Description of *Aquimarina muelleri* gen. nov., sp. nov., and proposal of the reclassification of [*Cytophaga*] *latercula* Lewin 1969 as *Stanierella latercula* gen. nov., comb. nov.

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The taxonomic position of three novel sea-water isolates was determined. The strains studied were strictly aerobic, heterotrophic, pigmented, motile by gliding, Gram-negative and oxidase-, catalase-, β -galactosidase- and alkaline phosphatase-positive. 16S rRNA gene sequence phylogenetic analysis indicated that the strains KMM 6020^T, KMM 6021 and KMM 6028 occupied a distinct lineage within the family *Flavobacteriaceae*. The major respiratory quinone was MK-6. The predominant fatty acids were i15:0, i15:1, i15:0 3-OH, i17:1 ω 9c and i17:0 3-OH. On the basis of phenotypic, chemotaxonomic, genotypic and phylogenetic characteristics, the novel bacteria were assigned to the genus *Aquimarina* gen. nov., as *Aquimarina muelleri* gen. nov., sp. nov. The type strain is KMM 6020^T (=KCTC 12285^T=LMG 22569^T). From the results of the 16S rRNA gene sequence analysis and phenotypic features, the species [*Cytophaga*] *latercula* Lewin 1969 is proposed to be reclassified in the new genus *Stanierella* as *Stanierella latercula* gen. nov., comb. nov., with type strain CIP 104806^T (=ATCC 23177^T=NCIMB 1399^T=LMG 1343^T).

The genus *Cytophaga* was proposed by Winogradsky (1929) to accommodate Gram-negative, motile by gliding, aerobic, pigmented and cellulolytic bacteria. Many other novel bacteria were later included in the genus *Cytophaga*, which was consequently emended by Reichenbach (1989) and Nakagawa & Yamasato (1996). The latter authors proposed to restrict the polyphyletic genus *Cytophaga* to the species *Cytophaga aurantiaca* and *Cytophaga hutchinsonii* according to phylogenetic analysis data based on 16S rRNA gene sequence analysis. Novel genera were proposed for some *Cytophaga* species. For example, [*Cytophaga*] *agarovorans*

Reichenbach 1989 and [*Cytophaga*] *salmonicolor* Veldkamp 1961 were reclassified as *Marinilabilia agarovorans* and *Marinilabilia salmonicolor*, respectively, by Nakagawa & Yamasato (1996). These species were subsequently merged into a single species *M. salmonicolor* on the basis of DNA–DNA hybridization experiments (Suzuki *et al.*, 1999). The novel genera *Flammeovirga* and *Persicobacter* were created, based on determination of their precise phylogenetic positions and polyamine compositions by Nakagawa *et al.* (1997), to accommodate [*Cytophaga*] *aprica* Reichenbach 1989 and [*Cytophaga*] *diffluens* Reichenbach 1989, respectively. Several *Cytophaga* species, [*Cytophaga*] *aquatilis* Strohl and Tait 1978, [*Cytophaga*] *columnaris* Bernardet and Grimont 1989, [*Cytophaga*] *flevense* van der Meulen *et al.* 1974, [*Cytophaga*] *johnsoniae* Stanier 1947, [*Cytophaga*] *pectinivora* Reichenbach 1989, [*Cytophaga*] *psychrophila* Reichenbach 1989, [*Cytophaga*] *saccharophila* Reichenbach 1989 and [*Cytophaga*] *succinicans* Reichenbach 1989, were transferred to the genus *Flavobacterium* (Bernardet *et al.*, 1996). [*Cytophaga*] *heparina* Christensen 1980 was reclassified

Published online ahead of print on 6 August 2004 as DOI 10.1099/ijs.0.63349-0.

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The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of *Aquimarina muelleri* KMM 6020^T, KMM 6021 and KMM 6028 are AY608406, AY608407 and AY608408, respectively.

as *Sphingobacterium heparinum* Takeuchi and Yokota 1993 (effective publication by Takeuchi & Yokota, 1992), and later transferred to the genus *Pedobacter* as *Pedobacter heparinum* (Steyn *et al.*, 1998). The marine bacteria [*Cytophaga*] *lytica* Lewin 1969 and [*Cytophaga*] *marina* Reichenbach 1989 were included in the new genera *Cellulophaga* (Johansen *et al.*, 1999) and *Tenacibaculum* (Suzuki *et al.*, 2001), respectively, as the type species of these taxa. A marine bacterium isolated from a mud sample and described as [*Flavobacterium*] *uliginosum* (ZoBell & Upham, 1944) is now included in the genus *Zobellia* (Barbeyron *et al.*, 2001). Currently, only two of the 20 species initially included in the genus *Cytophaga* by Reichenbach (1989), [*Cytophaga*] *latercula* and [*Cytophaga*] *marinoflava*, together with [*Cytophaga*] *fermentans* Bachmann 1955, [*Cytophaga*] *arvensicola* Oyaizu *et al.* 1983 (effective publication by Oyaizu *et al.*, 1982) and [*Cytophaga*] *xylanolytica* Haak and Breznak 1993, are considered as misnamed *Cytophaga* species and remain to be reclassified.

In the course of a study of a sea-water microbial population, novel heterotrophic, aerobic, Gram-negative, gliding and flexirubin-producing bacteria were isolated. 16S rRNA gene sequence analysis indicated that the isolates were members of the family *Flavobacteriaceae*, in which they form a distinct lineage. The closest relative of the strains studied was [*Cytophaga*] *latercula* (95.4 % sequence similarity). However, based on differences in the molecular and phenotypic features described here, we proposed that the KMM strains clearly differ from strain [*Cytophaga*] *latercula* CIP 104806^T and represent a separate genus of the family *Flavobacteriaceae*. Consequently, we propose the description of the novel genus and species *Aquimarina muelleri* gen. nov., sp. nov., with type strain KMM 6020^T, and the reclassification of [*Cytophaga*] *latercula* Lewin 1969 in the new genus *Stanierella* as *Stanierella latercula* gen. nov., comb. nov., with type strain CIP 104806^T.

Strains KMM 6020^T, KMM 6021 and KMM 6028 were isolated from a sea-water sample collected in Amursky Bay, Gulf of Peter the Great, Sea of Japan. After primary isolation and purification on marine agar, strains were cultivated at 28 °C on the same medium and stored at -80 °C in marine broth supplemented with 20 % (v/v) glycerol.

Genomic DNA extraction, PCR and sequencing of the 16S rRNA gene followed the procedures of Kim *et al.* (1998). The sequence data obtained were aligned together with those of representative members of the family *Flavobacteriaceae* by 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 from the models of Kimura (1980), and phylogenetic trees were constructed on the basis of the neighbour-joining (Saitou & Nei, 1987) and maximum-likelihood (Felsenstein, 1993) algorithms. Bootstrap analysis was performed with 1000 resamplings, using the SEQBOOT and CONSENSE programs of the PHYLIP package.

Phylogenetic 16S rRNA gene sequence analysis indicated

that strains KMM 6020^T, KMM 6021 and KMM 6028 are members of the family *Flavobacteriaceae* and form a cluster with species of the genera *Psychroflexus*, *Salegentibacter* and *Mesonía* (Fig. 1). The closest relative of these strains is [*Cytophaga*] *latercula* CIP 104806^T, with 95.4 % sequence similarity.

DNA was isolated following the method of Marmur (1961) and G + C content was determined by the thermal denaturation method of Marmur & Doty (1962). The G + C content of the DNA of the strains studied ranges from 31.6 to 32.5 mol%. DNA-DNA hybridizations were performed spectrophotometrically and initial renaturation rates were recorded as described by De Ley *et al.* (1970). The level of DNA-DNA relatedness between the KMM strains was 85–99 %. These values are significantly more than 70 %, and therefore suggest that the strains belong to the same species (Wayne *et al.*, 1987).

Analysis of fatty acid methyl esters was carried out according to the standard protocol of the Microbial Identification System (Microbial ID). The major cellular fatty acids of the sea-water isolates were i15:1, i15:0, i15:0 3-OH, i17:1ω9c and i17:0 3-OH (9.8–13, 19.3–21.1, 5.5–7.5, 9.3–10.6 and 21–29.5 %, respectively), and summed feature 3 (7–8.4 %), comprising 16:1ω7 and/or i15:0 2-OH fatty acids. Isoprenoid quinones were extracted from lyophilized cells and analysed as described by Nedashkovskaya *et al.* (2003c); the major respiratory quinone was MK-6.

Phenotypic analysis was performed using the methods of Nedashkovskaya *et al.* (2003a, b). Gliding motility was determined as described by Bowman (2000).

Physiological, biochemical and morphological characteristics of the strains studied are listed under the species

Fig. 1. Phylogenetic tree based on 16S rRNA gene sequences of strains KMM 6020^T, KMM 6021 and KMM 6028 and representative members of related genera in the family *Flavobacteriaceae*. The tree was generated using the neighbour-joining method (Saitou & Nei, 1987). Numbers at nodes indicate bootstrap values (%), and asterisks indicate branches that were also recovered in the maximum-likelihood tree. Bar, 0.01 substitutions per nucleotide position.

Table 1. Differential characteristics of the new genera *Aquimarina* and *Stanierella* and other allied genera of the family *Flavobacteriaceae*

Taxa: 1, *Aquimarina muelleri* gen. nov., sp. nov.; 2, *Stanierella latercula* gen. nov., comb. nov.; 3, *Psychroflexus*; 4, *Salegentibacter*; 5, *Mesonina*. Data from Reichenbach (1989), Dobson *et al.* (1993), Bowman *et al.* (1998), Nedashkovskaya *et al.* (2003c, 2004), Donachie *et al.* (2004) and this study. –, Negative; +, positive; v, variable; ND, not detected.

Characteristic	1	2	3	4	5
Gliding motility	+	–	v	–	–
Catalase	+	–	+	+	+
Flexirubins	+	–	–	–	–
Acid from carbohydrates	–	–	+	+	–
Growth at 15 % NaCl	–	–	v	v	+
Hydrolysis of:					
Agar	–	+	–	–	–
Casein	+	+	–	–	+
Starch	+	–	+	+	–
Alginate	–	+	ND	+	–
Chitin	+	+	–	–	–
DNA	+	+	+	+	–
Nitrate reduction	–	–	v	v	–
H ₂ S production	–	+	–	+	+
DNA G + C content (mol%)	31–33	34	32–36	37–38	32–34

description and are also given in Table 1. Phenotypic examination demonstrated many common traits between the strains studied and [*Cytophaga*] *latercula*. However, the KMM strains differ sufficiently from their closest relative on the basis of the ability to move by gliding motility, catalase activity, hydrolysis of agar and starch, flexirubin pigments and hydrogen sulphide production. Differential characteristics of the strains studied and their nearest relatives are shown in Table 1.

Based on the phenotypic, chemotaxonomic and molecular characteristics described here, we propose the creation of a novel genus and species *Aquimarina muelleri* gen. nov., sp. nov. for strains KMM 6020^T, KMM 6021 and KMM 6028. In addition, we propose the reclassification of [*Cytophaga*] *latercula* CIP 104106^T to the genus *Stanierella* as *Stanierella latercula* gen. nov., comb. nov.

Description of *Aquimarina* gen. nov.

Aquimarina (A.qui.ma.ri'na. L. fem. n. *aqua* water; L. adj. *marinus*, -a, -um marine; N.L. adj. *aquimarina* living in sea water).

Rod-shaped cells, motile by gliding. Gram-negative. Do not form endospores. Strictly aerobic. Produce non-diffusible yellow pigments. Chemo-organotroph. Cytochrome oxidase-, catalase- and alkaline phosphatase-positive. The predominant cellular fatty acids are straight-chain saturated, branched-chain saturated and unsaturated fatty acids:

i15:0, i15:1, i15:0 3-OH, i17:1ω9c, i17:0 3-OH and summed feature 3 (comprising 16:1ω7c and/or i15:0 2-OH fatty acids). The main lipoquinone is MK-6. 16S rRNA gene sequence analysis indicates the genus *Aquimarina* is a member of the family *Flavobacteriaceae*, phylum 'Bacteroidetes'. The type species is *Aquimarina muelleri*.

Description of *Aquimarina muelleri* sp. nov.

Aquimarina muelleri [muel'le.ri. N.L. gen. n. *muelleri* of Müller, in honour of Otto Friedrich Müller (1730–1784), the famous Danish naturalist, for his contributions to the development of marine microbiology].

Characteristics are as given for the genus. In addition, cells are 0.3–0.5 µm in width and 5–7 µm in length. Colonies are irregularly shaped, flat, with non-entire edges and 3–5 mm in diameter on marine agar 2216. Produces dark yellow to brown non-diffusible pigments. No growth is observed without Na⁺. Growth occurs at 1–8 % NaCl. Flexirubin pigments are formed. Growth occurs at 4–34 °C. Casein, gelatin, starch, DNA and Tweens 20, 40, 60 and 80 are degraded. Does not hydrolyse agar, alginate, urea, chitin or cellulose (CM-cellulose or filter paper). Does not form acid from arabinose, cellobiose, fucose, galactose, glucose, lactose, maltose, melibiose, raffinose, rhamnose, sucrose, xylose, adonitol, dulcitol, glycerol, inositol, mannitol or N-acetylglucosamine. Does not utilize arabinose, glucose, lactose, mannose, sucrose, inositol, mannitol, sorbitol, citrate or malonate as sole sources of carbon and energy. Nitrate reduction is negative. H₂S, indole and acetoin (Voges–Proskauer reaction) are not produced. Susceptible to ampicillin, carbenicillin, lincomycin and oleandomycin. Resistant to benzylpenicillin, gentamicin, kanamycin, neomycin and polymyxin B. The predominant cellular fatty acids are straight-chain unsaturated, branched-chain unsaturated and saturated: i15:0 (19.3–21.1 %), i15:1 (9.8–13 %), i15:0 3-OH (5.5–7.5 %), i17:1ω9c (9.3–10.6 %), i17:0 3-OH (21–29.5 %) and summed feature 3 (7–8.4 %; comprising i15:0 2-OH and/or 16:1ω7c fatty acids). G + C content of the DNA is 31.6–32.5 mol%.

The type strain, KMM 6020^T (=KCTC 12285^T=LMG 22569^T), was isolated from a sea-water sample collected in Amursky Bay, Gulf of Peter the Great, Sea of Japan.

Description of *Stanierella* gen. nov.

Stanierella [Sta'ni.er.el.la. L. dim. ending -ella; N.L. fem. n. *Stanierella* named in honour of the famous Canadian microbiologist Roger Y. Stanier (1916–1982), for his important contributions to the development of marine microbiology and the taxonomy of the *Cytophaga*-like bacteria].

Rod-shaped cells, non-motile. Gram-negative. Do not form endospores. Strictly aerobic. Produces non-diffusible pigments. No flexirubins are formed. Chemo-organotroph. Cytochrome oxidase- and alkaline phosphatase-positive; catalase-negative. The main lipoquinone is MK-6. 16S rRNA gene sequence analysis indicates the genus *Stanierella* is a

member of the family *Flavobacteriaceae*, phylum 'Bacteroidetes'. The type species is *Stanierella latercula*.

Description of *Stanierella latercula* comb. nov.

Stanierella latercula (la.ter'cu.la. L. masc. n. *laterculus* a small brick; N.L. fem. adj. *latercula* brick-like, brick-red colour).

Basonym: *Cytophaga latercula* Lewin 1969.

The description is as given for the genus and by Reichenbach (1989), with the addition that it is β -galactosidase-positive. Degrades casein, DNA and Tweens 20, 40 and 80, but not urea or cellulose (CM-cellulose or filter paper). Does not form acid from L-arabinose, D-cellobiose, L-fucose, D-galactose, D-glucose, D-lactose, D-maltose, D-melibiose, L- raffinose, L-rhamnose, D-sucrose, DL-xylose, adonitol, dulcitol, glycerol, inositol, mannitol or N-acetylglucosamine. Growth occurs at 4–34 °C and at 1–5 % NaCl. Susceptible to ampicillin, lincomycin, oleandomycin and streptomycin. Resistant to benzylpenicillin, carbenicillin, gentamicin, kanamycin, neomycin and polymyxin B. The predominant cellular fatty acids are straight-chain saturated, branched-chain saturated and unsaturated fatty acids: i15:0 (18.2 %), i15:1w10c (6.7 %), 15:0 (5.4 %), i15:0 3-OH (7.1 %), i17:1w7c (11.6 %) and i17:0 3-OH (34.7 %) (Bowman *et al.*, 1998). G+C content of the DNA is 34 mol%.

The type strain, CIP 104806^T (=ATCC 23177^T=NCIMB 1399^T=LMG 1343^T), was isolated from the outflow of a marine aquarium in La Jolla, CA, USA.

Acknowledgements

This research was supported by grants of the Federal Agency for Sciences and Innovations of the Ministry for Education and Sciences of the Russian Federation no. 2-2.16, Russian Foundation for Basic Research no. 05-04-48211 and Program of Fundamental Investigations of the Presidium of the Russian Academy of Sciences 'Molecular and Cell Biology'. S. B. K. and K. S. B. acknowledge support from the KRIBB Research Initiative Program.

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