for α-cyclodextrin, dextrin, glycogen, *N*-acetyl-D-glucosamine, adonitol, cellobiose, i-erythritol, gentiobiose, α-D-glucose, maltose, D-mannitol, D-mannose, raffinose, sucrose, pyruvic acid methyl ester, succinic acid monomethyl ester, citric acid, D-glucuronic acid, DL-lactic acid, quinic acid, succinic acid, L-alaninamide, L-glutamic acid, glycyl L-aspartic acid, glycyl L-glutamic acid, L-ornithine, L-proline, L-threonine, DL-carnitine, uridine, α-D-glucose 1-phosphate and D-glucose 6-phosphate, but negative for Tween 40, Tween 80, L-arabinose, *p*-hydroxyphenylacetic acid, itaconic acid, sebacic acid, D-alanine, L-asparagine, L-histidine, hydroxy-L-proline, L-leucine, D-serine, L-serine, γ-aminobutyric acid, urocanic acid and inosine. Both strains were susceptible to erythromycin, rifampicin and vancomycin, but resistant to ampicillin, gentamicin, kanamycin, penicillin G, streptomycin and tetracycline.

Characteristic	1	2
Temperature range for growth (°C)	4–37	5–40*
Growth with 7.5 % NaCl	+	–*
Anaerobic growth	+	–
Catalase	+	–
H_2S production	+	–
Aesculin hydrolysis	+	–
Nitrate reduction, glucose fermentation	–	–(+)†
Enzyme activities (API ZYM)		
Valine arylamidase, cystine arylamidase, trypsin, α-chymotrypsin, α-galactosidase, β-galactosidase	+	–
Acid production from carbohydrates (API 50CH)		
Glycerol, D-galactose, D-glucose, D-mannose, L-sorbose, L-rhamnose, *N*-acetylglucosamine, amygdalin, arbutin, D-cellobiose, gentiobiose	+	–
Potassium 5-ketogluconate	–	+
Carbon source oxidation (Biolog GN2)		
N-Acetyl-D-galactosamine, D-arabitol, D-fructose, L-fucose, D-galactose, *myo*-inositol, α-lactose, lactulose, melibiose, methyl β-D-glucoside, D-psicose, L-rhamnose, D-sorbitol, trehalose, turanose, xylitol, acetic acid, *cis*-aconitic acid, formic acid, D-galactonic acid lactone, D-galacturonic acid, D-gluconic acid, D-glucosaminic acid, α-hydroxybutyric acid, β-hydroxybutyric acid, γ-hydroxybutyric acid, α-ketobutyric acid, α-ketovaleric acid, malonic acid, propionic acid, D-saccharic acid, bromosuccinic acid, succinamic acid, glucuronamide, L-alanine, L-alanyl glycine, L-phenylalanine, L-pyroglutamic acid, thymidine, phenylethylamine, putrescine, 2-aminoethanol, 2,3-butanediol, glycerol, DL-α-glycerol phosphate	+	–
Cellobiose, pyruvic acid methyl ester, succinic acid monomethyl ester	+	+(–)†
α-Ketoglutaric acid	–	–(+)†
Chloramphenicol susceptibility	+	–
DNA G+C content (mol%)	37.3	34.0*

*Data for *K. algicida* KCTC 8814P^T obtained from Sohn *et al.* (2004).

†Conflicting results compared with the previous report (Sohn *et al.*, 2004). The results observed by Sohn *et al.* (2004) are shown in parentheses.

dextrin, glycogen, *N*-acetyl-D-galactosamine, *N*-acetyl-D-glucosamine, adonitol, D-arabitol, cellobiose, i-erythritol, D-fructose, L-fructose, D-galactose, gentiobiose, α-D-glucose, *myo*-inositol, α-lactose, lactulose, maltose, D-mannitol, D-mannose, melibiose, methyl β-D-glucoside, D-psicose, raffinose, L-rhamnose, D-sorbitol, sucrose, trehalose, turanose, xylitol, pyruvic acid methyl ester, succinic acid monomethyl ester, acetic acid, *cis*-aconitic acid, citric acid, formic acid, D-galactonic acid lactone, D-galacturonic acid, D-gluconic acid, D-glucosaminic acid, D-glucuronic acid, α-hydroxybutyric acid, β-hydroxybutyric acid, γ-hydroxybutyric acid, α-ketobutyric acid, α-ketoglutaric acid, α-ketovaleric acid, DL-lactic acid, malonic acid, propionic acid, quinic acid, D-saccharic acid, succinic acid, bromo-

Table 2. Comparison of cellular fatty acid composition of strain IMCC1412^T and *K. algicida* KCTC 8814P^T, obtained using different MIDI versions and databases

Methods: M1, MIDI version 4.5 and TSBA40 database; M2, MIDI version 6.1 and TSBA60 database; M3, MIDI version 6.1 and RTSBA60 database. Values are percentages of total fatty acids and all data were generated in this study. Both strains were grown under the same culture conditions (grown on MA at 30 °C for 4 days). Only fatty acids representing >1.0 % of the total fatty acids are shown. tr, Traces (<1.0 %); –, not detected.

Fatty acid	IMCC 1412^T			*K. algicida* KCTC 8814P^T		
	M1	M2	M3	M1	M2	M3
$C_{15:0}$	9.2	–	–	4.6	–	–
$C_{16:0}$	tr	4.7	1.2	2.4	tr	1.5
$C_{18:0}$	–	2.4	–	2.3	tr	tr
iso-$C_{14:0}$	tr	–	–	1.2	tr	–
iso-$C_{15:0}$	28.1	29.5	42.1	17.1	21.7	34.8
iso-$C_{15:1}$ F	6.9	7.3	11.4	1.5	1.7	5.5
iso-$C_{16:0}$	tr	tr	2.1	1.8	1.6	2.7
iso-$C_{16:1}$ H	–	–	–	tr	tr	2.2
iso-$C_{17:0}$	–	–	tr	–	–	1.0
anteiso-$C_{15:0}$	1.4	1.6	2.1	1.9	1.5	2.5
anteiso-$C_{17:0}$	–	–	–	1.8	–	tr
$C_{15:1}\omega6c$	–	–	tr	2.1	1.6	3.2
$C_{17:1}\omega6c$	–	–	–	1.1	1.2	3.2
$C_{15:0}$ 2-OH	tr	1.1	1.6	1.2	1.0	1.4
$C_{15:0}$ 3-OH	–	1.3	–	–	–	–
iso-$C_{15:0}$ 3-OH	11.2	10.9	8.5	12.3	14.4	8.8
iso-$C_{16:0}$ 3-OH	5.3	4.5	3.9	6.9	7.1	4.6
iso-$C_{17:0}$ 3-OH	16.3	16.4	–	17.8	24.1	8.0
iso-$C_{17:1}\omega9c$	–	–	tr	3.7	–	–
$C_{17:0}$ cyclo	–	–	1.2	–	–	–
Summed features*						
3	12.4	14.1†	20.7†	8.0	10.8†	6.2†
4	–	–	–	2.0	1.6	–
5	–	–	–	4.0	tr	–
9	–	tr	tr	–	4.4	7.3

*Summed features represent groups of two or three fatty acids that cannot be separated by the Microbial Identification System. Summed feature 3 contains $C_{16:1}\omega7c$ and/or iso-$C_{15:0}$ 2-OH, summed feature 4 contains iso-$C_{17:1}$ I and/or anteiso-$C_{17:1}$ B, summed feature 5 contains $C_{18:2}\omega6,9c$ and/or anteiso-$C_{18:0}$, summed feature 9 contains $C_{16:0}$ 10-methyl and/or iso-$C_{17:1}\omega9c$.
†For methods M2 and M3, summed feature 3 contains $C_{16:1}\omega7c$ and/or $C_{16:1}\omega6c$.

succinic acid, succinamic acid, glucuronamide, L-alaninamide, L-alanine, L-alanyl glycine, L-glutamic acid, glycyl L-aspartic acid, glycyl L-glutamic acid, L-ornithine, L-phenylalanine, L-proline, L-pyroglutamic acid, L-threonine, DL-carnitine, uridine, thymidine, phenylethylamine, putrescine, 2-aminoethanol, 2,3-butanediol, glycerol, DL-α-glycerol phosphate, α-D-glucose 1-phosphate and D-glucose 6-phosphate. Susceptible to erythromycin, rifampicin, chloramphenicol and vancomycin, but resistant to ampicillin, gentamicin, kanamycin, penicillin G, streptomycin and tetracycline. The major cellular fatty acids are iso-$C_{15:0}$, iso-$C_{17:0}$ 3-OH, iso-$C_{15:0}$ 3-OH and $C_{16:1}\omega7c$ and/or iso-$C_{15:0}$ 2-OH (by MIDI 4.5). The major respiratory quinone is MK-6. Polar lipids consist of phosphatidylethanolamine, unidentified aminolipids and unidentified polar lipids.

The type strain, IMCC1412^T (=KACC 14311^T=KCTC 22801^T=NBRC 106077^T), was isolated from a marine polychaete (*Periserrula leucophryna*) inhabiting a tidal flat of Donggum Island, Korea (37° 34′ 47″ N 126° 30′ 57″ E). The DNA G+C content of the type strain is 37.3 mol%.

Acknowledgements

This study was supported by the Korea Research Foundation Grant (MEST, Basic Research Promotion Fund, KRF-2008-521-C00263), by the 21C Frontier Program of Microbial Genomics and Applications from the MEST, and by the project on survey and excavation of Korean indigenous species from the National Institute of Biological Resources (NIBR).

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