Pibocella ponti gen. nov., sp. nov., a novel marine bacterium of the family *Flavobacteriaceae* isolated from the green alga *Acrosiphonia sonderi*

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A marine, heterotrophic, Gram-negative, aerobic, yellow-pigmented, bacterium that was motile by gliding, isolated from the green alga *Acrosiphonia sonderi*, was studied by polyphasic taxonomic methods. 16S rRNA gene sequence analysis indicated that strain KMM 6031^T formed a distinct lineage within the family *Flavobacteriaceae*. On the basis of phenotypic, chemotaxonomic, genotypic and phylogenetic analyses, the novel bacterium was classified as *Pibocella ponti* gen. nov., sp. nov. The type strain is KMM 6031^T (=KCTC 12262^T=NBRC 100591^T=LMG 22573^T).

The bacteria belonging to the family *Flavobacteriaceae* are one of the dominant groups of microbial populations inhabiting shallow marine environments and Antarctic meromictic lakes of marine origin (Bowman *et al.*, 1997; Glöckner *et al.*, 1999; Bano & Hollibaugh, 2002; Kirchman, 2002; Van Trappen *et al.*, 2002). Among flavobacteria, there are both halotolerant and moderately halophilic micro-organisms. The representatives of the genera *Chryseobacterium*, *Flavobacterium*, *Formosa* and *Gillisia* grow in the absence of NaCl or sea water in the nutrient medium (Vandamme *et al.*, 1994; Bernardet *et al.*, 1996; Ivanova *et al.*, 2004; Van Trappen *et al.*, 2004). However, the majority of members of the family *Flavobacteriaceae* require Na⁺ ions for growth (Bernardet *et al.*, 2002).

During investigation of the taxonomic diversity of the microbial population of the common green alga *Acrosiphonia sonderi* inhabiting the Sea of Japan, a novel moderately halophilic bacterium was isolated. Phylogenetic analysis based on 16S rRNA gene sequencing, supported by polyphasic taxonomic study, revealed that strain KMM 6031^T is

a member of the family *Flavobacteriaceae* and represents a new genus and species, for which the name *Pibocella ponti* gen. nov., sp. nov. is proposed.

The strain KMM 6031^T was isolated from a sample of the green alga *Acrosiphonia sonderi* collected in Troitsa Bay, Gulf of Peter the Great, Sea of Japan, during June 2000. For strain isolation, 0.1 ml homogenates of algal fronds were transferred onto plates of marine agar 2216. After primary isolation and purification, 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 previous procedures (Kim *et al.*, 1998). The sequence data obtained were aligned together with those of representative members of the family *Flavobacteriaceae* by using PHYDIT version 3.2 (<http://plaza.snu.ac.kr/~jchun/phydit/>). Phylogenetic trees were inferred by using suitable programs of the PHYLIP package (Felsenstein, 1993). Phylogenetic distances were calculated from the models of Kimura (1980) and the trees were constructed on the basis of the neighbour-joining (Saitou & Nei, 1987), least-squares (Fitch & Margoliash, 1967) and maximum-likelihood (Felsenstein, 1993) algorithms. Bootstrap analysis was performed with 1000 resampled datasets, using SEQBOOT and CONSENSE programs of the PHYLIP package.

A phylogenetic analysis of the almost-complete 16S rRNA

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The GenBank/EMBL/DBJ accession number for the 16S rRNA gene sequence of *Pibocella ponti* KMM 6031^T is AY576654.

Fig. 1. Phylogenetic tree based on the 16S rRNA gene sequences of strain KMM 6031^T and representative members of related genera in the family *Flavobacteriaceae*. The phylogenetic tree was generated by a neighbour-joining method (Saitou & Nei, 1987). Numbers at nodes indicate bootstrap values (%) and asterisks indicate branches that were also recovered in Fitch–Margoliash and maximum-likelihood trees. Bar, 0.01 substitutions per nucleotide position.

gene sequence (1447 nucleotide positions) revealed that strain KMM 6031^T formed a distinct lineage within a cluster group including members of the family *Flavobacteriaceae* such as *Aequorivita*, *Vitellibacter*, *Muricauda*, *Arenibacter*, *Zobellia* and *Maribacter* (Fig. 1). The 16S rRNA gene sequence similarity values of strain KMM 6031^T and its close relatives *Maribacter aquivivus*, *Maribacter orientalis* and *Maribacter ulvicola* were 95.8, 95.7 and 95 %, respectively. The low levels of sequence similarity of the strain tested with the other members of the family *Flavobacteriaceae* described to date (88.9–93 %) clearly demonstrate that the bacterium isolated in this study represents a new genus.

The DNA was extracted following the method of Marmur (1961) and the G+C content of the DNA (mol%) was determined by the thermal denaturation method (Marmur & Doty, 1962). The DNA G+C content of strain KMM 6031^T was 35.5 mol%.

The analysis of fatty acid methyl esters was carried out according to the standard protocol of the Microbial Identification System (Microbial ID). Isoprenoid quinones were extracted from lyophilized cells and analysed as described by Akagawa-Matsushita *et al.* (1992). Isoprenoid quinone composition was characterized by HPLC (Shimadzu instruments) using a reverse-phase type Zorbax ODS column (250 × 4.6 mm) and acetonitrile/2-propanol (65:35, v/v) as a mobile phase at a flow rate of 0.5 ml min⁻¹. The column was kept at 40 °C. Menaquinones were detected by monitoring absorbance at 270 nm and were identified by comparison with known quinones from reference strain *Salgentibacter salegens* DSM 5424^T.

The predominant cellular fatty acids of KMM 6031^T were branched-chain saturated and unsaturated, namely i-15:0

Table 1. Whole-cell fatty acid profiles (percentage content) of *Pibocella ponti* gen. nov., sp. nov. KMM 6031^T and *Maribacter* species

Strains: 1, *Pibocella ponti* KMM 6031^T; 2, *Maribacter sedimenticola* KMM 3903^T; 3, *Maribacter aquivivus* KMM 3949^T; 4, *Maribacter ulvicola* KMM 3951^T; 5, *Maribacter orientalis* KMM 3947^T. Data from Nedashkovskaya *et al.* (2004a) and this study. Values over 5 % are in bold; –, not detected.

Fatty acid	1	2	3	4	5
13:1	0.1	0.7	1.1	1.1	0.3
i-14:0	1.0	–	–	–	–
14:0	0.2	0.5	1.0	0.9	0.5
14:1ω5	–	–	1.0	0.9	–
i-15:0	8.7	20.5	12.3	13.6	10.6
a-15:0	5.4	1.2	1.3	1.9	2.3
i-15:1	11.7	16.9	13.6	18.9	10.1
a-15:1	2.1	–	–	–	–
15:0	4.2	6.3	14.5	8.1	12.3
15:1ω6c	1.5	1.7	4.8	1.6	2.5
i-16:0	12.1	1.1	0.7	0.3	0.3
i-16:1	6.2	–	–	–	–
16:0	1.0	1.0	0.5	1.0	1.2
Summed feature 3*	11.4	5.8	12.9	12.2	11.4
i-17:1ω5c	–	–	1.4	1.2	–
i-17:1ω9c	5.2	2.3	2.2	2.2	4.0
a-17:1ω9c	2.3	–	–	–	–
17:1ω6c	4.7	0.5	1.7	0.5	1.3
i-15:0 3-OH	0.9	5.4	3.2	4.1	2.9
15:0 3-OH	–	2.4	2.3	1.5	1.5
15:0 2-OH	1.8	–	–	–	–
i-16:0 3-OH	5.9	1.7	2.5	1.7	2.1
16:0 3-OH	1.0	2.2	2.9	3.7	3.0
i-17:0 3-OH	5.6	20.4	11.6	14.5	18.8
17:0 2-OH	2.8	–	–	–	–
i-18:1	–	–	–	–	2.4
Unknown	5.5	7.9	10.2	10.3	5.9

*Summed feature 3 consists of 16:1ω7c and/or i-15:0 2-OH.

(8.7 %), a-15:0 (5.4 %), i-15:1 (11.7 %), i-16:1 (6.2 %), i-16:0 (12.1 %), i-17:1ω9c (5.2 %), i-16:0 3-OH (5.9 %) and i-17:0 3-OH (5.6 %) fatty acids (Table 1). The major respiratory quinone is MK-6.

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

The physiological and biochemical characteristics of strain KMM 6031^T are listed in the species description and Table 2. The phenotypic features that separate the strain studied from close relatives of the family *Flavobacteriaceae* are shown in Table 2. The results of phenotypic examination demonstrated that the strain studied has many traits in common with *Maribacter* species. However, strain KMM

Table 2. Differential characteristics of *Pibocella* gen. nov. and other related genera of the family *Flavobacteriaceae*

Data from Barbeyron *et al.* (2001), Bruns *et al.* (2001), Ivanova *et al.* (2001), Bowman & Nichols (2002), Nedashkovskaya *et al.* (2003b, c, 2004a, b, c) and this study. +, Positive; –, negative; v, variable; ND, not determined. Members of all genera require Na⁺ or sea water for growth.

Characteristic	<i>Pibocella</i>	<i>Maribacter</i>	<i>Zobellia</i>	<i>Arenibacter</i>	<i>Muricauda</i>	<i>Vitellibacter</i>
Reaction to oxygen*	A	A	A	A	F	A
Oxidase/catalase	+/+	+/+	+/+	+/+	+/-	+/+
Gliding motility	+	+	+	–	–	–
Flexirubin	–	–	+	–	–	+
Growth at 37 °C	–	v	v	+	+	+
Growth at 12 % NaCl	+	–	–	–	–	–
Acid formation from carbohydrates	+	v	+	+	ND	–
Hydrolysis of:						
Agar	–	v	+	–	–	–
Casein	+	–	+	–	ND	+
Gelatin	+	v	+	v	–	+
Starch	+	v	+	–	–	–
DNA	–	v	+	+	ND	+
Urea	–	–	–	v	ND	–
Nitrate reduction	–	v	+	+	–	–
DNA G+C content (mol%)	35.5	35–39	42–43	37–40	41	41

*A, Aerobic; F, facultatively anaerobic.

6031^T grew at 12 % NaCl and degraded casein, in contrast to *Maribacter* species. Significant differences in the cellular fatty acid compositions of the strain studied and the type strains of the genus *Maribacter* were found (Table 1). For example, fatty acids a-15:1, i-16:1, a-17:1 ω 9c, 15:0 2-OH and 17:0 2-OH are present in KMM 6031^T (2.1, 6.2, 2.3, 1.8 and 2.8 %, respectively), but are absent in *Maribacter* species. The fatty acids i-16:0 and 17:1 ω 6c were present at significant levels in the cell extract of KMM 6031^T (12.1 and 4.7 %, respectively), but are only minor components in type strains of *Maribacter* species (0.3–1.1 and 0.5–1.7 %, respectively). The hydroxy fatty acid i-15:0 3-OH was only found in minor quantities in the strain KMM 6031^T (0.9 %), while in *Maribacter* species this component was more abundant, present at 2.9–5.4 %. In addition, 15:0 3-OH, present at 1.5–2.4 % in *Maribacter* type strains, was not detected in KMM 6031^T.

It is therefore evident from phylogenetic distinctness in combination with significant differences in cellular fatty acid composition and phenotypic findings, that the strain studied should be differentiated from its nearest neighbours *Maribacter aquivivus*, *Maribacter orientalis* and *Maribacter ulvicola*.

Thus, the results of the polyphasic analysis presented in this work demonstrate that the bacterium studied could not be assigned to any of the currently described taxa of the family *Flavobacteriaceae* and support the placement of strain KMM 6031^T in a new genus, *Pibocella* gen. nov., as *Pibocella ponti* sp. nov.

Description of *Pibocella* gen. nov.

Pibocella [Pi.bo.cel'la. N.L. fem. n. *Pibocella* arbitrary name, derived from the acronym PIBOC (Pacific Institute of Bioorganic Chemistry, FEB RAS), where the type species was first isolated and examined].

Rod-shaped cells. Gram-negative. Do not form endospores. Motile by gliding. Strictly aerobic. Produce non-diffusible yellow–orange pigments. No flexirubins are formed. Chemo-organotrophs. Cytochrome oxidase-, catalase- and alkaline phosphatase-positive. The major respiratory quinone is MK-6. The main cellular fatty acids are straight-chain unsaturated and branched-chain unsaturated fatty acids i-15:0, a-15:0, i-15:1, i-16:1, i-16:0, i-16:0 3-OH, i-17:1 ω 9c, i-17:0 3-OH and summed feature 3, consisting of i15:0 2-OH and/or 16:1 ω 7c. As determined by 16S rRNA gene sequence analysis, the genus *Pibocella* is a member of the family *Flavobacteriaceae*. The type species is *Pibocella ponti*.

Description of *Pibocella ponti* sp. nov.

Pibocella ponti (pon'ti. L. gen. n. *ponti* of the sea, a sea dweller).

Main characteristics are as given for the genus. In addition, cells range from 0.4 to 0.5 μ m in width and from 1.6 to 2.3 μ m in length. On marine agar colonies are 2–4 mm in diameter, circular, shiny, convex with entire edges, yellow in colour. Grows at 4–33 °C; optimum temperature for growth is 21–23 °C. Growth occurs at 1–13 % NaCl. Decomposes

gelatin, casein, starch and Tweens 20, 40 and 80; does not hydrolyse agar, DNA, urea, cellulose (CM-cellulose and filter paper) or chitin. Forms acid from D-maltose, but not from L-arabinose, D-cellobiose, L-fucose, D-galactose, D-glucose, D-lactose, D-melibiose, L-raffinose, L-rhamnose, D-sucrose, DL-xylose, citrate, adonitol, dulcitol, glycerol, inositol or mannitol. Utilizes L-arabinose, D-glucose, D-mannose and D-sucrose, but not D-lactose, mannitol, inositol, sorbitol, malonate or citrate. Nitrate is not reduced. Indole, H₂S and acetoin (Voges–Proskauer reaction) production are negative. Susceptible to ampicillin, carbenicillin, lincomycin, oleandomycin, streptomycin and tetracycline; resistant to benzylpenicillin, gentamicin, kanamycin, neomycin and polymyxin B. The predominant cellular fatty acids of KMM 6031^T are branched-chain saturated and unsaturated, namely i-15:0 (8.7%), a-15:0 (5.4%), i-15:1 (11.7%), i-16:1 (6.2%), i-16:0 (12.1%), i-17:1ω9c (5.2%), i-16:0 3-OH (5.9%), i-17:0 3-OH (5.6%) and summed feature 3 (11.4%), consisting of i-15:0 2-OH and/or 16:1ω7c. The major respiratory quinone is MK-6. The G+C content of the DNA is 35.5 mol%.

The type strain is KMM 6031^T (=KCTC 12262^T=NBRC 100591^T=LMG 22573^T), isolated from the green alga *Acrosiphonia sonderi* collected in Troitsa Bay, Gulf of Peter the Great, Sea of Japan.

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References

- Akagawa-Matsushita, M., Itoh, T., Katayama, Y., Kuraishi, H. & Yamasato, K. (1992). Isoprenoid quinone composition of some marine *Alteromonas*, *Marinomonas*, *Deleya*, *Pseudomonas* and *Shewanella* species. *J Gen Microbiol* **138**, 2275–2281.
- Bano, N. & Hollibaugh, J. (2002). Phylogenetic composition of bacterioplankton assemblages from the Arctic Ocean. *Appl Environ Microbiol* **68**, 505–518.
- Barbeyron, T., L'Haridon, S., Corre, E., Kloareg, B. & Potin, P. (2001). *Zobellia galactanovorans* gen. nov., sp. nov., a marine species of *Flavobacteriaceae* isolated from red alga, and classification of [*Cytophaga*] *uliginosa* (ZoBell and Upham 1944) Reichenbach 1989 as *Zobellia uliginosa* gen. nov., comb. nov. *Int J Syst Evol Microbiol* **51**, 985–997.
- Bernardet, J.-F., Segers, P., Vancanneyt, M., Berthe, F., Kersters, K. & Vandamme, P. (1996). Cutting a Gordian knot: emended classification and description of the genus *Flavobacterium*, emended description of the family *Flavobacteriaceae*, and proposal of *Flavobacterium hydatidis* nom. nov. (basonym *Cytophaga aquatilis* Strohl and Tait 1978). *Int J Syst Bacteriol* **46**, 128–148.
- Bernardet, J.-F., Nakagawa, Y. & Holmes, B. (2002). Proposed minimal standards for describing new taxa of the family *Flavobacteriaceae* and emended description of the family. *Int J Syst Evol Microbiol* **52**, 1049–1070.
- Bowman, J. P. (2000). Description of *Cellulophaga algicola* sp. nov., isolated from the surfaces of Antarctic algae, and reclassification of *Cytophaga uliginosa* (ZoBell and Upham 1944) Reichenbach 1989 as *Cellulophaga uliginosa* comb. nov. *Int J Syst Evol Microbiol* **50**, 1861–1868.
- Bowman, J. P. & Nichols, D. S. (2002). *Aequorivita* gen. nov., a member of the family *Flavobacteriaceae* isolated from terrestrial and marine Antarctic habitats. *Int J Syst Evol Microbiol* **52**, 1533–1541.
- Bowman, J. P., McCammon, S. A., Brown, M. V., Nichols, D. S. & McMeekin, T. A. (1997). Diversity and association of psychrophilic bacteria in Antarctic sea ice. *Appl Environ Microbiol* **63**, 3068–3078.
- Bruns, A., Rohde, M. & Berthe-Corti, L. (2001). *Muricauda ruestringensis* gen. nov., sp. nov., a facultatively anaerobic, appendaged bacterium from German North Sea intertidal sediment. *Int J Syst Evol Microbiol* **51**, 1997–2006.
- Felsenstein, J. (1993). PHYLIP (phylogenetic inference package), version 3.5c. Department of Genetics, University of Washington, Seattle, USA.
- Fitch, W. M. & Margoliash, E. (1967). Construction of phylogenetic trees: a method based on mutation distances as estimated from cytochrome c sequences is of general applicability. *Science* **155**, 279–284.
- Glöckner, F. O., Fuchs, B. M. & Amann, R. (1999). Bacterioplankton compositions of lakes and oceans: a first comparison based on fluorescence in situ hybridization. *Appl Environ Microbiol* **65**, 3721–3726.
- Ivanova, E. P., Nedashkovskaya, O. I., Chun, J. & 7 other authors (2001). *Arenibacter* gen. nov., a new genus of the family *Flavobacteriaceae* and description of a new species, *Arenibacter latericius* sp. nov. *Int J Syst Evol Microbiol* **51**, 1987–1995.
- Ivanova, E. P., Alexeeva, Y. A., Flavier, S., Wright, J. P., Zhukova, N. V., Gorshkova, N. M., Mikhailov, V. V., Nicolau, D. V. & Christen, R. (2004). *Formosa algae* gen. nov., sp. nov., a novel member of the family *Flavobacteriaceae*. *Int J Syst Evol Microbiol* **54**, 705–711.
- Kim, S. B., Falconer, C., Williams, E. & Goodfellow, M. (1998). *Streptomyces thermocarboxydovorans* sp. nov. and *Streptomyces thermocarboxydus* sp. nov., two moderately thermophilic carboxy-dotrophic species isolated from soil. *Int J Syst Bacteriol* **48**, 59–68.
- Kimura, M. (1980). A simple method for estimating evolutionary rates of base substitutions through comparative studies of nucleotide sequences. *J Mol Evol* **16**, 111–120.
- Kirchman, D. I. (2002). The ecology of *Cytophaga-Flavobacteria* in aquatic environments. *FEMS Microbiol Ecol* **39**, 91–100.
- Marmur, J. (1961). A procedure for the isolation of deoxyribonucleic acid from microorganisms. *J Mol Biol* **3**, 208–218.
- Marmur, J. & Doty, P. (1962). Determination of the base composition of deoxyribonucleic acid from its thermal denaturation temperature. *J Mol Biol* **5**, 109–118.
- Nedashkovskaya, O. I., Suzuki, M., Vysotskii, M. V. & Mikhailov, V. V. (2003a). *Reichenbachia agariperforans* gen. nov., sp. nov., a novel marine bacterium in the phylum *Cytophaga-Flavobacterium-Bacteroides*. *Int J Syst Evol Microbiol* **53**, 81–85.
- Nedashkovskaya, O. I., Suzuki, M., Vysotskii, M. V. & Mikhailov, V. V. (2003b). *Vitellibacter vladivostokensis* gen. nov., sp. nov., a new member of the phylum *Cytophaga-Flavobacterium-Bacteroides*. *Int J Syst Evol Microbiol* **53**, 1281–1286.
- Nedashkovskaya, O. I., Suzuki, M., Vysotskii, M. V. & Mikhailov, V. V. (2003c). *Arenibacter troitsensis* sp. nov., isolated from marine bottom sediment. *Int J Syst Evol Microbiol* **53**, 1287–1290.

- Nedashkovskaya, O. I., Kim, S. B., Han, S. K. & 7 other authors (2004a).** *Maribacter* gen. nov., a new member of the family *Flavobacteriaceae*, isolated from marine habitats, containing the species *Maribacter sedimenticola* sp. nov., *Maribacter aquivivus* sp. nov., *Maribacter orientalis* sp. nov. and *Maribacter ulvicola* sp. nov. *Int J Syst Evol Microbiol* **54**, 1017–1023.
- Nedashkovskaya, O. I., Kim, S. B., Han, S. K., Lysenko, A. M., Mikhailov, V. V. & Bae, K. S. (2004b).** *Arenibacter certesii* sp. nov., a novel marine bacterium isolated from the green alga *Ulva fenestrata*. *Int J Syst Evol Microbiol* **54**, 1173–1176.
- Nedashkovskaya, O. I., Suzuki, M., Vancanneyt, M., Cleenwerck, I., Lysenko, A. M., Mikhailov, V. V. & Swings, J. (2004c).** *Zobellia amurskyensis* sp. nov., *Zobellia laminariae* sp. nov. and *Zobellia russellii* sp. nov., novel marine bacteria of the family *Flavobacteriaceae*. *Int J Syst Evol Microbiol* **54**, 1643–1648.
- Saitou, N. & Nei, M. (1987).** The neighbor-joining method: a new method for reconstructing phylogenetic trees. *Mol Biol Evol* **4**, 406–425.
- Vandamme, P., Bernardet, J.-F., Segers, P., Kersters, K. & Holmes, B. (1994).** New perspectives in the classification of the flavobacteria: description of *Chryseobacterium* gen. nov., *Bergeyella* gen. nov. and *Empedobacter* nom. rev. *Int J Syst Bacteriol* **44**, 827–831.
- Van Trappen, S., Mergaert, J., Van Eygen, S., Dawyndt, P., Cnockaert, M. C. & Swings, J. (2002).** Diversity of 746 heterotrophic bacteria isolated from microbial mats from ten Antarctic lakes. *Syst Appl Microbiol* **25**, 603–610.
- Van Trappen, S., Vandecandelaere, I., Mergaert, J. & Swings, J. (2004).** *Gillisia limnaea* gen. nov., sp. nov., a new member of the family *Flavobacteriaceae* isolated from a microbial mat in Lake Fryxell, Antarctica. *Int J Syst Evol Microbiol* **54**, 445–448.