Reclassification of *Aurantimonas altamirensis* (Jurado *et al.* 2006), *Aurantimonas ureilytica* (Weon *et al.* 2007) and *Aurantimonas frigidaquae* (Kim *et al.* 2008) as members of a new genus, *Aureimonas* gen. nov., as *Aureimonas altamirensis* gen. nov., comb. nov., *Aureimonas ureilytica* comb. nov. and *Aureimonas frigidaquae* comb. nov., and emended descriptions of the genera *Aurantimonas* and *Fulvimarina*

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Members of the genera *Aurantimonas* and *Fulvimarina* have largely been described on the basis of 16S rRNA gene sequence analyses, biochemical tests and limited chemotaxonomic data. Examination of the polar lipid compositions of members of these two genera indicated that although the patterns were similar with regards the phospholipid and amino lipid compositions, there were clear differences in the presence or absence of the glycolipid sulfoquinovosyl-diacylglycerol (SQDG). This glycolipid was absent in members of the species *Aurantimonas coralicida* and *Fulvimarina pelagi* but was present in *Aurantimonas altamirensis*, *Aurantimonas ureilytica* and *Aurantimonas frigidaquae*. These results are also consistent with the 16S rRNA sequence-based grouping. We therefore propose that the genus *Aurantimonas* be divided further to reflect this additional information. Thus, it is recommended that *Aurantimonas altamirensis*, *Aurantimonas ureilytica* and *Aurantimonas frigidaquae* are transferred to a new genus, *Aureimonas* gen. nov., as *Aureimonas altamirensis* gen. nov., comb. nov. (type strain S21B^T = CECT 7138^T = CIP 109525^T = KCTC 22106^T = LMG 23375^T = DSM 21988^T), *Aureimonas ureilytica* comb. nov. (type strain 5715S-12^T = KACC 11607^T = DSM 18598^T = CIP 109815^T) and *Aureimonas frigidaquae* comb. nov. (type strain CW5^T = KCTC 12893^T = JCM 14755^T = DSM 21987^T). The type species of the new genus is *Aureimonas altamirensis*. Additionally, emended descriptions of the genera *Aurantimonas* and *Fulvimarina* are provided.

The genus *Aurantimonas* has been assigned to the family *Aurantimonadaceae* within the order *Rhizobiales* (Kuykendall, 2005) of the class *Alphaproteobacteria*. The genus was originally described by Denner *et al.* (2003) with *Aurantimonas coralicida* as the type species, which was isolated from a marine environment. At the time of writing, the genus *Aurantimonas* contained four species. Despite the fact that these species were

isolated from diverse environments such as a subterranean cave (*Aurantimonas altamirensis*; Jurado *et al.*, 2006), air (*Aurantimonas ureilytica*; Weon *et al.*, 2007) and a water-cooling system (*Aurantimonas frigidaquae*; Kim *et al.*, 2008), no attempt has been made to emend the genus description to take these different origins into account. Currently defined members of the genera *Fulvimarina* and *Aurantimonas* form two closely related but distinct monophyletic groups based on the comparison of 16S rRNA sequences. It should be also noted that, based on the 16S rRNA sequence data, representatives of the genus *Aurantimonas* that were isolated from terrestrial, aquatic or aerial environments formed a

Abbreviations: DPG, diphosphatidylglycerol; PC, phosphatidylcholine; PDE, phosphatidylmethylethanolamine; PE, phosphatidylethanolamine; PG, phosphatidylglycerol; PME, phosphatidylmonomethylethanolamine; SQDG, sulfoquinovosyldiacylglycerol.

subgroup distinct from those strains isolated from marine sources. A comprehensive study of the polar lipid compositions of all type strains of species with validly published names in the genus was undertaken in order to elucidate the taxonomic infrastructure within this group of prokaryotes.

Aurantimonas corallicida DSM 14790^T, *Aurantimonas ureilytica* DSM 18598^T, *Aurantimonas altamirensis* DSM 21988^T, *Aurantimonas frigidaquae* DSM 21987^T and *Fulvimarina pelagi* DSM 15513^T were obtained from the DSMZ. All strains were grown on Bacto marine agar 2216 or in Bacto marine broth (Difco). Agar plates and liquid cultures were incubated at 28 °C.

Phenotypic characterization of the following physiological and biochemical properties were performed using methods described by Tindall *et al.* (2007): cell morphology, Gram-reaction (KOH) (method 15.2.34.1), L-alanine-aminopeptidase (method 15.2.34.2), oxidase (tetramethyl-p-phenyldiamine dihydrochloride test) (method 15.2.63) and catalase (H₂O₂ test) (method 15.2.16.2) activities, phenylalanine utilization (method 15.2.68) and hydrolysis of tyrosine (Gordon *et al.*, 1973), casein (method 15.2.15), gelatin (method 15.2.32.2), starch (method 15.2.77), DNA (method 15.2.54.1) and Tween-80 (method 15.2.47.2). Furthermore, oxidation/fermentation of glucose (aerobe/anaerobe) (method 15.2.64) and arginine dihydrolase activity (method 15.2.6.2) were also analysed. All tests were performed with the modification that artificial seawater was used for preparation of the media. The strains tested were incubated under aerobic conditions at 28 °C and in the dark. The API 20 NE micro test system (bioMérieux) was used to determine physiological and biochemical characteristics according to the manufacturer's instructions with the modification that natural seawater (Biomaris) was added to the saline and AUX-medium. To test for the ability to metabolize various carbon sources Biolog GN2 microtitre plates were inoculated with exponential phase cultures (150 µl per well) with a cell density of 50 % transmission as determined with a Biolog turbidimeter. After incubation at 28 °C for 24 h and 48 h the development of a purple colour, indicative of substrate oxidation, was examined photometrically.

Chemotaxonomic analyses of quinones and polar lipids were performed using 100 mg freeze-dried cell material according to the two-stage method described by Tindall (1990a, b). Respiratory quinones were first separated by TLC and then subjected to separation by HPLC using an RP₁₈ column as described previously (Tindall 1990a, b). Polar lipids were separated by two dimensional chromatography and visualized using a combination of a non-specific spray reagents as well as specific spray reagents, as described previously (Tindall, 1990a, b; Tindall *et al.*, 2007). Fatty acids were analysed from 10 mg dry cell material. Cells were subjected to differential hydrolysis steps for detecting ester-linked and non-ester-linked (amide-bound) fatty acids (B. Tindall, unpublished).

16S rRNA gene sequences obtained from the GenBank database were aligned using the automatic alignment tool implemented in the ARB program package (<http://www.arb-home.de/>). Calculation of distance matrices for the aligned sequences and reconstruction of phylogenetic trees by the neighbour-joining (Saitou & Nei, 1987) and maximum-likelihood methods with bootstrap calculations (based on 1000 resamplings) were performed using programmes provided in the ARB package. Phylogenetic relationships between all members of the genera *Aurantimonas* and *Fulvimarina* are shown in Fig. 1.

All strains tested were catalase and oxidase-positive. Further phenotypic properties and patterns of substrate utilization (Biolog GN MicroPlate results) are given in Table 1.

Analyses using the API 20 NE system revealed that in all the strains tested, glucose, L-arabinose, D-mannitol and malic acid could be utilized. Nitrate reduction, indole production from tryptophan, fermentation of glucose, arginine dihydrolase activity, hydrolysis of β -glucosidase and gelatin, and assimilation of capric acid, N-acetylglucosamine, trisodium citrate and phenylacetic acid were negative in all strains tested (Table 1).

Analysis of the 16S rRNA gene sequences of type strains of the species *A. ureilytica*, *A. frigidaquae*, *A. altamirensis* and *A. corallicida* indicated that *A. corallicida* did not group with the other three species (Fig. 1).

Ubiquinone 10 (Q10) was the dominant respiratory lipokinone in all strains tested, which is consistent with their placement in the class *Alphaproteobacteria*. Polar lipid analyses (Fig. 2) gave patterns that were largely consistent

Fig. 1. Neighbour-joining tree showing the phylogenetic positions of species of the family *Aurantimonadaceae* and related genera of the class *Alphaproteobacteria* based on 16S rRNA gene sequences. Bootstrap values >50 % (based on 1000 replications) are given at branch points. Bar, 0.1 substitutions per nucleotide position.

Table 1. Biochemical characteristics of type strains of species of the genera *Aurantimonas* and *Fulvimarina*

Strains: 1, *Aurantimonas corallicida* DSM 14790^T; 2, *Aurantimonas ureilytica* DSM 18598^T; 3, *Aurantimonas altamirensis* DSM 21988^T; 4, *Aurantimonas frigidaquae* DSM 21987^T; 5, *Fulvimarina pelagi* DSM 15515^T. All data were from this study, except for Biolog data for *Fulvimarina pelagi* DSM 15515^T, from this study and Cho & Giovannoni (2003). All strains were positive for catalase, oxidase, hydrolysis of DNA and assimilation of glucose, arabinose, mannitol and malic acid; negative for arginine dihydrolase (aerobe/anaerobe) activity, hydrolysis of casein, gelatin (API 20 NE), and aesculin, assimilation of capric acid, trisodium citrate and phenylacetic acid, reduction of nitrates to nitrites, indole production and fermentation of glucose. In Biolog GN2 tests, all strains were negative for Tween 80, α -keto glutaric acid, malonic acid, L-pyroglutamic acid and 2,3-butanediol utilization. +, Positive; +*, colour change restricted to the surface; –, negative; w, weakly positive.

Characteristic	1	2	3	4	5
L-Alanine-aminopeptidase	–	–	–	–	–
Phenylalanine deaminase	–	–	–	+	–
Hydrolysis of:					
Starch	+	+	+	+	–
DNA	+	+	+	+	+
Gelatin	–	–	+	+	–
Tyrosine	+	–	–	–	+
Oxidation/fermentation test for glucose (aerobe)	–	–	+	+	–
Oxidation/fermentation test for glucose (anaerobe)	+*	+*	+*	+*	+*
API 20 NE					
Release of urea	+	+	+	+	–
Hydrolysis with β -galactosidase	–	+	–	–	–
Assimilation of:					
Mannose	+	+	+	+	–
N-Acetylglucosamine	–	–	–	–	–
Maltose	–	+	+	–	+
Potassium gluconate	+	+	+	+	–
Adipic acid	+	–	–	–	–
Utilization of (Biolog GN MicroPlate):					
α -Cyclodextrin, Tween 40, gentiobiose, β -methyl-D-glucoside, raffinose, propionic acid, thymidine, glycerol	–	–	–	–	+
Dextrin	+	w	w	–	+
Glycogen, melibiose, α -keto butyric acid, D-saccharic acid, L-leucine	–	–	+	–	+
N-Acetyl-D-galactosamine, γ -hydroxybutyric acid, D-glucosaminic acid, itaconic acid, α -keto valeric acid, glycyl-L-aspartic acid, L-histidine, L-ornithine, urocanic acid, putrescine	–	–	+	–	–
Adonitol, D-arabitol, L-arabinose, D-fructose, D-galactose, α -D-glucose, D-mannitol, D-mannose, D-sorbitol, xylitol, acetic acid, L-proline	–	w	+	+	+
Succinamic acid mono-methyl-ester, pyruvic acid methyl ester, DL-lactic acid, succinamic acid, L-alaninamide, L-glutamic acid, L-serine	–	–	+	+	+
Cellobiose	–	+	–	–	+
i-Erythritol, L-fucose, inositol, D-psicose, L-rhamnose, D-gluconic acid, succinic acid, bromosuccinic acid, L-alanyl-glycine, L-asparagine, hydroxy-L-proline	–	w	+	+	–
Maltose, sucrose, glycyl-L-glutamic acid	–	w	+	–	+
Turanose	–	–	+	–	–
Formic acid	+	w	+	+	+
D-Galactonic acid lactone	–	w	–	+	–
α -Hydroxybutyric acid, D-alanine, L-alanine, L-threonine	–	–	+	+	–
β -Hydroxybutyric acid	–	w	+	w	+
γ -Hydroxybutyric acid, quinic acid, L-pyroglutamic acid	–	w	+	–	–
Glucuronamide	–	–	w	–	+
L-Aspartic acid	–	w	w	–	–
DL-Carnitine, γ -amino butyric acid	–	–	w	+	–
Uridine	–	w	–	–	+
DL- α -Glycerol phosphate	–	–	w	w	–

Fig. 2. Polar lipid compositions of strains *Aurantimonas coralicida* DSM 14790^T (a), *Aurantimonas ureilytica* DSM 18598^T (b), *Aurantimonas altamirensis* DSM 21988^T (c), *Aurantimonas frigidaquae* DSM 21987^T (d) and *Fulvimarina pelagi* DSM 15515^T (e). All data were from this study. Separation was in two dimensions: first dimension, chloroform/methanol/water (65:25:4, v/v/v); second dimension, chloroform/methanol/acetic acid/water (80:12:15:4, v/v/v/v). Plates were stained with 5% molybdophosphoric acid in ethanol and heated for 15 min at 150 °C. DPG, diphosphatidylglycerol; PG, phosphatidylglycerol; PE, phosphatidylethanolamine; PME, phosphatidylmonomethylethanolamine; PC, phosphatidylcholine; AL1, AL2, unidentified aminolipids; L1–L2, lipids; SQDG, sulfoquinovosyldiacylglycerol.

with previous reports, although there were differences in the identity of the lipids. The phospholipid profiles of the strains tested all contained diphosphatidylglycerol (DPG), phosphatidylglycerol (PG), phosphatidylethanolamine (PE), phosphatidylmonomethylethanolamine (PME) and phosphatidylcholine (PC). This differs from the reports of Denner *et al.* (2003) and Weon *et al.* (2007), both of which reported the presence of phosphatidylmethylethanolamine (PDE). However, the lipid running with an R_f value similar to that of PDE in the supplementary images presented by Weon *et al.* (2007) was shown, in the present study, to be ninhydrin (primary amines)-positive and Zinzadze (phosphate)-negative. Denner *et al.* (2003) did not provide an image of their TLC plate. It should be noted that the lipid labelled PME was both ninhydrin- and phosphate-positive, and was checked against an authentic sample of PME purchased from Sigma; the head group structure was also checked using mass spectrometry (B. Tindall, unpublished). Authentic samples of PDE are phosphate positive and ninhydrin negative. Denner *et al.* (2003) and Weon *et al.* (2007) did not mention aminolipids, although the lipid labelled L3 in the TLC images of Weon *et al.* (2007) has an R_f value similar to that of the second amino lipid (AL2) reported here. All lipids labelled AL1 or AL2 reacted with the ninhydrin reagent. The polar lipid profiles of the type strains of *Aurantimonas altamirensis* DSM 21988^T, *Aurantimonas ureilytica* DSM 18598^T and *Aurantimonas frigidaquae* DSM 21987^T contained a polar lipid that stained positively with the α -naphthol reagent, indicating that it contained a carbohydrate head group. The R_f value was consistent with it being identified as sulfoquinovosyldiacylglycerol (SQDG), a sulfonic acid containing a glycolipid derivative. Significantly, this polar lipid was not present in either *Fulvimarina pelagi* or *Aurantimonas coralicida*. The presence of this or other glycolipids was

not mentioned by Weon *et al.* (2007), although the lipid labelled L2 in TLC images from that study had an R_f value similar to that of SQDG. This lipid only appeared to be present in *Aurantimonas ureilytica* in these images, which is consistent with the data reported in the present study. It should be noted that the presence/absence of SQDG may be of taxonomic significance as discussed by Biebl *et al.* (2007). We therefore propose that the genus *Aurantimonas* be split into two groups based on the presence or absence of the glycolipid sulfoquinovosyldiacylglycerol (SQDG), a grouping that is consistent with that of both the results of 16S rRNA gene sequence analysis and the divide between taxa from marine and non-marine habitats. Thus, we suggest that *A. ureilytica*, *A. frigidaquae* and *A. altamirensis* form a new genus named *Aureimonas* with *Aureimonas altamirensis* as type species. *A. coralicida* remains as the only representative species of the genus *Aurantimonas*.

Previous work has shown that in all members of these bacterial taxa, the predominant fatty acid is C_{18:1} ω 7c, which is a feature of the vast majority of members of the class *Alphaproteobacteria*. Our studies confirmed this (Table 2). However, distinct differences have been observed within members of the species *A. ureilytica*, *A. frigidaquae* and *A. altamirensis* and *A. coralicida* regarding the fatty acids C_{16:0} and C_{20:1} ω 7c. Although all the strains contained C_{16:0} the amount was up to five times higher in strains of *A. ureilytica*, *A. frigidaquae* and *A. altamirensis* when compared to strains of *A. coralicida*. Furthermore, the fatty acid C_{20:1} ω 7c could only be detected in proportions greater than trace levels in strains of *A. coralicida*. On the basis of the chemotaxonomic analysis, significant differences between the strains were detected, emphasizing the fact that chemotaxonomic features contribute considerably to the classification of organisms (Tindall, 1994).

Table 2. Cellular fatty acid contents (%) of strains of species of the genus *Aurantimonas*

Strains: 1, *A. coralicida* DSM 14790^T; 2, *A. ureilytica* KACC 11607^T; 3, *A. altamirensis* DSM 21988^T; 4, *A. frigidaquae* DSM 21987^T. All data from this study except for *A. ureilytica* KACC 11607^T (Weon *et al.*, 2007). Method 1 (M1) releases only ester-linked fatty acids; method 2 (M2) releases ester-linked and non-ester-linked fatty acids. tr, Trace (<1 % of total); ND, not detected.

Fatty acid	1		2		3		4	
	M1	M2			M1	M2	M1	M2
C _{16:0}	1.8	2.2	9.0		6.7	6.5	5.7	6.4
C _{18:1} ω7c	88.9	86.6	62.2		85.4	85.0	70.2	80.5
C _{18:0} 3-OH	ND	tr	1.4		tr	tr	tr	1.0
C _{18:0}	2.8	3.6	1.1		1.7	1.7	2.84	3.3
C _{19:0} cyclo ω8c	2.2	1.8	1.6		2.4	2.4	3.7	4.8
C _{20:1} ω7c	1.5	1.8	ND		tr	tr	tr	tr

Due to the evident heterogeneity of the genus *Aurantimonas*, based on differences in habitat (*Aurantimonas coralicida* being the only isolate obtained from a marine environment), fatty acid profiles and polar lipid patterns (including the significant absence of the polar lipid SQDG), we propose the transfer of the species *A. ureilytica*, *A. frigidaquae* and *A. altamirensis* from the genus *Aurantimonas* to a new genus, *Aureimonas* gen. nov., as *Aureimonas altamirensis* gen. nov., comb. nov., *Aureimonas ureilytica* comb. nov. and *Aureimonas frigidaquae* comb. nov., with *Aureimonas altamirensis* as the type species.

It should be noted that although members of the genera *Fulvimarina* and *Aurantimonas* have been included in the order *Rhizobiales* (Kuykendall, 2005, 2006), the circumscription of that order includes the genus *Hyphomicrobium*. The genus *Hyphomicrobium* is the type genus of the order *Hyphomicrobiales* (Douglas, 1957; Approved Lists 1980). Although the name *Hyphomicrobiales* (Douglas, 1957; Approved Lists 1980) has priority over the name *Rhizobiales* (Kuykendall, 2006), according to Rule 51b 1 of the Bacterial Code, this name is illegitimate and Rule 51a clearly states that 'a name contrary to a Rule is illegitimate and may not be used'. While an emended description and circumscription of the order *Hyphomicrobiales* (Douglas, 1957; Approved Lists 1980) is clearly overdue, it is beyond the scope of the present article.

Description of *Aureimonas* gen. nov.

Aureimonas (Au.re.i.mo'nas. L. adj. *aureus* golden; Gr. fem. n. *monas* a unit; N.L. fem. n. *Aureimonas* golden-coloured bacterium).

Cells are Gram-reaction-negative, short rods of mean size 1.0 × 2.0 μm. Colonies are yellow in colour. Growth occurs at 4–40 °C (optimum 25–30 °C) and in 0–3 % (w/v) NaCl.

Cells are catalase-, urease- and oxidase-positive but negative for L-alanine-aminopeptidase. Positive for hydrolysis of DNA and starch, but negative for hydrolysis of tyrosine, Tween 80 and casein. Cells are able to assimilate glucose, L-arabinose, D-mannitol and malic acid. Negative for nitrite reduction, production of indole from tryptophan, fermentation of glucose, arginine dihydrolase activity, hydrolysis of β-glucosidase and assimilation of capric acid, N-acetylglucosamine, trisodium citrate and phenylacetic acid. Positive for utilization of D-arabitol, L-arabinose, i-erythritol, D-fructose, L-fucose, D-galactose, α-D-glucose, inositol, D-mannitol, D-mannose, D-psicose, L-rhamnose, D-sorbitol, xylitol, acetic acid, adonitol, formic acid, D-gluconic acid, β-hydroxybutyric acid, succinic acid, bromosuccinic acid, L-alanyl-glycine, hydroxy-L-proline and L-proline. The major respiratory lipoquinone is Q10. Polar lipids comprise DPG, PME, PC, PG, PE, two lipids, two unidentified aminolipids and SQDG. The predominant fatty acid is C_{18:1}ω7c with significant proportions of C_{16:0}, C_{18:1} 2-OH, C_{18:1} and cyclo-C_{19:0}ω8c. Members of the genus have been isolated predominantly from non-marine habitats. The genus comprises three species *Aureimonas altamirensis*, *Aureimonas ureilytica* and *Aureimonas frigidaquae*. The type species is *Aureimonas altamirensis*.

Description of *Aureimonas altamirensis* comb. nov.

Aureimonas altamirensis [al.ta.mi.ren'sis. N.L. fem. adj. *altamirensis* referring to Altamira Cave (Cantabria, Spain), where the type strain was isolated].

Basonym: *Aurantimonas altamirensis* (Jurado *et al.* 2006).

Description of *Aureimonas altamirensis* is as given by Jurado *et al.* (2006), with the following additions. The polar lipids and respiratory lipoquinone compositions are consistent with those listed in the genus description.

The type strain is S21B^T (=CECT 7138^T =CIP 109525^T =KCTC 22106^T =LMG 23375^T =DSM 21988^T).

Description of *Aureimonas ureilytica* comb. nov.

Aureimonas ureilytica (ur.e.i.ly'ti.ca. N.L. n. *urea* urea; N.L. fem. adj. *lytica* from Gr. adj. *lutikos* dissolving; N.L. fem. adj. *ureilytica* urea-dissolving).

Basonym: *Aurantimonas ureilytica* (Weon *et al.* 2007).

Description of the species is as given by Weon *et al.* (2007), with the following additions. The polar lipid and respiratory lipoquinone compositions are consistent with those listed in the genus description. It should be noted that the polar lipid pattern differs from that given by Weon *et al.* (2007) but these components are not mentioned as part of the species description.

The type strain is 5715S-12^T (=KACC 11607^T =DSM 18598^T =CIP 109815^T).

Description of *Aureimonas frigidaquae* comb. nov.

Aureimonas frigidaquae (fri.gi.da'quae. L. adj. *frigidus* cold; L. fem. n. *aqua* water; N.L. gen. n. *frigidaquae* from/of cold water, because the type strain was isolated from a water-cooling system).

Basonym: *Aurantimonas frigidaquae* (Kim *et al.* 2008).

Description of the species *Aureimonas frigidaquae* is as given by Kim *et al.* (2008), with the following additions. The polar lipids and respiratory lipoquinone compositions are consistent with those listed in the genus description.

The type strain is CW5^T (=KCTC 12893^T =JCM 14755^T =DSM 21987^T).

Emended description of the genus *Aurantimonas* (Denner *et al.* 2003)

Aurantimonas (Au.ran.ti.mo'nas. M.L. adj. *aurantiaca* orange-coloured; Gr. fem. n. *monas* a unit; N.L. fem. n. *Aurantimonas* orange-coloured unicellular organism).

The genus *Aurantimonas* exhibits the following properties in addition to those given by Denner *et al.* (2003). The polar lipids PE [listed in the genus description by Denner *et al.* (2003)] and SQDG are not detected. Additionally, two amino lipids are observed. Isolated from marine environments and does not grow in the absence of NaCl. The type species is *Aurantimonas corallicida*. The genus currently consists of one species, *Aurantimonas corallicida*.

Emended description of *Aurantimonas corallicida* (Denner *et al.* 2003)

Aurantimonas corallicida [co.ra.li'ci.da. L. n. *coralium* (red) coral; L. masc./fem. suffix *-cida* murderer, killer; N.L. masc./fem. n. *corallicida* coral-killer].

The species has the characteristics listed in the emended genus description in addition to those listed by Denner *et al.* (2003). The type strain is strain WP1^T (=CIP 107386^T =DSM 14790^T =CCUG 53900^T).

Emended description of the genus *Fulvimarina* (Cho & Giovannoni 2003)

Fulvimarina (Ful.vi.ma.ri'na. L. adj. *fulvus* brownish-yellow; L. fem. adj. *marina* of the sea; N.L. fem. n. *Fulvimarina* brownish-yellow bacterium isolated from sea water).

Description of the genus *Fulvimarina* is as given by Cho & Giovannoni (2003) with the following additions. The polar lipids comprise DPG, PME, PC, PG, PE, two lipids and two unidentified aminolipids. The sole respiratory lipoquinone is Q10. The type, and currently only, species of the genus is *Fulvimarina pelagi* HTCC 2506^T (=ATCC BAA-666^T =KCTC 12091^T =DSM 15513^T).

Emended description of *Fulvimarina pelagi* (Cho & Giovannoni 2003).

Fulvimarina pelagi (pe.la'gi. L. fem. adj. *pelagi* from the open sea).

The species has the characteristics listed in the emended genus description in addition to those listed by Cho & Giovannoni (2003). The type strain is strain HTCC2506^T (=ATCC BAA-666^T =DSM 15513^T =KCTC 12091^T).

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References

- Biebl, H., Pukall, R., Lünsdorf, H., Schulz, S., Allgaier, M., Tindall, B. J. & Wagner-Döbler, I. (2007). Description of *Labrenzia alexandrii* gen. nov., sp. nov., a novel alphaproteobacterium containing bacteriochlorophyll *a*, and a proposal for reclassification of *Stappia aggregata* as *Labrenzia aggregata* comb. nov., of *Stappia marina* as *Labrenzia marina* comb. nov. and of *Stappia alba* as *Labrenzia alba* comb. nov., and emended descriptions of the genera *Pannonibacter*, *Stappia* and *Roseibium*, and of the species *Roseibium denhamense* and *Roseibium hamelinense*. *Int J Syst Evol Microbiol* **57**, 1095–1107.
- Cho, J. C. & Giovannoni, S. J. (2003). *Fulvimarina pelagi* gen. nov., sp. nov., a marine bacterium that forms a deep evolutionary lineage of descent in the order 'Rhizobiales'. *Int J Syst Evol Microbiol* **53**, 1853–1859.
- Denner, E. B. M., Smith, G. W., Busse, H.-J., Schumann, P., Narzt, T., Polson, S. W., Lubitz, W. & Richardson, L. L. (2003). *Aurantimonas corallicida* gen. nov., sp. nov., the causative agent of white plague type II on Caribbean scleractinian corals. *Int J Syst Evol Microbiol* **53**, 1115–1122.
- Gordon, R. E., Haynes, W. C. & Pang, C. H. (1973). *The genus Bacillus*. (Agricultural handbook no. 427). Washington, DC: US Department of Agriculture.
- Jurado, V., Gonzalez, J. M., Laiz, L. & Saiz-Jimenez, C. (2006). *Aurantimonas altamirensis* sp. nov., a member of the order Rhizobiales isolated from Altamira Cave. *Int J Syst Evol Microbiol* **56**, 2583–2585.
- Kim, M. S., Hoa, K. T. Q., Baik, K. S., Park, S. C. & Seong, C. N. (2008). *Aurantimonas frigidaquae* sp. nov., isolated from a water-cooling system. *Int J Syst Evol Microbiol* **58**, 1142–1146.
- Kuykendall, L. D. (2005). Order VI. Rhizobiales ord. nov. In *Bergey's Manual of Systematic Bacteriology*, 2nd edn, vol. 2 (*The Proteobacteria*), part C (*The Alpha-, Beta-, Delta-, and Epsilonproteobacteria*), p. 324. Edited by D. J. Brenner, N. R. Krieg, J. T. Staley & G. M. Garrity. New York: Springer.
- Kuykendall, L. D. (2006). List of new names and new combinations previously effectively, but not validly, published – Validation List no. 107. *Int J Syst Evol Microbiol* **56**, 1–6.
- Saitou, N. & Nei, M. (1987). The neighbor-joining method: a new method for reconstructing phylogenetic trees. *Mol Biol Evol* **4**, 406–425.
- Stackebrandt, E. & Goebel, B. M. (1994). Taxonomic note: a place for DNA–DNA reassociation and 16S rRNA sequence analysis in the present species definition in bacteriology. *Int J Syst Bacteriol* **44**, 846–849.

Tindall, B. J. (1990a). Lipid composition of *Halobacterium lacusprofundi*. *FEMS Microbiol Lett* **66**, 199–202.

Tindall, B. J. (1990b). A comparative study of the lipid composition of *Halobacterium saccharovororum* from various sources. *Syst Appl Microbiol* **13**, 128–130.

Tindall, B. J. (1994). Chemical analysis of *Archaea* and *Bacteria*: a critical evaluation of its use in taxonomy and identification. In *Bacterial Diversity and Systematics (FEMS Symposium no. 75)*, pp. 243–258. Edited by F. G. Priest, A. Ramos-Cormenzana & B. J. Tindall. New York: Plenum.

Tindall, B. J., Sikorski, J., Smibert, R. M. & Kreig, N. R. (2007). Phenotypic characterization and the principles of comparative systematics. In *Methods for General and Molecular Microbiology*, pp. 332–393. Edited by C. A. Reddy, T. J. Beveridge, J. A. Breznak, G. A. Marzluf, T. M. Schmidt & L. R. Snyder. Washington, DC: American Society for Microbiology.

Weon, H.-Y., Kim, B.-Y., Yoo, S.-H., Joa, J.-H., Lee, K. H., Zhang, Y.-S., Kwon, S.-W. & Koo, B.-S. (2007). *Aurantimonas ureilytica* sp. nov., isolated from an air sample. *Int J Syst Evol Microbiol* **57**, 1717–1720.