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ORIGINAL PAPER

Jejudonia soesokkakensis gen. nov., sp. nov., a member of the family *Flavobacteriaceae* isolated from the junction between the ocean and a freshwater spring, and emended description of the genus *Aureitalea* Park et al. 2012

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Abstract A Gram-negative, non-flagellated, non-gliding and rod-shaped bacterial strain, designated SSK1-1^T, was isolated from the junction between the ocean and a freshwater spring at Jeju island of South Korea. Strain SSK1-1^T was found to grow optimally at 30 °C, at pH 7.0–7.5 and in the presence of 2 % (w/v) NaCl. Neighbour-joining, maximum-likelihood and maximum-parsimony phylogenetic trees based on 16S rRNA gene sequences revealed that strain SSK1-1^T is phylogenetically most closely related to members of the genera *Ulvibacter* and *Aureitalea*, with which it exhibited 16S rRNA gene sequence similarities of 93.1–95.3 %. The results of chemotaxonomic analyses distinguish strain SSK1-1^T from the genera *Ulvibacter* and *Aureitalea*. Strain SSK1-1^T was determined to contain MK-6 as the predominant menaquinone and iso-$C_{15:0}$, anteiso-$C_{15:0}$ and iso-$C_{16:0}$ as the major fatty acids. The major polar lipids of strain SSK1-1^T were identified as phosphatidylethanolamine and one unidentified lipid. The DNA G + C content of strain SSK1-1^T was determined to be 39.9 mol%. The phylogenetic analysis, chemotaxonomic data and other phenotypic properties revealed that the strain SSK1-1^T can be distinguished from the members of previously known genera of the family *Flavobacteriaceae*. On the basis of the data presented, strain SSK1-1^T is considered to represent a novel genus and species, for which the name *Jejudonia soesokkakensis* gen. nov., sp. nov. is proposed. The type strain is SSK1-1^T (=KCTC 32325^T = CCUG 63830^T). An emended description of the genus *Aureitalea* is also proposed.

Keywords *Jejudonia soesokkakensis* · Novel genus · Novel species · Ocean · Freshwater spring · *Aureitalea*

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Introduction

Soesokkak, that is located in Jeju island of South Korea and designated a Natural Environment Preservation Zone by UNESCO, is an interesting place where the ocean and a freshwater spring meet. During a screening of novel bacteria from this junction, many novel bacterial taxa have been isolated and characterized taxonomically. One of these isolates, designated SSK1-1^T, is described in this study. Comparative 16S rRNA gene sequence analysis indicated that the novel strain has its closest phylogenetic affiliation to the genus *Ulvibacter*, a member of the family *Flavobacteriaceae* of the phylum *Bacteroidetes* (Bernardet

2011). The genus *Ulvibacter* was created by Nedashkovskaya et al. (2004) and at the time of writing the genus comprises two species with validly published names, *Ulvibacter litoralis* (Nedashkovskaya et al. 2004) and *Ulvibacter antarcticus* (Choi et al. 2007). The aim of the present work was to determine the exact taxonomic position of strain SSK1-1^T by using a polyphasic characterisation that included the determinations of chemotaxonomic and other phenotypic properties and detailed phylogenetic analyses based on 16S rRNA gene sequences.

Materials and methods

Bacterial strains and culture conditions

Water was collected from the junction between the ocean and a freshwater spring at Jeju island, South Korea, and used as a source for the isolation of bacterial strains. Strain SSK1-1^T was isolated by the dilution plating technique on marine agar 2216 (MA; Becton–Dickinson) at 25 °C and cultivated routinely on MA at 30 °C. Strain SSK1-1^T was maintained on MA at 4 °C for short-term preservation and as a glycerol suspension (20 %, w/v, in distilled water) at −80 °C for long-term preservation. Strain SSK1-1^T has been deposited in the Korean Collection for Type Cultures (KCTC; South Korea) and the Culture Collection, University of Göteborg (CCUG; Sweden) as KCTC 32325^T and CCUG 63830^T, respectively. *U. litoralis* CCUG 47093^T, *U. antarcticus* IMCC3101^T and *Aureitalea marina* KCTC 23434^T were used as reference strains for fatty acid and polar lipid analyses. *U. litoralis* CCUG 47093^T and *A. marina* KCTC 23434^T were obtained from the CCUG and the KCTC, respectively. *U. antarcticus* IMCC3101^T was obtained from corresponding author (Prof. Jang-Cheon Cho) of laboratory that described it.

Cell biomass of strain SSK1-1^T for DNA extraction and for the analyses of isoprenoid quinones and polar lipids was obtained from cultures grown for 3 days at 30 °C in marine broth 2216 (MB; Becton–Dickinson). Cell biomass of *U. litoralis* CCUG 47093^T, *U. antarcticus* IMCC3101^T and *A. marina* KCTC 23434^T for polar lipid analysis was obtained from cultures grown for 3 days at 30 °C in MB. For fatty acid methyl ester analysis, cell mass of strain SSK1-1^T, *U. litoralis* CCUG 47093^T, *U. antarcticus* IMCC3101^T and *A. marina* KCTC 23434^T was harvested from MA after incubation at 25 °C for 5 days.

Morphological, physiological and biochemical characterization

Cell morphology was examined by using light microscopy (BX51; Olympus) and transmission electron microscopy (JEM1010; JEOL). The latter technique was also used to assess the presence of flagella on cells from an exponentially growing MA culture. For this purpose, the cells were negatively stained with 1 % (w/v) phosphotungstic acid and the grids were examined after being air-dried. Gliding motility was investigated according to the method described by Bowman (2000). The Gram reaction was determined by using the bioMérieux Gram stain kit according to the manufacturer's instructions. Growth under anaerobic conditions was determined after incubation for 10 days in an anaerobic jar (MGC) with AnaeroPack (MGC) on MA; the jar was kept overnight at 4 °C to establish anoxic conditions before incubation at 30 °C. Growth at 4, 10, 15, 20, 25, 28, 30 and 37 °C was measured on MA to determine the optimal temperature and temperature range for growth. Growth in the absence of NaCl and in the presence of 0.5, 1.0, 2.0 and 3.0 % (w/v) NaCl was investigated by using trypticase soy broth prepared according to the formula of the Becton–Dickinson medium except that NaCl was excluded and that 0.45 % (w/v) $MgCl_2{\cdot}6H_2O$ was added. Growth in the presence of 2.0–7.0 % (as final concentration, w/v, at increments of 1.0 %) NaCl was investigated in MB. The pH range for growth was determined in MB adjusted to pH 4.5–9.5 (using increments of 0.5 pH unit) by using sodium acetate/acetic acid and Na_2CO_3 buffers. The pH values were verified after autoclaving. The presence of flexirubin-type pigments was investigated as described previously (Reichenbach 1992; Bernardet et al. 2002). Catalase and oxidase activities were determined as described by Barrow and Feltham (1993). Hydrolysis of casein, hypoxanthine, starch, Tween 80, L-tyrosine and xanthine was tested on MA using the substrate concentrations described by Barrow and Feltham (1993). Hydrolysis of gelatin and urea was investigated by using Nutrient gelatin and Urea agar base media (BD), respectively, with the modification that artificial seawater was used for the preparation of media. Hydrolysis of aesculin and

nitrate reduction were investigated as described previously (Lányí 1987) with the modification that artificial seawater was used for preparation of media. The artificial seawater contained (l^{-1} distilled water) 23.6 g NaCl, 0.64 g KCl, 4.53 g $MgCl_2 \cdot 6H_2O$, 5.94 g $MgSO_4 \cdot 7H_2O$ and 1.3 g $CaCl_2 \cdot 2H_2O$ (Bruns et al. 2001). Utilization of various substrates for growth was tested according to Baumann and Baumann (1981), using medium supplemented with 1 % (v/v) vitamin solution (Staley 1968) and 2 % (v/v) Hutner's mineral salts (Cohen-Bazire et al. 1957). The carbon sources were added at a concentration of 0.2 % (w/v) after sterilization by filtration. Acid production from carbohydrates was determined as described by Leifson (1963). Susceptibility to antibiotics was tested on MA plates using antibiotic discs (Advantec) containing the following (μg per disc unless otherwise stated): ampicillin (10), carbenicillin (100), cephalothin (30), chloramphenicol (100), gentamicin (30), kanamycin (30), lincomycin (15), neomycin (30), novobiocin (5), oleandomycin (15), penicillin G (20 U), polymyxin B (100 U), streptomycin (50) and tetracycline (30). Enzyme activities were determined, after incubation for 8 h at 30 °C, by using the API ZYM system (bioMérieux).

16S rRNA gene sequencing and phylogenetic analysis

Chromosomal DNA was extracted 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 as described previously (Yoon et al. 1998) using two universal primers, 9F (5′-GAGTTTGATCCTGGCTCAG-3′) and 1512R (5′-ACGGTTACCTTGTTACGACTT-3′), and the PCR products were purified by using a QIAquick PCR purification kit (Qiagen). Sequencing of the amplified 16S rRNA gene was performed as described by Yoon et al. (2003). The identification of phylogenetic neighbours was achieved using the EzTaxon server (http://eztaxon-e.ezbiocloud.net/; Kim et al. 2012). Alignment of sequences was carried out with CLUSTAL W software (Thompson et al. 1994). Gaps at the 5′ and 3′ ends of the alignment were omitted from further analysis. Phylogenetic analysis was performed as described by Yoon et al. (2012).

Chemotaxonomic characterization

Isoprenoid quinones were extracted according to the method of Komagata and Suzuki (1987) and analyzed using reversed-phase HPLC and a YMC ODS-A (250 × 4.6 mm) column. The isoprenoid quinones were eluted by a mixture of methanol/isopropanol (2:1, v/v) using a flow rate of 1 ml min^{-1} at room temperature and detected by UV absorbance at 270 nm. Fatty acids were saponified, methylated and extracted using the standard protocol of the MIDI (Sherlock Microbial Identification System, version 6.1). The fatty acids were analysed by GC (Hewlett Packard 6890) and identified by using the TSBA6 database of the Microbial Identification System (Sasser 1990). Polar lipids were extracted according to the procedures described by Minnikin et al. (1984) and separated by two-dimensional TLC using chloroform/methanol/water (65:25:3.8, v/v/v) for the first dimension and chloroform/methanol/acetic acid/water (40:7.5:6:1.8, v/v/v/v) for the second dimension as described by Minnikin et al. (1977). Individual polar lipids were identified by spraying with the ethanolic molybdophosphoric acid, molybdenum blue, ninhydrin and α-naphthol reagents (Minnikin et al. 1984; Komagata and Suzuki 1987) and with Dragendorff's reagent (Sigma).

The DNA G + C content was determined by the method of Tamaoka and Komagata (1984) with the modification that DNA was hydrolysed and the resultant nucleotides were analysed by reversed-phase HPLC equipped with a YMC ODS-A (250 × 4.6 mm) column. The nucleotides were eluted by a mixture of 0.55 M $NH_4H_2PO_4$ (pH 4.0) and acetonitrile (40:1, v/v), using flow rate of 1 ml min^{-1} at room temperature and detected by UV absorbance at 270 nm. *Escherichia coli* DNA was used as a standard.

Results and discussion

Morphological, cultural, physiological and biochemical characteristics

Strain SSK1-1^T was found to be an aerobic, non-motile, Gram-negative, non-spore-forming bacterium. Cells of strain SSK1-1^T were observed to be rod-shaped; filamentous cells longer than 10 μm also occurred. Strain SSK1-1^T was observed to grow

optimally at 30 °C and pH 7.0-7.5 and was determined to be a moderate halophile as it grew optimally in the presence of 2 % (w/v) NaCl; the strain grew in the presence of 1.0–5.0 % NaCl. Mg^{2+} ions were required for growth. Strain SSK1-1^T was found to show catalase and oxidase activities and to be unable to reduce nitrate to nitrite. Strain SSK1-1^T was found to be susceptible to carbenicillin, chloramphenicol, gentamicin, lincomycin and novobiocin, but resistant to ampicillin, cephalothin, kanamycin, neomycin, oleandomycin, penicillin G, polymyxin B, streptomycin and tetracycline.

Morphological, cultural, physiological and biochemical characteristics of strain SSK1-1^T are given in the genus and species descriptions (see below) and in Table 1.

Table 1 Differential phenotypic characteristics of SSK1-1^T and two phylogenetically related genera of the family *Flavobacteriaceae*

Characteristic	1	2	3
Cell length (μm)	0.7–>10.0	0.5–7.3	0.5–6
Gliding motility	–	v	–
Production of flexirubin-type pigments	–	+	–
NaCl concentration of growth (%,w/v)	1.0–5.0	1.0–6.0	1.0–4.0
Optimal growth temperature (°C)	30	21–25	20–25
Growth at:			
4 °C	–	+	–
30 °C	+	v	+
Catalase	+	+	–
Nitrate reduction	–	v	+
Hydrolysis of:			
Casein	+	–	ND
Gelatin	–	+	+
Starch	–	v	+
Acid production from glucose	–	–	+
DNA G + C content (mol%)	39.9	36.7–38.0	48.1

Taxa: *1* SSK1-1^T, *2 Ulvibacter* data taken from Nedashkovskaya et al. (2004) and Choi et al. (2007), *3 Aureitalea* data taken from Park et al. (2012)

+ positive reaction, – negative reaction, *v* variable reaction, *ND* not described

Phylogenetic analysis

The almost complete 16S rRNA gene sequence of strain SSK1-1^T determined in this study (GenBank/EMBL/DDBJ accession number KC792554) comprised 1,445 nucleotides, representing approximately 95 % of the *E. coli* 16S rRNA sequence. Comparative 16S rRNA gene sequence analysis showed that strain SSK1-1^T was most closely affiliated to members of the family *Flavobacteriaceae* of the phylum *Bacteroidetes* (Fig. 1). In the neighbour-joining phylogenetic tree based on 16S rRNA gene sequences, strain SSK1-1^T clustered with the type strains of the two *Ulvibacter* species and *A. marina* (Fig. 1). In the phylogenetic trees constructed using the maximum-likelihood and maximum-parsimony algorithms, strain SSK1-1^T was found to be closely related to the type strains of the two *Ulvibacter* species, *A. marina*, *Marixanthomonas ophiurae* and *Gilvibacter sediminis* (Supplementary Figs 1 and 2). Strain SSK1-1^T exhibited the highest 16S rRNA gene sequence similarity value to the type strain of *U. antarcticus* (95.3 %). It exhibited sequence similarity values of 93.5, 93.1, 92.4 and 92.3 % to the type strains of *U. litoralis*, *A. marina*, *M. ophiurae* and *G. sediminis*, respectively and of less than 93.3 % to those of other species used in the phylogenetic analysis.

Chemotaxonomic characteristics

The predominant isoprenoid quinone detected in strain SSK1-1^T was determined to be menaquinone-6 (MK-6) in line with all members of the family *Flavobacteriaceae* (Bernardet 2011). The cellular fatty acid profile of strain SSK1-1^T consisted of large amounts of branched, hydroxy, straight-chain and unsaturated fatty acids (Table 2). The major fatty acids (>10 % of the total fatty acids) identified in strain SSK1-1^T were iso-$C_{15:0}$ (18.1 %), anteiso-$C_{15:0}$ (11.7 %) and iso-$C_{16:0}$ (11.1 %) (Table 2). The fatty acid profile of strain SSK1-1^T was distinguished from those of the type strains of the two *Ulvibacter* species by differences in the proportions of some fatty acids, particularly iso-$C_{17:0}$ 3-OH and anteiso-$C_{15:0}$ (Table 2). It was clearly distinguished from that of the type strain of *A. marina* by differences in the proportions of iso-$C_{17:0}$ 3-OH, anteiso-$C_{15:0}$ and iso-$C_{15:1}$ G (Table 2). The major polar lipids detected in strain SSK1-1^T were phosphatidylethanolamine (PE) and one unidentified

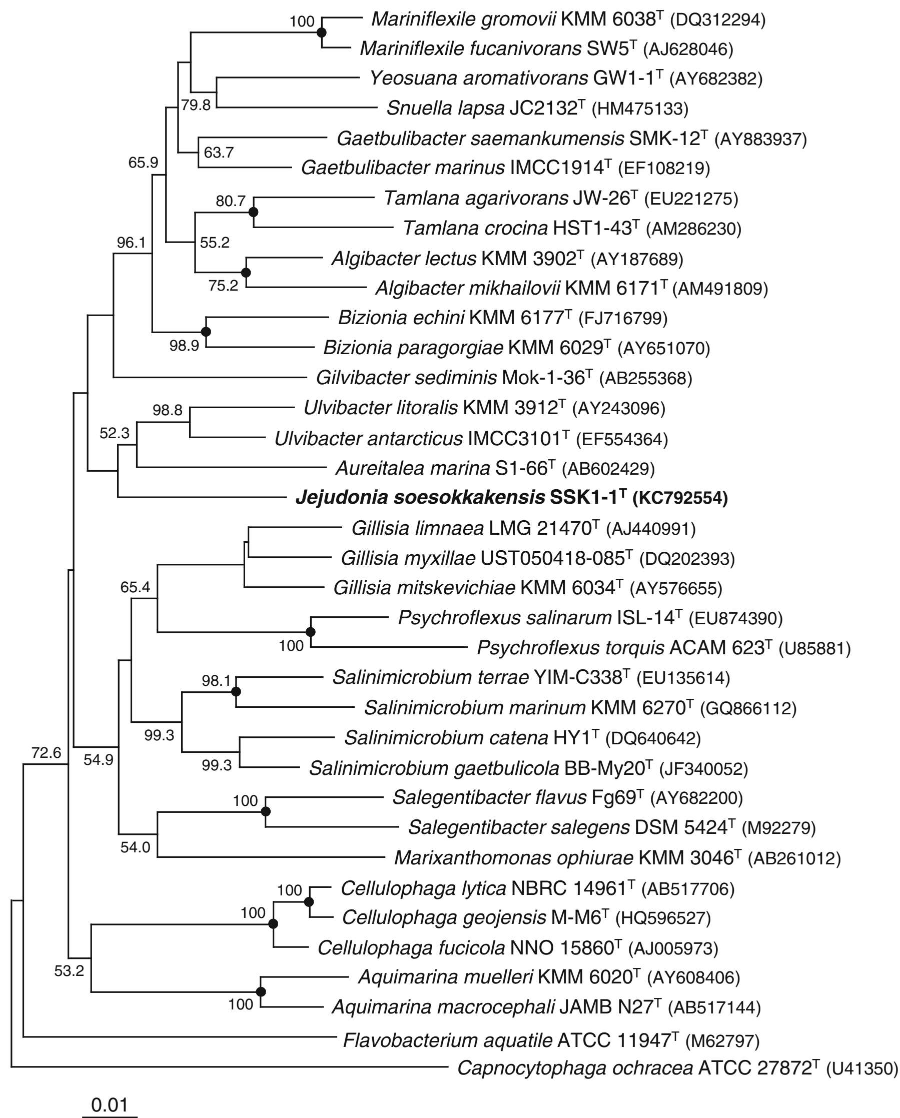

Fig. 1 Neighbour-joining phylogenetic tree based on 16S rRNA gene sequences showing the positions of *Jejudonia soesokkakensis* SSK1-1^T and representatives of other related taxa in the family *Flavobacteriaceae*. Bootstrap values (expressed as percentages of 1,000 replications) of >50 % are shown at branching points. Filled circles indicate that the corresponding nodes were also recovered in the trees generated with the maximum-likelihood and maximum parsimony algorithms. *Capnocytophaga ochracea* ATCC 27872^T (GenBank accession number, U41350) was used as an outgroup. Scale bar, 0.01 substitutions per nucleotide position

lipid; minor amounts of one other unidentified lipid and one unidentified aminolipid were also present (Fig. 2). The polar lipid profile of strain SSK1-1^T was distinguished from those of the type strains of *U. litoralis* and *U. antarcticus* in that one additional unidentified lipid (L3), which is a major component in the type strains of the two *Ulvibacter* species, is absent (Fig. 2). It was also distinguished from those of the type strains of *U. litoralis* and *A. marina* in that a major or significant amount of one unidentified glycolipid is absent (Fig. 2). However, there is discrepancy in the polar lipid profiles of the type strain of *A. marina* between this study and the study of Park et al. (2012). It was reported by Park et al. (2012) that PE is absent and that phosphatidylglycerol and diphosphatidylglycerol, which were not detected in this study, are

present as major components. It appears that the polar lipid profile of the type strain of *A. marina* has been misinterpreted by Park et al. (2012). These data therefore suggest that the description of the genus *Aureitalea* Park et al. (2012) should be emended.

The G + C content of strain SSK1-1^T was 39.9 mol%, a value similar with that reported for members of the genus *Ulvibacter* but lower than that of the genus *Aureitalea* (Table 1).

Conclusion

From the results of the phylogenetic analyses, it is likely not to be appropriate to assign strain SSK1-1^T to any recognized genera of the family *Flavobacteriaceae*. Strain SSK1-1^T was chemotaxonomically compared with the two phylogenetically most closely related genera, *Ulvibacter* and *Aureitalea.* The predominant menaquinone type (MK-6) found in strain SSK1-1^T is the same as that found in all members of the family *Flavobacteriaceae* (Bernardet 2011) as well as the genera *Ulvibacter* and *Aureitalea* (Nedashkovskaya et al. 2004; Park et al. 2012). The fatty acid profile of strain SSK1-1^T showed differences in the nature and proportion of the major fatty acids compared to the genera *Ulvibacter* and *Aureitalea* (Table 2). Strain SSK1-1^T was also distinguishable from members of the genera *Ulvibacter* and *Aureitalea* in differences in their polar lipid profiles (Fig. 2). The differences in several phenotypic properties served to differentiate strain SSK1-1^T from the two phylogenetically most closely related genera (Table 1). Accordingly, the phylogenetic distinctiveness and chemotaxonomic and phenotypic data suggest that strain SSK1-1^T should be classified in a novel genus within the family *Flavobacteriaceae*. On the basis of the data presented, we propose a novel genus and novel species, *Jejudonia soesokkakensis* gen. nov., sp. nov., for strain SSK1-1^T.

Description of *Jejudonia* gen. nov.

Jejudonia (Je.ju.do'ni.a. N.L. fem. n. *Jejudonia* named after Jejudo, the largest island located in South Korea, from where the organism was isolated).

Cells are aerobic, Gram-negative, non-flagellated, non-gliding and rod-shaped. Catalase- and oxidase-positive. Nitrate reduction is negative. The predominant menaquinone is MK-6. The major fatty acids (>10 % of the total fatty acids) are iso-$C_{15:0}$, anteiso-$C_{15:0}$ and iso-$C_{16:0}$. The major polar lipids are

Table 2 Cellular fatty acid compositions (%) of strain SSK1-1^T and the type strains of two *Ulvibacter* species and *Aureitalea marina*

Fatty acid	1	2	3	4
Straight-chain				
$C_{12:0}$	–	1.8	–	–
$C_{14:0}$	–	1.7	–	–
$C_{16:0}$	4.0	1.4	1.5	0.9
$C_{18:0}$	3.0	–	–	–
Unsaturated				
$C_{17:1}$ $\omega 6c$	1.1	–	2.9	tr
$C_{18:1}$ $\omega 7c$	4.0	–	–	–
$C_{18:1}$ $\omega 9c$	1.3	–	–	–
Branched				
iso-$C_{12:0}$	1.1	–	–	–
iso-$C_{13:0}$	1.9	–	–	tr
anteiso-$C_{13:0}$	0.8	–	–	tr
iso-$C_{14:0}$	2.6	–	0.6	tr
anteiso-$C_{14:0}$	–	1.8	–	–
iso-$C_{15:1}$ G[a]	4.1	11.7	6.5	17.8
iso-$C_{15:0}$	18.1	20.7	14.8	18.3
anteiso-$C_{15:1}$ A[a]	tr	1.1	1.3	1.7
anteiso-$C_{15:0}$	11.7	3.0	2.8	3.2
iso-$C_{16:1}$ G[a]	1.3	1.9	5.2	2.9
iso-$C_{16:0}$	11.1	2.9	10.3	5.4
anteiso-$C_{17:1}$ A[a]	–	–	1.5	–
iso-$C_{17:1}$ $\omega 9c$	–	3.6	3.5	–
Hydroxy				
$C_{13:0}$ 2-OH	–	1.0	–	–
$C_{15:0}$ 2-OH	1.1	–	1.5	0.8
$C_{17:0}$ 2-OH	9.4	5.5	8.8	2.0
iso-$C_{13:0}$ 3-OH	1.3	–	1.2	–
iso-$C_{15:0}$ 3-OH	1.1	3.4	2.1	5.0
iso-$C_{16:0}$ 3-OH	9.3	3.4	6.4	4.6
iso-$C_{17:0}$ 3-OH	6.7	30.2	23.1	28.6
Summed feature 3[b]	4.7	4.9	5.9	6.4

Strains: 1 SSK1-1^T, 2 *U. litoralis* CCUG 47093^T, 3 *U. antarcticus* IMCC3101^T, 4 *A. marina* KCTC 23434^T. All data obtained from this study. Fatty acids that represented <0.5 % in all strains were omitted. tr, traces (<0.5 %)

– not detected

[a] Double bond position indicated by a capital letter is unknown

[b] Summed feature 3 contained $C_{16:1}$ $\omega 7c$ and/or $C_{16:1}$ $\omega 6c$

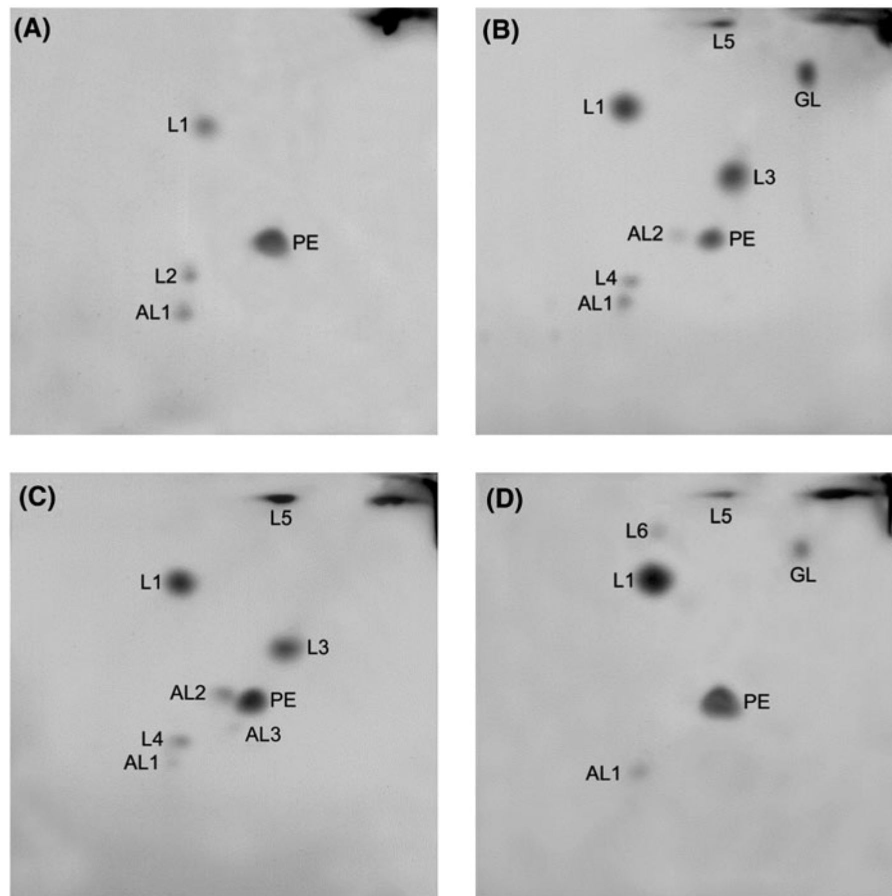

Fig. 2 Thin layer chromatograms of the total polar lipids of strain SSK1-1^T (**A**), *U. litoralis* CCUG 47093^T (**B**), *U. antarcticus* IMCC3101^T (**C**) and *A. marina* KCTC 23434^T (**D**). *Spots* were revealed by spraying the plates with the 10 % ethanolic molybdophosphoric acid. Abbreviations: *PE* phosphatidylethanolamine, *L1–L6* unidentified lipids, *AL1–AL3* unidentified aminolipids, *GL* unidentified glycolipid

phosphatidylethanolamine and one unidentified lipid. The DNA G + C content of the type strain of the type species is 39.9 mol %. The type species is *Jejudonia soesokkakensis*. A member of the family *Flavobacteriaceae*, phylum *Bacteroidetes*, according to 16S rRNA gene sequence analysis.

Description of *Jejudonia soesokkakensis* sp. nov.

Jejudonia soesokkakensis (so.e.so.kkak.en'sis. N.L. fem. adj. *soesokkakensis* pertaining to Soesokkak, from where the type strain was isolated).

Cells are Gram-negative, non-flagellated, non-gliding and rod-shaped, approximately 0.2–0.5 µm in diameter and 0.7–>10.0 µm in length; a few cells longer than 10.0 µm occur. Colonies on MA are circular, convex, smooth, glistening, deep-yellow in colour and 1.0–2.0 mm in diameter after incubation for 5 days at 30 °C. Growth does not occur under anaerobic conditions on MA. Optimal growth temperature is 30 °C; growth occurs at 10 °C, but not at 4 and 37 °C. Optimal pH for growth is between 7.0 and 7.5. Optimal growth occurs in the presence of 2.0 % (w/v) NaCl; growth occurs in the presence of 1.0–5.0 % (w/v) NaCl. Mg^{2+} ions are required for growth. Aesculin, casein and L-tyrosine are hydrolysed but gelatin, hypoxanthine, starch, Tween 80, urea and xanthine are not. D-Galactose, D-glucose, maltose, acetate (weak) and L-malate are utilized as carbon and energy sources but L-arabinose, D-cellobiose, D-fructose, D-mannose, sucrose, D-trehalose, D-xylose, benzoate, citrate, formate, pyruvate, succinate, salicin and L-glutamate are not. Acid is not produced from L-arabinose, D-cellobiose, D-fructose, D-galactose,

D-glucose, lactose, maltose, D-mannose, D-melezitose, melibiose, D-raffinose, L-rhamnose, D-ribose, sucrose, D-xylose, D-trehalose, *myo*-inositol, D-mannitol and D-sorbitol. In assays with the API ZYM system, alkaline phosphatase, esterase lipase (C 8), leucine arylamidase and valine arylamidase activities are present but esterase (C 4), lipase (C 14), cystine arylamidase, trypsin, α-chymotrypsin, acid phosphatase, naphthol-AS-BI-phosphohydrolase, α-galactosidase, *β*-galactosidase, *β*-glucuronidase, α-glucosidase, *β*-glucosidase, *N*-acetyl-*β*-glucosaminidase, α-mannosidase and α-fucosidase activities are absent. The predominant menaquinone is MK-6. The major fatty acids (>10 % of the total fatty acids) are iso-$C_{15:0}$, anteiso-$C_{15:0}$ and iso-$C_{16:0}$. The major polar lipids are phosphatidylethanolamine and one unidentified lipid. The DNA G + C content of the type strain is 39.9 mol%.

The type strain, SSK1-1^T (=KCTC 32325^T = CCUG 63830^T), was isolated from the junction between the ocean and a freshwater spring at Jeju island of South Korea. The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain SSK1-1^T is KC792554.

Emended description of the genus *Aureitalea* Park et al. 2012

The description of the genus *Aureitalea* is as given by Park et al. (2012) with the following amendment. The major polar lipids are phosphatidylethanolamine and one unidentified lipid.

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