Proposal of *Algoriphagus vanfongensis* sp. nov., transfer of members of the genera *Hongiella* Yi and Chun 2004 emend. Nedashkovskaya *et al.* 2004 and *Chimaereicella* Tiago *et al.* 2006 to the genus *Algoriphagus*, and emended description of the genus *Algoriphagus* Bowman *et al.* 2003 emend. Nedashkovskaya *et al.* 2004

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A taxonomic study of a novel marine, heterotrophic, non-gliding, halotolerant and light-pink-pigmented bacterium was carried out using a polyphasic approach. 16S rRNA gene sequence analysis revealed that strain KMM 6241^T is a member of the phylum *Bacteroidetes*. Strain KMM 6241^T formed a cluster with the genera *Algoriphagus*, *Chimaereicella* and *Hongiella* with sequence similarities of 94.0–98.2%. *Hongiella ornithinivorans* was the closest relative of the novel isolate. Comparative analysis of phenotypic, chemotaxonomic and genotypic characteristics of strain KMM 6241^T and representatives of the genera *Algoriphagus*, *Chimaereicella* and *Hongiella* revealed many similar features. Consequently, phylogenetic evidence supported by phenotypic and genotypic similarities support the transfer of members of the genera *Chimaereicella* and *Hongiella* to the genus *Algoriphagus* and the establishment of a novel species, *Algoriphagus vanfongensis* sp. nov., with strain KMM 6241^T (=DSM 17529^T=KCTC 12716^T) as the type strain.

The genus *Algoriphagus* accommodates heterotrophic, strictly aerobic, Gram-negative, non-motile, rod-shaped and pink-pigmented bacteria. Originally, the strains of the single species of the genus, *Algoriphagus ratkovskyi*, were isolated from sea ice and from saline lake cyanobacterial mats collected in Antarctica (Bowman *et al.*, 2003). Therefore, members of the genus were described as cold-adapted micro-organisms. Later, mesophilic *Algoriphagus* spp. were found and the description of the genus *Algoriphagus* was emended (Nedashkovskaya *et al.*, 2004). Currently the genus *Algoriphagus* contains nine species, the majority being isolated from marine environments or meromictic saline lakes. Only *Algoriphagus terrigena* was

recovered from a soil sample, from Dokdo (Yoon *et al.*, 2006). The members of the genus *Algoriphagus* form a phylogenetic cluster with the genera *Chimaereicella* and *Hongiella*. Three *Hongiella* species, *H. halophila*, *H. mannitolivorans* and *H. ornithinivorans*, were isolated from marine sediments of the East Sea (near the Korean Peninsula), and *H. marincola* was a seawater dweller (Yi & Chun, 2004; Yoon *et al.*, 2004). Later, the species *H. halophila* was reclassified in the genus *Algoriphagus* on the basis of phylogenetic, phenotypic, chemotaxonomic and genotypic similarities, and the description of the genus *Hongiella* was emended (Nedashkovskaya *et al.*, 2004). The genus *Chimaereicella* was proposed recently for strictly aerobic and mesophilic bacteria isolated from non-saline, highly alkaline groundwater in Southern Portugal (Tiago *et al.*, 2006). From the results of phylogenetic analysis

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of *Algoriphagus vanfongensis* KMM 6241^T is EF392675.

based on the sequence of the 16S rRNA gene, *Chimaericella alkaliphila* AC-74^T was equidistant from members of the genera *Algoriphagus* and *Hongiella*, showing 94.9–97.0 % similarity. The authors argued the creation of a new genus and species based on fatty acid composition and on the unique isolation source. Recently, another *Chimaericella* species, *C. boritolerans*, which was isolated from a soil sample, was described (Ahmed *et al.*, 2007). The 16S rRNA gene sequence similarity between *C. boritolerans* and its closest relative *C. alkaliphila* was 97.6 %. Sequence similarities between *C. boritolerans* and representative members of the genera *Algoriphagus* and *Hongiella* were 94.7–96.0 and 95.1–96.7 %, respectively.

During a study of the bacterial diversity of coral *Palithoa* sp., an unknown heterotrophic, strictly aerobic, pale-pink and rod-shaped bacterium was isolated. Phylogenetic analysis showed that strain KMM 6241^T was related to the genus *Hongiella* of the phylum *Bacteroidetes*. The high 16S rRNA gene sequence similarities between the novel isolate and members of the genera *Algoriphagus*, *Hongiella* and *Chimaericella*, together with similar phenotypic, chemotaxonomic and genotypic characteristics, support reclassification of members of the genera *Chimaericella* and *Hongiella* in the genus *Algoriphagus* and establishment of a novel species within the genus *Algoriphagus*, for which the name *Algoriphagus vanfongensis* sp. nov. is proposed.

Strain KMM 6241^T was isolated by direct plating on medium containing (l⁻¹): Bacto peptone (Difco), 5.0 g; sucrose, 5.0 g; glucose, 1.0 g; yeast extract (Difco), 2.5 g; KH₂PO₄, 0.1 g; MgSO₄, 0.1 g; and Bacto agar (Difco), 15.0 g; in 30 % (v/v) natural seawater and 70 % (v/v) distilled water, from 0.1 ml tissue homogenates collected from Vanfong Bay, South China Sea, Vietnam, in January 2005. After primary isolation and purification on marine agar 2216 (Difco), the strains were cultivated on the same medium at 25 °C for 48 h and stored at –80 °C in marine broth (Difco) supplemented with 20 % (v/v) glycerol.

Genomic DNA extraction, PCR and sequencing of the 16S rRNA gene followed the procedures given by Kim *et al.* (1998). To establish the precise taxonomic position of strain KMM 6241^T, an almost-complete sequence of its 16S rRNA gene (1375 nucleotides) was determined, 1308 nucleotides of which were used for comparative phylogenetic analysis. Sequence data obtained were aligned with those of representative members of the family *Flexibacteraceae*, class *Sphingobacteria*, phylum *Bacteroidetes* using PHYDIT version 3.2 (<http://plaza.snu.ac.kr/~jchun/phydit/>). Phylogenetic trees were inferred using suitable programs of the PHYLIP package (Felsenstein, 1993). Phylogenetic distances were calculated using the Jukes–Cantor model (Jukes & Cantor, 1969) and trees were constructed on the basis of the neighbour-joining (Saitou & Nei, 1987) algorithm. The tree topology was also evaluated using maximum-likelihood (Felsenstein, 1993) and maximum-parsimony (Kluge & Farris, 1969) methods. Bootstrap analysis was performed with 1000 resampled datasets

using the programs SEQBOOT and CONSENSE of the PHYLIP package.

Phylogenetic analysis based on almost-complete 16S rRNA gene sequences revealed that strain KMM 6241^T occupied a distinct lineage within the genus *Hongiella* and possessed a sequence similarity of 98.2 % with its nearest neighbour, *H. ornithinivorans* (Fig. 1).

DNA was isolated according to the method of Marmur (1961) and the G+C content was determined using the thermal denaturation method (Marmur & Doty, 1962). The G+C content of the DNA of strain KMM 6241^T was 43.8 mol%. DNA–DNA hybridization experiments were performed using HPLC, as described by Grimont *et al.* (1980). The DNA–DNA relatedness between strain KMM 6241^T and *H. ornithinivorans* was 32 %. Consequently, strain KMM 6241^T represents a novel species within the genus *Hongiella* (Wayne *et al.*, 1987).

Analysis of fatty acid methyl esters was carried out according to the standard protocol of the Sherlock Microbial Identification System (Microbial ID). The predominant cellular fatty acids of strain KMM 6241^T were iso-C_{15:0}, iso-C_{15:1} G, iso-C_{17:1} ω9c, iso-C_{15:0} 3-OH, iso-C_{17:0} 3-OH, summed feature 3 comprising C_{16:1} ω7c and/or iso-C_{15:0} 2-OH, and summed feature 4 comprising iso-C_{17:1} I and/or anteiso-C_{17:1} B. Strains of the genus *Hongiella* were found to possess a similar fatty acid composition (Nedashkovskaya *et al.*, 2004).

Physiological and biochemical properties of strain KMM 6241^T were examined as described by Nedashkovskaya *et al.* (2004, 2006) and by using the API 20NE gallery (bio-Mérieux), according to the manufacturer's instructions.

Strain KMM 6241^T, similar to *Hongiella* species, grew under aerobic conditions, produced cytochrome oxidase, catalase, alkaline phosphatase and β-galactosidase, utilized carbohydrates and hydrolysed aesculin (Table 1). However, several differences were found to be useful for distinguishing strain KMM 6241^T from recognized species of the genus *Hongiella*. Moreover, the novel isolate could be clearly distinguished from *Hongiella* species by its inability to decompose starch and DNA. Therefore, data from the phylogenetic analysis taken together with similarities in fatty acid composition and phenotypic features support the inclusion of strain KMM 6241^T in the genus *Hongiella*. The significant molecular distinctiveness and phenotypic differences allow the creation of a novel species within the genus *Hongiella* to accommodate strain KMM 6241^T.

Taxonomic analysis using a polyphasic approach revealed the very close phylogenetic positions of the recently described species *C. alkaliphila* and *C. boritolerans* (Tiago *et al.*, 2006; Ahmed *et al.*, 2007) to representatives of the genus *Algoriphagus*, with similarities of 95.1–97.0 %. *C. alkaliphila* AC-74^T was isolated from a non-saline, highly alkaline groundwater sample and *C. boritolerans* T-22^T was recovered from a soil sample, in contrast to the majority of *Algoriphagus* species. However, an isolate of non-marine

Fig. 1. Rooted neighbour-joining tree based on nearly complete 16S rRNA gene sequences (1308 unambiguously aligned bases) showing the relationships between strain KMM 6241^T and closely related members of the family *Flexibacteraceae*. Bootstrap values of 1000 resampled datasets are shown. Circles at nodes indicate nodes recovered with >70% (closed circles) or >50% (open circles) bootstrap values in a maximum-likelihood-parsimony tree. Bar, 0.03 nucleotide substitutions per nucleotide position.

origin, *A. terrigena* KCTC 12545^T, was described recently (Yoon *et al.*, 2006). The cellular fatty acid compositions of members of the above-mentioned genera are in accordance with each other (Table 2). These facts, taken together with the similar phenotypic features, including the presence of oxidase activity and aesculin hydrolysis and the absence of gliding motility and glucose fermentation, indicate that members of the genus *Chimaereicella* should be reclassified as belonging to the genus *Algoriphagus*. Comparative examination of the phenotypic and chemotaxonomic characteristics of *C. alkaliphila* AC-74^T and *C. boritolerans* T-22^T with those of members of the genus *Hongiella* also indicate that many similar features are present (Tables 1 and 2). Phylogenetically, members of the genera *Chimaereicella* and *Hongiella* demonstrate a very close relatedness, showing 16S rRNA gene similarities of 94.7–96.0%. In addition, species of the genus *Hongiella* possess close relatedness with recognized *Algoriphagus* species with sequence similarities ranging from 93.7 to 96.5%. Therefore, based on phylogenetic evidence and similar chemotaxonomic and phenotypic data, it is proposed that members of the genera *Algoriphagus*, *Chimaereicella* and *Hongiella* should be combined in a single genus, *Algoriphagus*. We also propose that strain KMM 6241^T

represents a novel species, *Algoriphagus vanfongensis* sp. nov.

Description of *Algoriphagus vanfongensis* sp. nov.

Algoriphagus vanfongensis (van.fong.en'sis. N.L. masc. adj. *vanfongensis* pertaining to Vanfong Bay, from which the type strain was isolated).

Main characteristics are the same as those given in the genus description. In addition, cells are 0.4–0.5 × 1.0–2.5 µm. Gliding motility is not observed. On marine agar, colonies are circular, 2–3 mm in diameter, convex, shiny, smooth and light-pink-coloured. β-Galactosidase-positive. Does not require Na⁺ ions or seawater for growth, but Na⁺ ions are sufficient for growth. Grows in 0–8% NaCl. Optimal growth occurs in 1–4% NaCl. Growth occurs at 12–35 °C. Flexirubin-type pigments are not formed. Degrades gelatin and aesculin, but not agar, casein, starch, Tweens 20, 40 or 80, urea, cellulose (CM-cellulose and filter paper) or chitin. Produces acid from D-cellobiose, D-glucose, DL-xylose, maltose, L-rhamnose and N-acetylglucosamine, but not from L-arabinose, D-fructose, D-galactose, D-lactose, D-melibiose, D-raffinose, L-sorbose,

Table 1. Phenotypic characteristics of *Algoriphagus* species

Taxa: 1, strain KMM 6241^T (*Algoriphagus vanfongensis* sp. nov.); 2, *Algoriphagus alkaliphilus*; 3, *Algoriphagus antarcticus*; 4, *Algoriphagus aquimarinus*; 5, *Algoriphagus boritolerans*; 6, *Algoriphagus chordae*; 7, *Algoriphagus halophilus*; 8, *Algoriphagus localis*; 9, *Algoriphagus mannitolivorans*; 10, *Algoriphagus marincola*; 11, *Algoriphagus ornithinivorans*; 12, *Algoriphagus ratkowskyi*; 13, *Algoriphagus terrigena*; 14, *Algoriphagus winogradskyi*; 15, *Algoriphagus yeomjeoni*. All are positive for the following tests: aerobic metabolism, oxidase, catalase, β -galactosidase and alkaline phosphatase activities, and aesculin hydrolysis. All are negative for following tests: fermentation of glucose, gliding motility, tryptophan deaminase, arginine dihydrolase and urease activities, acid formation from mannitol and *myo*-inositol, and production of flexirubin-type pigments, H₂S, indole and acetoin. Data from Ahmed *et al.* (2007), Bowman *et al.* (2003), Nedashkovskaya *et al.* (2004), Tiago *et al.* (2006), Van Trappen *et al.* (2004), Yi & Chun (2004), Yoon *et al.* (2005a, b, 2006) and this study. v, Variable; ND, not determined. Results in parentheses are for the type strain.

Characteristic	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
Nitrate reduction	–	+	–	–	–	–	–	–	+	v	–	v	+	+	–
NaCl requirement for growth	–	–	–	–	–	+	–	+	–	+	–	v	+	–	+
Salinity range for growth (%)	0–8	0–3	0–5	0–10	0–3	1–10	0–8	1–9	0–7	1–9	0–10	0–6	1–7	0–6	1–9
Temperature range (°C)	12–35	11–39	5–25	4–34	17–37	4–32	10–41	4–35	10–42	10–45	10–40	–2–25	10–36	4–39	4–35
Hydrolysis of:															
Agar	–	–	–	+	–	+	–	–	–	–	–	v	–	+	–
Casein	–	–	–	+	ND	–	–	–	–	+	–	+	+	–	+
Gelatin	+	+	–	+	–	–	+	–	+	–	+	v	–	+	v
Starch	–	+	–	–	+	–	+	–	+	+	+	v	–	+	–
DNA	–	+	–	+	ND	–	–	ND	+	+	+	v	ND	–	–
Tween 20	–	ND	ND	+	ND	+	+	+	–	+	–	+	+	+	+
Tween 40	–	ND	ND	+	ND	+	+	+	–	+	+	+	+	+	+
Tween 80	–	ND	ND	+	ND	–	+	+	–	+	+	–	+	–	+
Acid production from:															
L-Arabinose	–	+	–	–	–	–	–	+	–	+	–	+	+	–	–
D-Cellobiose	+	+	–	+	+	+	–	+	+	+	–	+	+	+	+
D-Fructose	–	+	–	ND	–	ND	ND	+	–	v	–	+	+	ND	+
D-Galactose	–	+	–	–	+	+	–	+	–	+	–	+	+	+	+
D-Glucose	+	+	–	+	+	+	+	+	–	+	+	+	+	+	+
D-Lactose	–	+	–	+	+	+	–	+	–	+	–	–	+	+	+
Maltose	+	+	–	–	+	+	+	+	–	+	–	+	+	+	+
D-Mannose	+	+	–	+	+	+	ND	+	–	+	–	+	+	+	v (–)
D-Melibiose	–	+	–	+	–	+	–	+	–	+	–	+	+	+	+
D-Raffinose	–	–	–	–	+	+	–	+	–	+	–	+	+	+	v (+)
L-Rhamnose	+	–	–	+	+	+	–	+	–	–	–	+	–	+	+
Sucrose	–	+	–	+	–	+	+	+	+	+	–	–	+	+	+
Trehalose	–	+	–	ND	–	ND	ND	v	ND	+	–	+	+	ND	+
DL-Xylose	+	–	–	+	–	+	+	+	–	+	–	+	+	+	+
N-Acetylglucosamine	+	–	–	+	+	–	+	ND	–	–	–	+	ND	+	–
Utilization of:															
L-Arabinose	+	+	–	+	–	+	+	+	+	+	–	+	+	+	–
D-Galactose	ND	+	ND	ND	+	+	+	+	–	+	–	+	+	+	+
D-Glucose	+	+	–	+	+	+	+	+	+	+	+	+	+	+	+
D-Lactose	+	+	ND	+	+	+	+	+	+	+	+	+	+	+	+
Maltose	+	+	–	+	+	+	+	+	+	+	+	+	+	+	+
D-Mannose	+	+	–	+	+	+	+	+	+	+	+	+	+	+	+
D-Xylose	+	–	ND	+	–	+	+	+	+	+	+	+	+	+	+
D-Mannitol	–	–	–	+	+	–	–	–	+	–	–	+	–	–	–
Sorbitol	–	+	ND	–	–	–	–	ND	–	–	–	+	ND	–	ND
myo-Inositol	–	–	ND	–	–	–	–	–	–	–	–	+	–	–	–
Glycerol	–	–	ND	–	ND	–	–	–	–	–	–	–	ND	–	–
N-Acetylglucosamine	+	–	–	+	–	+	+	ND	+	–	+	+	ND	+	–
Susceptibility to:															
Ampicillin	–	ND	ND	–	ND	–	–	–	+	+	+	–	–	–	–
Benzylpenicillin	–	ND	ND	–	+	–	–	–	+	+	+	–	–	–	–
Carbenicillin	+	ND	ND	+	ND	–	+	–	+	–	+	+	–	v	+

Table 1. cont.

Characteristic	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
Gentamicin	+	ND	ND	—	+	—	—	—	—	—	—	—	—	—	—
Kanamycin	—	+	ND	—	—	—	—	—	—	—	+	—	—	—	—
Lincomycin	+	ND	ND	+	ND	+	+	+	+	—	+	+	—	v	+
Oleandomycin	+	ND	ND	+	ND	—	+	+	+	+	+	+	—	+	+
Neomycin	+	ND	ND	—	ND	—	—	—	—	—	—	—	—	—	—
Polymyxin B	+	ND	ND	—	ND	—	—	—	—	+	+	—	—	—	—
Streptomycin	+	ND	ND	—	+	—	—	—	+	+	—	—	—	—	—
Tetracycline	+	ND	ND	+	+	—	+	—	+	+	+	+	—	v	—
DNA G + C content (mol%)	43.8	43.5	39–41	41	42.5	37–40	37	42	42	43	38	35	49	39–42	41

sucrose, trehalose, glycerol, adonitol, dulcitol, *myo*-inositol or mannitol. Utilizes L-arabinose, D-lactose, D-mannose and sucrose. Does not utilize *myo*-inositol, mannitol,

sorbitol, gluconate, caprate, adipate, malate, citrate or phenylacetate. D-Glucose is not fermented. Nitrate is not reduced to nitrite. Indole and hydrogen sulfide are

Table 2. Fatty acid composition (%) of *Algoriphagus* species

Strains: 1, strain KMM 6241^T (*Algoriphagus vanfongensis* sp. nov.); 2, *Algoriphagus alkaliphilus* AC-74^T; 3, *Algoriphagus aquimarinus* KMM 3958^T; 4, *Algoriphagus boritolterans* T-22^T; 5, *Algoriphagus chordae* KMM 3957^T; 6, *Algoriphagus halophilus* KCTC 12051^T; 7, *Algoriphagus locisalis* KCTC 12310^T; 8, *Algoriphagus mannitolivorans* KCTC 12050^T; 9, *Algoriphagus ornithinivorans* KCTC 12052^T; 10, *Algoriphagus ratkowskyi* ACAM 646^T; 11, *Algoriphagus terrigena* KCTC 12545^T; 12, *Algoriphagus winogradskyi* KMM 3956^T; 13, *Algoriphagus yeomjeoni* KCTC 12309^T. Values of less than 1 % are not shown. Values for predominant fatty acids are shown in bold. Data from Ahmed *et al.* (2007), Nedashkovskaya *et al.* (2004), Tiago *et al.* (2006), Yoon *et al.* (2005a, b, 2006) and this study.

Fatty acid	1	2	3	4	5	6	7	8	9	10	11	12	13
C _{15:0}	0.7	1.6	1.6	0.6	2.5	1.0	1.5	3.0	2.7	1.6	0.3	1.2	0.6
C _{16:0}	0.3	0.4	1.7	3.2	1.4		0.7	0.2	0.3	2.9		1.0	0.8
iso-C _{11:0}	2.2	0.9		0.2			0.7				1.1		
anteiso-C _{11:0}	2.6	2.6	0.6	0.4	1.0	1.5	1.6	0.9		2.1	1.6	1.2	
iso-C _{14:0}		0.3	0.7	2.1	0.3	0.6	0.3	2.3	0.6	1.4	1.0	0.3	1.6
anteiso-C _{15:0}	1.6	3.4	3.2	6.4	1.9	2.8	0.8	3.7	6.1	3.6	2.4	1.6	1.2
iso-C _{15:0}	21.5	32.4	38.9	16.6	38.1	28.4	31.2	32.7	26.5	30.5	35.3	36.6	28.6
iso-C _{15:1} G	6.8	1.4	0.3	0.2			0.8	0.4	0.2	1.1	1.0	2.9	
iso-C _{16:0}	0.3	3.2	2.4	20.7	5.8	7.7	3.5	6.5	12.3	3.4	1.0	3.9	4.8
iso-C _{16:1}	0.6	3.8	2.4	10.9	1.5	3.5	1.6	3.5	6.4	1.7	2.5	2.1	1.9
anteiso-C _{17:1} ω9c				1.6					1.0				
iso-C _{17:1} ω9c	4.2	14.6	5.3	5.0	4.4	9.0	2.8	6.0	12.2	1.5	8.5	4.0	2.3
C _{15:1} ω6c	0.5	1.9	2.3		1.0	1.8	1.6	4.1	1.1	2.1	1.0	1.3	0.8
C _{16:1} ω5c		1.2	5.2	0.5	3.6	3.5	3.7	0.6	1.1	5.8	2.8	3.6	3.3
C _{17:1} ω6c	0.7	1.7	0.7	1.3	1.2	3.4	1.7	7.0	4.5	0.5	0.7	0.8	1.0
iso-C _{15:0} 3-OH	5.1	3.2	1.8	0.6	1.6	2.5	2.7	2.7	1.8	2.9	3.2	2.0	3.0
C _{16:0} 2-OH							0.8						1.3
C _{16:0} 3-OH	0.6		0.5		1.9	0.7	1.9			1.9	0.6	0.8	1.1
iso-C _{16:0} 3-OH		1.3	1.0	4.5	0.9	3.1	1.7	4.7	3.4	2.8	0.6	1.9	3.3
C _{17:0} 2-OH				1.1				0.4	1.8				
iso-C _{17:0} 3-OH	10.7	7.4	5.9	4.9	6.4	5.9	7.5	6.4	6.7	9.2	6.9	6.4	7.8
iso-C _{19:1} I	1.3												
Summed feature 3*	32.6	9.2	20.4	8.9	22.2	19.0	29.0	7.4	6.0	22.3	24.5	24.6	33.7
Summed feature 4*	4.9	3.9	1.8		1.7	2.7	1.5	2.5	2.0	0.9	2.5	1.6	1.3

*Summed feature 3 consists of one or more of the following fatty acids which could not be separated by the Microbial Identification System: iso-C_{15:0} 2-OH, C_{16:1}ω7c and/or C_{16:1}ω7t. Summed feature 4 consists of one or more of the following fatty acids: iso-C_{17:1} I and/or anteiso-C_{17:1} B.

not produced. Sensitive to gentamicin, carbenicillin, lincomycin, neomycin, oleandomycin, polymixin B, streptomycin, tetracycline, chloramphenicol, doxycycline and erythromycin. Resistant to ampicillin, benzylpenicillin and kanamycin. Fatty acids accounting for greater than 1% of the total are anteiso-C_{11:0} (2.6%), iso-C_{11:0} (2.2%), anteiso-C_{15:0} (1.6%), iso-C_{15:0} (21.5%), iso-C_{15:1} G (6.8%), iso-C_{17:1} ω9c (4.2%), iso-C_{15:0} 3-OH (5.1%), iso-C_{17:0} 3-OH (10.7%), iso-C_{19:1} I (1.3%), summed feature 3 (32.6%) comprising C_{16:1} ω7c and/or iso-C_{15:0} 2-OH, and summed feature 4 (4.9%) comprising iso-C_{17:1} I and/or anteiso-C_{17:1} B. The DNA G+C content of the type strain is 43.8 mol%.

The type strain is KMM 6241^T (=DSM 17529^T=KCTC 12716^T), which was isolated from coral *Palithoa* sp. collected in Vanfong Bay, South China Sea, Vietnam.

Emended description of the genus *Algoriphagus* Bowman et al. 2003, emend. Nedashkovskaya et al. 2004

Algoriphagus (Al.go.ri.pha'gus. L. masc. n. *algor* cold; Gr. masc. n. *phagos* glutton; N.L. masc. n. *Algoriphagus* the cold eater).

Main characteristics are as those given for the genus description by Nedashkovskaya et al. (2004). In addition, produce non-diffusible pink and red pigments. The DNA G+C content is 35–44 mol%. Habitat: sea ice and seawater, algae, marine sediments, soil and fresh water.

Description of *Algoriphagus alkaliphilus* comb. nov.

Algoriphagus alkaliphilus (al.ka.li.phi'lus. N.L. n. *alkali* from Arabic article *al* the, and Arabic n. *qaliy* ashes of saltwort, soda; Gr. adj. *philos* loving; N.L. masc. adj. *alkaliphilus* loving alkaline environments).

Basonym: *Chimaereicella alkaliphila* Tiago et al. 2006

The description is identical to that given for *Chimaereicella alkaliphila* by Tiago et al. (2006). The type strain is AC-74^T (=CIP 108470^T=LMG 22694^T), which was isolated from water taken from a borehole at Cabeço de Vide, Southern Portugal.

Description of *Algoriphagus boritolerans* comb. nov.

Algoriphagus boritolerans (bo'ri.to'le.rans. N.L. n. *borum* boron; L. part. adj. *tolerans* tolerating; N.L. part. adj. *boritolerans* boron-tolerating).

Basonym: *Chimaereicella boritolerans* Ahmed et al. 2007

The description is identical to that given for *Chimaereicella boritolerans* by Ahmed et al. (2007).

The type strain is strain T-22^T (=ATCC BAA-1189^T=DSM 17298^T=NBRC 101277^T), which was isolated from

naturally boron-contaminated soil of Hisarcik area in the Kutahya province of Turkey.

Description of *Algoriphagus mannitolivorans* comb. nov.

Algoriphagus mannitolivorans (man.ni.to.li.vo'rans. N.L. n. *mannitolium* mannitol; L. v. *vorare* to devour; N.L. part. adj. *mannitolivorans* utilizing mannitol).

Basonym: *Hongiella mannitolivorans* Yi and Chun 2004

The description is identical to that given for *Hongiella mannitolivorans* by Yi & Chun (2004). In addition, forms acid from D-cellobiose and sucrose, but not from L-arabinose, D-fructose, D-galactose, D-glucose, D-lactose, maltose, D-melibiose, D-raffinose, L-rhamnose, DL-xylose, N-acetylglucosamine, D-adonitol, glycerol, *myo*-inositol, D-mannitol or sorbitol. Sensitive to ampicillin, benzylpenicillin, carbenicillin, lincomycin, chloramphenicol, doxycycline, erythromycin, oleandomycin, streptomycin and tetracycline; resistant to gentamicin, kanamycin, neomycin and polymixin B.

The type strain is JC2050^T (=DSM 15301^T=IMSNU 14012^T=KCTC 12050^T), which was isolated from sediment of getbol, the Korean tidal flat.

Description of *Algoriphagus marincola* comb. nov.

Algoriphagus marincola (ma.rin'co.la. L. gen. n. *maris* of the sea; L. n. *incola* inhabitant; N.L. n. *marincola* inhabitant of the sea).

Basonym: *Hongiella marincola* Yoon et al. 2004

The description is identical to that given for *Hongiella marincola* by Yoon et al. (2004). In addition, hydrolyses Tweens 20 and 40. Does not degrade chitin. Does not produce acid from glycerol or N-acetylglucosamine. Sensitive to ampicillin, benzylpenicillin, chloramphenicol, doxycycline, erythromycin, oleandomycin, polymixin B, streptomycin and tetracycline; resistant to gentamicin, kanamycin, carbenicillin, lincomycin and neomycin.

The type strain is strain SW-2^T (=DSM 16067^T=KCTC 12180^T), which was isolated from seawater of the East Sea of Korea.

Description of *Algoriphagus ornithinivorans* comb. nov.

Algoriphagus ornithinivorans (or'ni.thi.ni.vo'rans. N.L. n. *ornithinum* ornithine; L. v. *vorare* to devour; N.L. part. adj. *ornithinivorans* utilizing ornithine).

Basonym: *Hongiella ornithinivorans* Yi and Chun 2004

The description is identical to that given for *Hongiella ornithinivorans* by Yi & Chun (2004). In addition, hydrolyses Tween 40, but not Tween 20. Forms acid from D-glucose, but not from L-arabinose, D-cellobiose, D-fructose, D-galactose,

D-lactose, maltose, D-melibiose, D-raffinose, L-rhamnose, sucrose, DL-xylose, N-acetylglucosamine, D-adonitol, glycerol, *myo*-inositol, D-mannitol or sorbitol. Sensitive to ampicillin, benzylpenicillin, kanamycin, carbenicillin, lincomycin, chloramphenicol, doxycycline, erythromycin, oleandomycin, polymixin B and tetracycline; resistant to gentamicin, neomycin and streptomycin.

The type strain is strain JC2052^T (=DSM 15282^T=IMSNU 14014^T=KCTC 12052^T), which was isolated from sediment of getbol, the Korean tidal flat.

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