Flavobacterium chuncheonense sp. nov. and Flavobacterium luteum sp. nov., isolated from a freshwater lake

Miri Park, Gi Gyun Nam, Suhyun Kim, Hyoung Tae Jeon, Yochan Joung and Jang-Cheon Cho

Abstract

Two Gram-staining-negative, orange coloured, non-motile, rod-shaped bacterial strains, designated strains IMCC26013T and IMCC26026T, were isolated from a freshwater sample collected from Lake Soyang in Korea. The 16S rRNA gene-based phylogenetic analyses showed that both strains belonged to the genus Flavobacterium and that strains IMCC26013T and IMCC26026T were most closely related to Flavobacterium psychrophilum (96.5%) and Flavobacterium myungsense (97.7%), respectively. DNA G+C contents of strains IMCC26013T and IMCC26026T were 37.8 and 33.7 mol%, respectively. DNA–DNA relatedness between strain IMCC26026T and F. myungsense HMD1033T was 56.4%, showing a novel species status of strain IMCC26026T. Major fatty acid constituents (>10%) of strain IMCC26013T were iso-C15:0 G, C15:1 ω6c, C17:1 ω7c and summed feature 3 (C16:1 ω5c and/or C16:1 ω7c) and those of strain IMCC26026T were iso-C15:0 anteiso, anteiso-C15:0 and summed feature 3. Respiratory quinone detected in the two strains was MK-6. Both strains contained phosphatidylethanolamine as a major polar lipid. On the basis of these results, strains IMCC26013T and IMCC26026T were considered to represent novel species in the genus Flavobacterium, for which the names Flavobacterium chuncheonense (type strain IMCC26013=KCTC 52573T=NBRC 112526T), and Flavobacterium luteum (type strain IMCC26026=KCTC 52572T=NBRC 112527T) are proposed, respectively.

The initial liquid cultures of strains IMCC26013T and IMCC26026T were isolated from a freshwater sample collected from a depth of 1 m at Lake Soyang, Chuncheon, Korea (37° 56’ 51” N, 127° 49’ 8” E), using the high-throughput culturing method based on dilution-to-extinction [21, 22]. The freshwater sample was diluted to 5 cells ml-1 in a liquid medium (0.2 µm-filtered and autoclaved lake water) supplemented with NH4Cl (10 µM), KH2PO4 (10 µM), pyruvic acid (50 µM), each 5 µM of D-glucose, D-ribose, N-acetyl-D-glucosamine and methyl alcohol, and a 10−4 dilution of a vitamin mixture [23]. The microtiter plates containing dilution-to-extinction liquid cultures were incubated at 15 °C for 4 weeks and growth-positive cultures were spread onto R2A agar (BD Diagnostics). Strains IMCC26013T and IMCC26026T were isolated as single colonies after incubating the agar plates at 15 °C for 7 days.

The 16S rRNA genes of strains IMCC26013T and IMCC26026T were amplified with the universal primers 27F and 1492R and sequenced by the standard chain-termination method. The resultant almost-complete 16S rRNA gene sequences of strains IMCC26013T (1414 nt) and IMCC26026T (1422 nt) were obtained and sequence similarities of both strains to closely related species were analyzed using the EzTaxon-e server implemented in the EzBioCloud [24]. For phylogenetic analyses, the 16S rRNA gene sequences of IMCC26013T and IMCC26026T were aligned using the SILVA Incremental Aligner and imported into the ARB software [25]. Using the pre-aligned 16S rRNA sequences, maximum likelihood (ML) and neighbour-joining (NJ) trees were constructed. The best ML tree was selected from 1000 bootstrap replications. Cladograms of the two trees were highly congruent, with bootstrap support values of ≥70% for all branches, and were rooted with Flavobacterium sp. IMCC26019 and Flavobacterium myungsense HMD1033T (KX505860).

One supplementary table and two supplementary figures are available with the online Supplementary Material.

Author affiliation: Department of Biological Sciences, Inha University, Incheon 22212, Republic of Korea.
*Correspondence: Jang-Cheon Cho, choc@inha.ac.kr
Keywords: Flavobacterium; freshwater; taxonomy; new species.
Abbreviations: MA, marine broth 2216 agar; NA, nutrient agar; PCA, plate count agar; TSA, tryptic soy agar.
The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of strains IMCC26013T and IMCC26026T are KX505859 and KX505860, respectively.

DOI 10.1099/ijsem.0.002304
gene sequences exported from the ARB, phylogenetic trees were generated based on the neighbour-joining method [26] using the Jukes-Cantor correction, maximum-likelihood method [27] using the Tamura-Nei model and maximum-parsimony method [28] using Tree-Bisection-Reconnection (TBR) in the MEGA6 program [29]. The robustness of the phylogenetic trees was confirmed by bootstrap analyses based on 1000 random replicates.

The 16S rRNA gene sequence similarity and phylogenetic analyses showed that strains IMCC26013\(^T\) and IMCC26026\(^T\) belonged to the genus Flavobacterium (Fig. 1). Strain IMCC26013\(^T\) was closely related to F. psychrophilum IFO 15942\(^T\) (96.5\%) and F. swingsii WB2.3-68\(^T\) (96.3\%) while strain IMCC26026\(^T\) was related most closely to F. myungsuense HMD 1033\(^T\) (97.7\%). All phylogenetic trees generated based on 16S rRNA gene sequences indicated that strains IMCC26013\(^T\) and IMCC26026\(^T\) were placed within the clade of the genus Flavobacterium. Strain IMCC26013\(^T\) formed a robust clade with F. psychrophilum IFO 15942\(^T\) and F. swingsii WB2.3-68\(^T\). Strain IMCC26026\(^T\) formed a robust clade with F. myungsuense HMD 1033\(^T\) and also formed a larger clade with F. flevense and F. oryzae. These phylogenetic relationships were well resolved in all phylogenetic trees (Fig. 1).

As the 16S rRNA gene sequence similarity between strain IMCC26026\(^T\) and F. myungsuense HMD 1033\(^T\) exceeded 97\%, DNA–DNA hybridization method was applied to measure genomic DNA relatedness. Membrane based slot-blot hybridization was performed using DIG-High Prime DNA Labeling and Detection Starter kit II (Roche) using the genomic DNA extracted with DNeasy blood and tissue (Qiagen). DNA–DNA relatedness was calculated from the relative signal intensities of triplicate slot-blots estimated by densitometric analysis (LAS-3000, Fujifilm). The level of DNA–DNA relatedness between strain IMCC26026\(^T\) and F. myungsuense HMD 1033\(^T\) was 39.9±1.9\% (IMCC26026\(^T\) as the probe) and 58.3±2.5\% (HMD 1033\(^T\) as the probe), which was below 70\% recommended threshold value for the bacterial species demarcation [30].

Since the results of phylogenetic analysis and genomic DNA relatedness showed that strain IMCC26013\(^T\) and strain IMCC26026\(^T\) represented each genomic species separated from other Flavobacterium species, type strains of closely

![Phylogenetic Tree](image)

**Fig. 1.** Neighbour-joining phylogenetic tree based on 16S rRNA gene sequences showing the positions of strains IMCC26013\(^T\) and IMCC26026\(^T\) among the related species of the genus Flavobacterium. Bootstrap values (expressed as percentages of 1000 replications) over 70\% are shown at nodes for neighbour-joining, maximum-parsimony and maximum-likelihood methods, respectively. Filled circles indicate that the corresponding nodes were recovered by all treeing methods. Dokdonia donghaensis DSW-1\(^T\) (DQ003276) was used as an outgroup. Bar, 0.01 substitutions per nucleotide position.
related species were chosen for comparative phenotypic characterization. *F. psychrophilum* KACC 14825T, *F. swing-
siit* DSM 21789T, *F. myungsuense* HMD1033T, *F. flevense* KACC 11416T and *F. oryzae* KCTC 33240T were obtained either from the Korean Agricultural Culture Collection (KACC), German Collection of Microorganisms and Cell Cultures (DSMZ) and Korean Collection for Type Cultures (KCTC) or the original isolator and used as reference strains for the following phenotypic characterization.

For phenotypic characterization, strains IMCC26013T and IMCC26026T were routinely grown on R2A agar medium for 3 days at 25 °C and at 20 °C, respectively. Gram staining was performed using a Gram-staining kit (bioMérieux) and cell morphology was examined by transmission electron microscopy (TEM; CM200, Philips) using the cells stained with 2.0 % uranyl acetate. Gliding motility was examined by hanging drop method with phase-contrast microscopy (Nikon 80i). Cellular growth was tested on several bacteriological media (BD Diagnostics): R2A agar, nutrient agar (NA), plate count agar (PCA), tryptic soy agar (TSA), and marine broth 2216 agar (MA). Growth at different temperatures was investigated at 4, 10, 15, 20, 25, 30, 37 and 42 °C in R2A broth and salt tolerance was tested in R2A broth supplemented with 0, 0.5, 1.0, 1.5, 2.0, 2.5 and 3.0 % (w/v) NaCl. The pH range for cellular growth was monitored in R2A broth adjusted to pH 5.0–10.0 using the following buffer systems: MES, MOPS, HEPES and CHES buffer. Growth under anaerobic conditions was investigated for 4 weeks using the GasPak EZ anaerobe pouch system with indicator (BD Diagnostics). Catalase activity was determined using 3 % (v/v) H2O2 solution (Sigma-Aldrich) and oxidase activity was determined using the Kovac’s reagent (bioMérieux). Production of flexirubin-type pigment was investigated by using 20 % KOH solution. Hydrolysis of the following macromolecules was determined by the observation of clear zones around colonies after 7 days of incubation: 1.0 % (w/v) Tween 20, 1.0 % (w/v) Tween 80, 1.0 % (w/v) CM-cellulose and 1.0 % (w/v) colloidal chitin. DNase test agar (BD Diagnostics) was used for determining DNA degradation activity and Triple-sugar iron agar (BD Diagnostics) was applied for the test of H2S production. For other biochemical tests including carbon source oxidation test, API 20NE, API ZYM strips (bioMérieux) and GN2 microplate (Biolog) were used according to the manufacturer’s instructions. Characteristics of strains IMCC26013T and IMCC26026T are shown in Tables 1 and S1, Fig. S1 (available in the online Supplementary Material) and the species protologues.

The DNA G+C contents of both strains were determined by a thermal denaturation fluorimetric method [31] using SYBR Green I (Invitrogen) and real-time PCR thermocycler (iQ5, Bio-Rad). The DNA G+C contents of strains IMCC26013T and IMCC26026T were 37.8 mol% and 33.7 mol%, respectively that were within the range of 30–52 mol% reported for the genus *Flavobacterium* [6].

Cellular fatty acid methyl ester analysis was performed by a gas chromatography (Agilent 7890 GC) using Sherlock Microbial Identification System version 6.1 (MIDI) with TSBA6 database [32]. For analysis of fatty acid profiles, strains IMCC26013T and IMCC26026T and all reference strains were grown on R2A agar at 25 °C for 3 days. Strains IMCC26013T and IMCC26026T contained iso-C15:0 as one of predominant fatty acids (>5%) in common with other related species of the genus *Flavobacterium* (Table 2). In addition, iso-C15:1 G, C15:1ω6c, C17:1ω6c and summed feature 3 (C16:1ω7c and/or C16:1ω6c) were major fatty acids of strain IMCC26013T and anteiso-C15:0 and summed feature 3 (comprised C16:1ω6c and/or C16:1ω7c) were major fatty acids of strain IMCC26026T. Fatty acid profiles including higher proportions of C15:1ω7c and C17:1ω6c in strain IMCC26013T and higher proportion of summed feature 3 in strain IMCC26026T clearly differentiated the novel strains from other reference strains.

For respiratory quinone and polar lipid analysis, freeze-dried cells of strains IMCC26013T and IMCC26026T grown on R2A for 3 days were used. Respiratory isoprenoid quinones were extracted by a thin-layer chromatography (TLC) according to Minnikin et al. [33] and analyzed using TLC system [34]. Both strains contained menaquinone-6 (MK-6) as the sole respiratory quinone that was the major quinone detected in the genus *Flavobacterium*. For two dimensional TLC of polar lipid analysis, TLC on silica gel 60 F254 plates (Merck) were developed with chloroform/methanol/water (65 : 25 : 3.8, by vol.) for the first dimension and chloroform/acetic acid/methanol/water (40 : 7.5 : 6 : 1.8, by vol.) for the second dimension. Polar lipids were detected by spraying with molybdatophosphoric acid, ninhydrin, molybdenum blue, α-naphthol and Dragendorff’s solution. The major polar lipids of strain IMCC26013T were phosphatidylethanolamine (PE), two unidentified aminolipids and one unidentified lipid, which was similar to those of the genus *Flavobacterium* (Fig. S2). Strain IMCC26026T differed from strain IMCC26013T only by the absence of one unidentified aminolipid (Fig. S2).

On the basis of 16S rRNA gene phylogeny, DNA G+C contents, polar lipids and respiratory quinone, it was clear that strains IMCC26013T and IMCC26026T belonged to the genus *Flavobacterium*. However, the low 16S rRNA gene sequence similarities, low level of DNA–DNA relatedness and many differential phenotypic characteristics including major fatty acid constituents, macromolecule hydrolysis and enzyme activities confirmed that strains IMCC26013T and IMCC26026T represent two novel species of the genus *Flavobacterium*. Therefore, the names *Flavobacterium chuncheonense* sp. nov. and *Flavobacterium luteum* sp. nov., are proposed for strains IMCC26013T and IMCC26026T, respectively.

**DESCRIPTION OF FLAVOBACTERIUM CHUNCHEONENSE SP. NOV.**

*Flavobacterium chuncheonense* (chun.cheon.en’se. N. L. neut. adj. chuncheonense from Chuncheon city, where the type strain was isolated.)
Table 1. Differential characteristics of IMCC26013T, IMCC26026T and related species in the genus Flavobacterium

Strains: 1, IMCC26013T; 2, IMCC26026T; 3, F. psychrophilum KACC 14825T; 4, F. swingsii DSM 21789T; 5, F. myungsuense HMD 33240T. All data were obtained in this study except for the DNA G+C content of the reference strains [35–37]. All strains are positive for alkaline phosphatase, acid phosphatase and naphthol-AS-BI-phosphohydrolase. All strains are negative for nitrate reduction, indole production, glucose fermentation and arginine dihydrolase; lipase (C14), α-chymotrypsin, β-glucuronidase, α-mannosidase and α-fucosidase; hydrolysis of chitin and Tween 20; and H2S production. +, positive; −, negative.

<table>
<thead>
<tr>
<th>Characteristics</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
</tr>
</thead>
<tbody>
<tr>
<td>Gliding motility</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>+</td>
</tr>
<tr>
<td>Growth on</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>37°C</td>
<td>−</td>
<td>+</td>
<td>−</td>
<td>+</td>
<td>−</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>TSA</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>−</td>
</tr>
<tr>
<td>PCA</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>−</td>
<td>+</td>
<td>−</td>
<td>+</td>
</tr>
<tr>
<td>MA</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>−</td>
<td>+</td>
</tr>
<tr>
<td>NA</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>−</td>
<td>+</td>
</tr>
<tr>
<td>Hydrolysis of:</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Starch</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Aesculin hydrolysis</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Gelatinase</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>−</td>
<td>+</td>
</tr>
<tr>
<td>PNP (β-galactosidase)</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>−</td>
<td>+</td>
</tr>
<tr>
<td>API ZYM</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Esterase (C4)</td>
<td>−</td>
<td>+</td>
<td>−</td>
<td>+</td>
<td>−</td>
<td>+</td>
<td>−</td>
</tr>
<tr>
<td>Esterase lipase (C8)</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>Leucine ary lamidase</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Valine ary lamidase</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Cysteine ary lamidase</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>+</td>
<td>−</td>
</tr>
<tr>
<td>Trypsin</td>
<td>−</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>−</td>
<td>+</td>
</tr>
<tr>
<td>α-Galactosidase</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>−</td>
</tr>
<tr>
<td>β-Galactosidase</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>−</td>
</tr>
<tr>
<td>α-Glucosidase</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>−</td>
</tr>
<tr>
<td>β-Glucosidase</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>−</td>
</tr>
<tr>
<td>N-Acetyl-β-glucosaminidase</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>−</td>
</tr>
<tr>
<td>DNA G+C (mol%)</td>
<td>37.8</td>
<td>33.7</td>
<td>32.5</td>
<td>33.3</td>
<td>32.2</td>
<td>34.9</td>
<td>34.2</td>
</tr>
</tbody>
</table>

Gram-staining-negative, aerobic, non-motile, non-gliding and rod-shaped. Cells are 1.0–1.5 μm in length and 0.3–0.5 μm in width. Colonies are circular, convex, smooth with regular margin and orange-coloured on R2A agar plate grown for 3 days at 25°C. Growth occurs on R2A at 15–30°C (optimum, 25°C), at 0–1.0% NaCl (optimum 0%) and at pH 6–8 (optimum, pH 8) but not on MA, NA, PCA and TSA. Flexirubin-type pigment is absent. Cells are positive for catalase and oxidase activities. Starch and casein are hydrolysed but not Tween 20, Tween 80, CM-cellulose, chitin and DNA. In the API 20NE test, hydrolysis of aesculin is positive but nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis and β-galactosidase activity are negative. In the API ZYM test, positive for alkaline phosphatase, esterase lipase (C8), leucine ary lamidase, valine ary lamidase, acid phosphatase and naphthol-AS-BI-phosphohydrolase, but negative for esterase (C4), lipase (C14), cysteine ary lamidase, trypsin, α-chymotrypsin, α-galactosidase, β-galactosidase, β-glucuronidase, α-glucosidase, β-glucosidase, N-acetyl-β-glucosaminidase, α-mannosidase and α-fucosidase. In carbon source oxidation test (GN2 Microplate; Biolog), the following positive results are observed for: α-cyclodextrin, dextrin, glyco gen, N-acetyl-d-galactosamine, N-acetyl-d-glucosamine, adonitol, d-galactose, α-D-glucose, maltose, α-keto glutaric acid, α-keto valeric acid, D, L-lactic acid, L-alanyl glycine, L-aspartic acid, L-glutamic acid, glycyll-L-glutamic acid, hydroxy-L-proline, L-ornithine, L-proline, inosine and uridine. The respiratory quinone of the type strain is MK-6. The major fatty acids (>10%) are C15:1 ω6c, C17:1 ω6c, iso-
Table 2. Cellular fatty acid composition of IMCC26013 T, IMCC26026 T and related species of the genus Flavobacterium

![Table 2](image)

Strains: 1, IMCC26013 T; 2, IMCC26026 T; 3, F. psychrophilum KACC 14825 T; 4, F. swingsii DSM 21789 T; 5, F. myungsuense HMD 1033 T; 6, F. revente KACC 11418 T; 7, F. oryzae KCTC 33240 T. All data were obtained in this study. Cells of strains IMCC26013 T and IMCC26026 T and reference strains were cultured for 3 days at 25 °C. Fatty acids amounting to less than 1.0 % in all strains are not listed. tr, traces (<1.0 %).

**DESCRIPTION OF FLAVOBACTERIUM LUTEUM SP. NOV.**

*Flavobacterium luteum* (lu’tee.um L. neut. adj. luteum orange coloured).

Gram-staining-negative, aerobic, non-motile, non-gliding and rod-shaped. Cells are 1.2–1.5 μm in length and 0.3–0.5 μm in width. Colonies are circular, smooth and orange-coloured on R2A agar plate grown for 3 days at 20 °C. Growth occurs on R2A at 4–37 °C (optimum, 20 °C), at 0–1.0 % NaCl (optimum 0 %) and at pH 6–8 (optimum, pH 7) but not on MA, NA, PCA and TSA. Flexirubin-type pigments are absent. Cells are positive for catalase and oxidase activities. Starch is hydrolysed but casein, Tween 20, Tween 80, CM-cellulose, chitin and DNA are not hydrolysed. In the API 20NE test, hydrolysis of urea and aesculin are positive but nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, gelatin hydrolysis and β-galactosidase activity are negative. In the API ZYM test, positive for alkaline phosphatase, esterase (C4), esterase lipase (C8), leucine arylamidase, valine arylamidase, trypsin, acid phosphatase and naphthol-AS-BI-phosphohydrolase but negative for lipase (C14), cysteine arylamidase, α-

C15:1 G, 0, and summed feature 3 (C16:1ω6c and/or C16:1ω7c). Major polar lipids are phosphatidylethanolamine, two unknown aminolipids and an unidentified polar lipid. The genomic DNA G+C content is 37.8 mol%.

The type strain, IMCC26013 T (KCTC 52573 T=NBRC 112526 T), was isolated from a freshwater lake (Lake Soyang), Chuncheon, Republic of Korea.
chymotrypsin, α-galactosidase, β-galactosidase, β-glucuronidase, α-glucosidase, β-glucosidase, N-acetyl-β-glucosaminidase, α-mannosidase and α-fucosidase. In carbon source oxidation test (GN2 Microplate; Biolog), the following positive results are observed for: α-cyclodextrin, dextrin, glyco-
gen, D-galactose, α-D-glucose, maltose, D-mannose, sucrose, succinic acid mono-methyl-ester, L-ornithine, L-proline, inosine, uridine and thymidine. The respiratory quinone of the type strain is MK-6. The major fatty acids (≥10%) are iso-C_{15:0} anteiso, anteiso-C_{15:0} and summed feature 3 (C_{16:1}ω6c and/or C_{16:1}ω7c). Major polar lipids are phosphatidylethanol-
olamine, an unknown aminolipid and an unidentified polar lipid. The genomic DNA G+C content is 33.7 mol%.

The type strain, IMCC26026ᵀ (KCTC 52572ᵀ=NBRC 112527ᵀ), was isolated from a freshwater lake (Lake Soyang), Chuncheon, Republic of Korea.

Funding information
This work was supported by the project on survey of indigenous spe-
cies of Korea of the National Institute of Biological Resources (NIBR) under the Ministry of Environment (MOE) and by the Mid-Career Research Program through the National Research Foundation (NRF) funded by the Ministry of Science, ICT, and Future Planning (NRF-
2016R1A2B015142).

Conflicts of interest
The authors declare that there are no conflict of interest.

References
2. Bernardet J-F, Segers P, Vancanneyt M, Berthe F, Kersters K et al. Cutting a Gordian knot: emended classification and descrip-
tions of the type strain, IMCC26026ᵀ, isolated from freshwater, and emended descriptions of Flavobacterium chungangense
sp. nov., isolated from a freshwater reservoir, and emended description of the genus Flavobacterium tructae

Five reasons to publish your next article with a Microbiology Society journal

1. The Microbiology Society is a not-for-profit organization.
2. We offer fast and rigorous peer review – average time to first decision is 4–6 weeks.
3. Our journals have a global readership with subscriptions held in research institutions around the world.
4. 80% of our authors rate our submission process as ‘excellent’ or ‘very good’.
5. Your article will be published on an interactive journal platform with advanced metrics.

Find out more and submit your article at microbiologyresearch.org.