Snuella lapsa gen. nov., sp. nov., isolated from tidal flat sediment

Hana Yi1 and Jongsik Chun1,2

1Institute of Molecular Biology and Genetics, Seoul National University, 599 Kwanak-ro, Kwanak-gu, Seoul 151-742, Republic of Korea
2School of Biological Sciences & Institute of Bioinformatics (BIOMAX), Seoul National University, 599 Kwanak-ro, Kwanak-gu, Seoul 151-742, Republic of Korea

A yellow-coloured, rod-shaped, Gram-reaction-negative, aerobic bacterial strain, designated JC2132T, was isolated from a tidal flat sediment sample from Ganghwa Island, Korea. The isolate required sea salts for growth. Cells produced non-diffusible carotenoid pigments, but flexirubin-type pigments were absent. Gliding motility was observed. Phylogenetic analyses based on 16S rRNA gene sequences showed that strain JC2132T represented a distinct phyletic line that reflected a novel generic status within the family Flavobacteriaceae with relatively low sequence similarities (<95%) to members of other genera with validly published names. The predominant isoprenoid quinone (MK-6) and DNA G+C content (35 mol%) were consistent with assignment of the isolate to the family Flavobacteriaceae, but overall phenotypic traits demonstrated that strain JC2132T was not closely affiliated with any previously described genera. Based on taxonomic data obtained using a polyphasic approach, it is proposed that strain JC2132T represents a novel species in a new genus belonging to the family Flavobacteriaceae, for which the name Snuella lapsa gen. nov., sp. nov. is proposed; the type strain of the type species is JC2132T (=KACC 14152T=JCM 17111T).

The family Flavobacteriaceae, proposed by Reichenbach (1991) and emended by Bernardet et al. (1996, 2002), is one of the major groups in the phylum ‘Bacteroidetes’ and currently accommodates 87 genera with validly published names. It is known that bacteria belonging to this family have diverse ecological niches and dynamic physiological features even within a genus (Bernardet & Nakagawa, 2006). A yellow-pigmented flavobacterial strain, designated JC2132T, was isolated from tidal flat sediment and was the subject of a taxonomic study according to the minimal standards for describing new taxa of the family Flavobacteriaceae (Bernardet et al., 2002). On the basis of evidence obtained using a polyphasic approach, the isolate represents a novel species in a new genus in the family Flavobacteriaceae.

Strain JC2132T was isolated from a tidal flat sediment sample of Ganghwa Island, Korea (37° 35’ 32” N 126° 27’ 25” E), using a standard dilution plating method on marine agar 2216 (MA; Difco). The isolate was routinely cultured on MA and maintained as glycerol suspensions (20%, w/v) at −80°C. Yeosuana aromativorans GW1-T was selected as a reference strain and evaluated under identical experimental conditions to those for strain JC2132T.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain JC2132T is HM475133.
libacter marinus
new genus of the family
Growth at various temperatures (5–50°C)
media including cetrimide agar (Difco), MacConkey agar
and phase-contrast microscopy, respectively. Gliding moti-
lity was observed by direct phase-contrast microscopic
examination of cells initially grown in marine broth 2216
(Difco) at 30°C for 2 days and subsequently incubated
for 16, 48 and 72 h on microscope slides coated with
MA at 30°C for 2 days by transmission electron
microscopy, respectively. The presence of flexirubin-type pigments
was determined by flooding the cell mass taken from agar
plates with 20% (w/v) KOH and confirmed by examining
bathycromatic shift of the absorbance spectrum of ethanol
and alkaline-ethanol extracts of lysed cells (Weeks, 1981).

Standard physiological and biochemical tests were performed
as described previously (Smibert & Krieg, 1994). Hydrolysis of alginic acids (0.5%; Sigma), casein (5% skimmed milk; Difco),
microcrystalline cellulose (0.5%; Sigma), chitin (0.5%; Sigma), egg yolk (0.5%; Oxoid), elastin (0.5%; Sigma), pectin (0.5%; Sigma), starch (0.2%; Difco),
Tween 20 (1%; Sigma), Tween 40 (1%; Junsei), Tween 60 (1%; Junsei) and Tween 80 (1%; Sigma) was tested using
MA as basal medium. Decomposition of adenine (0.5%; Sigma),
hypoxanthine (0.5%; Sigma), L-tyrosine (0.5%; Sigma) and xanthine (0.4%; Sigma) was tested using MA
according to Gordon et al. (1974). Other enzymic activities
were determined using API 20NE, API 20E and API ZYM
kits (bioMérieux). Acid production from carbohydrates
was tested by using API 50CH with CHB/E medium
(bioMérieux) supplemented with half-strength seawater.
API kits were inoculated with a heavy bacterial suspension in
half-strength artificial seawater and data were recorded for
up to five consecutive days.

DNA G+C content was determined by the thermal
denaturation method (Marmur & Doty, 1962). Mena-
quiones were isolated from 3-day-old cells according to
Minnikin et al. (1984) and analysed by HPLC (Waters) as
described by Collins (1985). For fatty acid analysis, strain
JC2132T and the reference strain were grown on MA at 30
and 25°C, respectively, for 2 days. Extraction of fatty acid
methyl esters and their separation by GC were performed
by using the Instant FAME method of the Microbial
Identification System (MIDI) version 6.1 and the RTSBA6
6.10 database. The fatty acids of strain JC2132T were
iso-C15:0 (18.6%), iso-C15:1 G (17.2%), iso-C17:0 3-OH
(16.4%), iso-C15:0 3-OH (8.4%), summed feature 3
(comprising C16:1ω6c and/or C16:1ω7c 8.4%), iso-C16:0
3-OH (5.5%), anteiso-C15:0 (4.9%), summed feature 9
(C16:0 10-methyl and/or iso-C17:1ω9c 3.3%), C15:1ω6c
(2.7%), anteiso-C15:1 (1.7%), C16:0 (1.6%), C17:1ω6c
(1.5±0.3%), C15:0 2-OH (1.3±0.0%), iso-C13:0 (1.2±0.0%),
iso-C14:0 (1.2±0.1%) and C16:0 3-OH (1.1±0.0%).

Results of morphological, cultural, biochemical, physio-
logical and chemotaxonomic tests are presented in the
species description.

Phylogenetic analyses based on 16S rRNA gene sequences
showed that strain JC2132T represents a distinct phyletic
line that reflects novel genus status. Overall phenotypic
traits also demonstrated that strain JC2132T was not closely
affiliated with members of any recognized genera (Table 1).
Thus, based on data obtained in this polyphasic study,
strain JC2132T represents a novel species in a new genus
belonging to the family Flavobacteriaceae, for which the
name Snuella lapsa gen. nov., sp. nov. is proposed.

**Description of Snuella gen. nov.**

*Snuella* (Snu.e’lla. N.L. fem. dim. n. *Snuella* arbitrary name
derived from the acronym of the Seoul National University,
SNU, where this taxon was studied).
Gram-reaction-negative, oxidase- and catalase-positive and aerobic. Cells are rod-shaped with rounded ends and gliding ability. Spores are not formed. Produces non-diffusible carotenoid pigments, but flexirubin-type pigments are absent. Requires sea salts, but not yeast extract for growth. Major isoprenoid quinone is MK-6. Predominant cellular fatty acids are iso-C_{15}:0, iso-C_{15}:1 G and iso-C_{17}:0 3-OH. Maximum absorption peak of pigments is at 452 nm and the next shoulder peak is at 480 nm. A member of the family Flavobacteriaceae, class
**Table 1. Characteristics that differentiate strain JC2132TX from other phylogenetically related genera in the family Flavobacteriaceae**

Taxa: 1, strain JC2132T (data from this study); 2, Yeosuana aromativorans GW1-1T (all data from this study except the DNA G+C content and isoprenoid quinone); 3, Gaetbulibacter (n=2; Jung et al., 2005; Yang & Cho, 2008); 4, Gelidibacter (n=4; Bowman et al., 1997; Bowman & Nichols, 2005; Macián et al., 2002); 5, Meridianimaribacter flavus NH57NT (Wang et al., 2010); 6, Subsaximicrobium (n=2; Bowman & Nichols, 2005). n, Number of type strains in each genus; +, positive; −, negative; w, weakly positive; ND, no data available; V, varies among different species within the same genus. All taxa are positive for catalase and leucine arylamidase and negative for β-glucuronidase activity and production of flexirubin-type pigments (no data available for Meridianimaribacter flavus), indole or H₂S.

<table>
<thead>
<tr>
<th>Characteristic</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>DNA G+C content (mol%)</td>
<td>35</td>
<td>51.4*</td>
<td>34.7–38.1</td>
<td>36–42</td>
<td>32.7</td>
<td>35</td>
<td>38–41</td>
</tr>
<tr>
<td>Major isoprenoid quinone(s)</td>
<td>MK-6</td>
<td>MK-5, MK-6*</td>
<td>MK-6</td>
<td>MK-6</td>
<td>MK-6</td>
<td>MK-6</td>
<td>MK-6</td>
</tr>
<tr>
<td>Major fatty acids</td>
<td>i-C₁₅₀, i-C₁₅₀, i-C₁₅₀, i-C₁₅₀</td>
<td>i-C₁₅₀, i-C₁₅₀, i-C₁₅₀, i-C₁₅₀</td>
<td>i-C₁₅₀, i-C₁₅₀, i-C₁₅₀, i-C₁₅₀</td>
<td>i-C₁₅₀, i-C₁₅₀, i-C₁₅₀, i-C₁₅₀</td>
<td>i-C₁₅₀, i-C₁₅₀, i-C₁₅₀, i-C₁₅₀</td>
<td>i-C₁₅₀, i-C₁₅₀, i-C₁₅₀, i-C₁₅₀</td>
<td></td>
</tr>
<tr>
<td>i-C₁₇₀ 3-OH, i-C₁₇₀ 3-OH, i-C₁₇₀ 3-OH</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Growth requirements:</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Sea salts†</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>Oxygen</td>
<td>+</td>
<td>+</td>
<td>V</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Yeast extract</td>
<td>−</td>
<td>−</td>
<td>ND</td>
<td>−</td>
<td>ND</td>
<td>+</td>
<td>−</td>
</tr>
<tr>
<td>Gliding motility</td>
<td>+</td>
<td>+‡</td>
<td>V</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Oxidase activity</td>
<td>+</td>
<td>+</td>
<td>V</td>
<td>−</td>
<td>+</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>Urease activity</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>V</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>Acid production from glucose</td>
<td>−</td>
<td>−</td>
<td>V</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>Acid production from carbohydrates</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>ND</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>Production of acetoin</td>
<td>−</td>
<td>+</td>
<td>ND</td>
<td>ND</td>
<td>+</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>Nitrate reduction</td>
<td>+</td>
<td>−</td>
<td>V</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>Degradation of:</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Casein</td>
<td>−</td>
<td>−</td>
<td>V</td>
<td>V</td>
<td>−</td>
<td>−</td>
<td>+</td>
</tr>
<tr>
<td>Egg yolk</td>
<td>−</td>
<td>−</td>
<td>ND</td>
<td>V</td>
<td>ND</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>Aesculin</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>W</td>
<td>+</td>
</tr>
<tr>
<td>Gelatin</td>
<td>−</td>
<td>+</td>
<td>−</td>
<td>V</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Starch</td>
<td>+</td>
<td>+</td>
<td>V</td>
<td>V</td>
<td>W</td>
<td>−</td>
<td>+</td>
</tr>
<tr>
<td>Tween 20</td>
<td>+</td>
<td>−</td>
<td>+</td>
<td>ND</td>
<td>−</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>Tween 40</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>ND</td>
<td>W</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>Tween 60</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>Tween 80</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>V</td>
<td>−</td>
<td>−</td>
<td>+</td>
</tr>
<tr>
<td>L-Tyrosine</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>V</td>
<td>ND</td>
<td>+</td>
<td>V</td>
</tr>
<tr>
<td>API ZYM/API ID32A:</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Alkaline phosphatase</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>V</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Esterase (C4), esterase</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>ND</td>
<td>+</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>Lipase (C8)</td>
<td>−</td>
<td>−</td>
<td>V</td>
<td>ND</td>
<td>−</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>Lipase (C14)</td>
<td>−</td>
<td>−</td>
<td>V</td>
<td>ND</td>
<td>−</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>Valine arylamidase, acid phosphatase</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>ND</td>
<td>+</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>Cystine arylamidase</td>
<td>−</td>
<td>+</td>
<td>+</td>
<td>ND</td>
<td>W</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>Trypsin</td>
<td>W</td>
<td>+</td>
<td>V</td>
<td>ND</td>
<td>W</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>α-Chymotrypsin</td>
<td>−</td>
<td>−</td>
<td>V</td>
<td>ND</td>
<td>+</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>Naphthol-AS-BI-phosphohydrolase</td>
<td>+</td>
<td>+</td>
<td>V</td>
<td>ND</td>
<td>+</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>α-Galactosidase</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>V</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>β-Galactosidase</td>
<td>+∥</td>
<td>+</td>
<td>−</td>
<td>V</td>
<td>+</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>α-Glucosidase</td>
<td>W</td>
<td>−</td>
<td>V</td>
<td>V</td>
<td>W</td>
<td>−</td>
<td>+</td>
</tr>
<tr>
<td>β-Glucosidase</td>
<td>−</td>
<td>−</td>
<td>V</td>
<td>V</td>
<td>+</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>N-Acetyl-β-glucosaminidase</td>
<td>+</td>
<td>+</td>
<td>V</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
</tbody>
</table>
*Flavobacteria*, phylum ‘Bacteroidetes’. The type species is *Snuella lapsa*.

**Description of Snuella lapsa sp. nov.**

*Snuella lapsa* [lap’sa. L. fem. part. adj. lapsa (from L. v. labor to glide) gliding].

In addition to properties given in the genus description, grows under aerobic and microaerobic conditions, but not under anaerobic conditions. Cells are rod-shaped with rounded ends and approximately 0.6–0.7 μm in diameter. It grows under aerobic and microaerobic conditions, but not under anaerobic conditions. Egg yolk decomposition was negative but a clear zone was formed around colonies.

<table>
<thead>
<tr>
<th>Characteristic</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>α-Mannosidase, z-fucosidase</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>ND</td>
<td>–</td>
<td>ND</td>
<td>ND</td>
</tr>
</tbody>
</table>

*Data from Kwon et al. (2006).*

†Cannot grow in the presence of NaCl alone.

‡Data differs from that in a previous report (Kwon et al., 2006).

§Egg yolk decomposition was negative but a clear zone was formed around colonies.

||Positive in the API ZYM and API 20E tests, but negative in the API 20E test.

The type strain is JC2132T (=KACC 14152T =JCM 17111T), isolated from a tidal flat sediment sample from Ganghwa Island, Korea. The DNA G+C content of the type strain is 35 mol%.

**Acknowledgements**

We thank Dr K. K. Kwon for providing *Y. aromativorans* GW 1-1T used in this study. This work was supported by the Priority Research Centers Program (2008-00530201) and National Research Foundation grant (2010-0017955) funded by the Korean Government (MEST), and a grant from Regional SubGenBank Support Program of Rural Development Administration, Republic of Korea.

**References**


Bowman, J. P. (2000). Description of *Cellulophaga algicola* sp. nov., isolated from the surfaces of Antarctic algae, and reclassification of...


Felsenstein, J. (1993). PHYLIP (phylogenetic inference package) version 3.5.1. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle, USA.


