Mesonia mobilis sp. nov., isolated from seawater, and emended description of the genus Mesonia

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The taxonomic position of a novel marine, heterotrophic, strictly aerobic, gliding and yellow-pigmented bacterium, designated strain KMM 6059T, was determined. 16S rRNA gene sequence analysis revealed that this strain represents a member of the genus Mesonia. Phenotypic and chemotaxonomic data showed that the isolate represents a novel species of the genus Mesonia, for which the name Mesonia mobilis sp. nov. is proposed. The type strain is KMM 6059T (=KCTC 12708T =LMG 23670T). An emended description of the genus Mesonia based on the new data is also given.

The genus Mesonia, comprising the single species Mesonia algæ (Nedashkovskaya et al., 2003), was erected to accommodate Gram-negative, strictly aerobic, heterotrophic, yellow-pigmented and non-motile marine bacteria belonging to the family Flavobacteriaceae (Bernardet et al., 2002). Strains of M. algæ were isolated from the common Pacific green alga Acrosiphonia sonderi. The genus Mesonia forms a phylogenetic cluster with the genera Salegentibacter and Gramella.

During June 2000 we isolated an unknown bacterial strain, designated KMM 6059T, from a seawater sample collected in Troitsa Bay, Gulf of Peter the Great, Sea of Japan. A polyphasic taxonomic study of this strain indicated that it represents a novel species of the genus Mesonia.

Genomic DNA extraction, PCR and sequencing of the 16S rRNA gene followed the procedures given in Kim et al. (1998). To establish the precise taxonomic position of strain KMM 6059T, 1434 nt of its 16S rRNA gene sequence was determined, 1405 bp of which were used for comparative phylogenetic analysis. The sequence data obtained were aligned with sequences of representative members of the family Flavobacteriaceae retrieved from EMBL using 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 Kimura’s two-parameter model (Kimura, 1980), and 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 the SEQBOOT and CONSENSE programs of the PHYLIP package.

16S rRNA gene sequence analysis indicated that strain KMM 6059T was a member of the family Flavobacteriaceae and formed a distinct branch within the genus Mesonia (Fig. 1). The level of 16S rRNA gene sequence similarity between KMM 6059T and M. algæ KMM 3909T was 95-8 %.

Genomic DNA was isolated according to the method of Marmur (1961) and the G + C content of the DNA was determined by the thermal denaturation method (Marmur & Doty, 1962). The DNA base composition of KMM 6059T was 36-1 mol% G + C.

In order to determine whole-cell fatty acid and polar lipid profiles, strains KMM 6059T and M. algæ KMM 3909T were grown at 28 °C for 48 h on marine agar 2216 (Difco). Lipids were extracted by a method modified from that of Bligh & Dyer (1959). Polar lipids were separated by two-dimensional micro-TLC in solvent systems as described by Vaskovsky & Terekhova (1979). Lipids were detected by TLC using 10 % H2SO4 in methanol with subsequent

**Abbreviation:** FAME, fatty acid methyl ester.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of Mesonia mobilis KMM 6059T is DQ367409.
heating to 180°C, and using specific reagents for phospho-
liquids (Vaskovsky et al., 1975) and amino group-containing
lipids (2% ninhydrin in acetone). The lipids were treated
with 5% HCl in methanol at 80°C for 180 min to produce
fatty acid methyl esters (FAMEs) (Christie, 1982). FAMEs
were analysed in a flame ionization detector gas chromato-
graph (Shimadzu GC-17) with a fused silica capillary
column (30 m × 0.25 mm) coated with Supelcowax 10 at
210°C. Helium was used as carrier gas. FAMEs were
identified by comparing the retention times with those of
authentic standards and using equivalent chain length
measurements. To ensure correct identification, FAMEs
were also analysed by GC-MS (Shimadzu QP5050A) with an
MDN-5S capillary column (30 m × 0.25 mm). The column
temperature was programmed as follows: 1 min hold at
170°C, followed by an increase to 240°C at 2°C min⁻¹, and
a hold at 240°C for 20 min. The temperature of the injector
and detector was 250°C.

Phosphatidylethanolamine was the only phospholipid
identified. The predominant cellular fatty acids of KMM
6059T and M. algae KMM 3909T were straight-chain
unsaturated, branched-chain unsaturated and saturated,
namely iso-C₁₅:₀, anteiso-C₁₅:₀, C₁₅:₀, iso-C₁₅:₁, C₁₆:₁₀₇,
iso-C₁₇:₁ and iso-C₁₅:₀ 2-OH (Table 1).

The physiological, morphological and biochemical char-
acteristics of strain KMM 6059T were tested as described
previously (Nedashkovskaya et al., 2003, 2004); they are
given in the species description below and in Table 2.
Similarities in phenotypic characteristics and cellular fatty
acid composition support the inclusion of strain KMM
6059T within the genus Mesonia. However, strain KMM
6059T differed from M. algae based on several phenotypic
features, including its ability to move by gliding, to grow at
39°C, to produce acid from D-glucose and D-maltose and to
utilize L-arabinose and D-mannose (Table 2). Whereas
M. algae strains were able to degrade casein and Tween 40,
KMM 6059T could not hydrolyse these substrates.

Susceptibility to benzylpenicillin, resistance to carbenicillin
and oleandomycin and higher G + C content of the DNA

Fig. 1. Neighbour-joining tree based on 16S rRNA gene
sequences of KMM 6059T and members of related genera of
the family Flavobacteriaceae. The topology was not changed in
trees constructed with the least-squares or maximum-likelihood
methods. Numbers at nodes are bootstrap values (percentages
of 1000 resampled datasets). Bar, 0.01 substitutions per
nucleotide position.

<table>
<thead>
<tr>
<th>Table 1. Fatty acid compositions of Mesonia type strains</th>
</tr>
</thead>
<tbody>
<tr>
<td>Values are percentages of the total fatty acids. Only those accounting for 1.0% or more in one of the strains are given. –, Not detected.</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Fatty acid</th>
<th>M. mobilis KMM 6059T</th>
<th>M. algae KMM 3909T</th>
</tr>
</thead>
<tbody>
<tr>
<td>iso-C₁₅:₁</td>
<td>38.3</td>
<td>36.7</td>
</tr>
<tr>
<td>anteiso-C₁₅:₀</td>
<td>4.0</td>
<td>11.4</td>
</tr>
<tr>
<td>iso-C₁₅:₀</td>
<td>9.7</td>
<td>9.8</td>
</tr>
<tr>
<td>C₁₅:₀</td>
<td>7.6</td>
<td>6.0</td>
</tr>
<tr>
<td>C₁₅:₁₀₆</td>
<td>2.3</td>
<td>2.9</td>
</tr>
<tr>
<td>iso-C₁₆:₀</td>
<td>1.0</td>
<td>3.4</td>
</tr>
<tr>
<td>anteiso-C₁₆:₁</td>
<td>0.6</td>
<td>1.0</td>
</tr>
<tr>
<td>C₁₆:₀</td>
<td>2.2</td>
<td>0.9</td>
</tr>
<tr>
<td>C₁₆:₁₀₇</td>
<td>8.1</td>
<td>3.6</td>
</tr>
<tr>
<td>iso-C₁₇:₁</td>
<td>6.2</td>
<td>6.5</td>
</tr>
<tr>
<td>C₁₇:₀</td>
<td>0.4</td>
<td>1.0</td>
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<tr>
<td>C₁₇:₁₀₈</td>
<td>1.0</td>
<td>1.0</td>
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<tr>
<td>C₁₇:₁₀₆</td>
<td>2.6</td>
<td>1.9</td>
</tr>
<tr>
<td>C₁₈:₁₀₇</td>
<td>1.0</td>
<td>0.5</td>
</tr>
<tr>
<td>iso-C₁₅:₀ 2-OH</td>
<td>8.3</td>
<td>2.9</td>
</tr>
<tr>
<td>iso-C₁₆:₀ 2-OH</td>
<td>0.7</td>
<td>1.0</td>
</tr>
<tr>
<td>iso-C₁₆:₀ 3-OH</td>
<td>0.5</td>
<td>1.4</td>
</tr>
<tr>
<td>iso-C₁₇:₀ 3-OH</td>
<td>2.3</td>
<td>3.7</td>
</tr>
<tr>
<td>anteiso-C₁₇:₀ 3-OH</td>
<td>–</td>
<td>1.0</td>
</tr>
</tbody>
</table>
Table 2. Differential phenotypic characteristics of Mesonia species

All strains were positive for the following tests: presence of oxidase, catalase and alkaline phosphatase, Na⁺ requirement for growth, growth with 1–12 % NaCl and at 4–34°C, hydrolysis of gelatin and Tween 20, susceptibility to lincomycin and resistance to gentamicin, kanamycin, neomycin, polymyxin B and streptomycin. All of the strains were negative for the following tests: requirement for organic Tween 20, susceptibility to lincomycin and resistance to gentamicin, kanamycin, neomycin, polymyxin B and streptomycin. Degradation of agar, DNA, starch, cellulose (carboxymethylcellulose and filter paper), chitin and urea, acid production from L-arabinose, D-cellubiose, L-fucose, D-galactose, D-lactose, L-raffinose, D-melibiose, L-rhamnose, sucrose, L-sorbitol, adonitol, dulcitol, glycerol, inositol, mannitol, malate, fumarate and citrate and utilization of D-lactose, sucrose, adonitol, dulcitol, inositol, mannitol, sorbitol, malonate and citrate. Data are taken from Nedashkovskaya et al. (2003) (for four strains of M. algae) and this study.

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>M. mobilis KMM 6059T</th>
<th>M. algae</th>
</tr>
</thead>
<tbody>
<tr>
<td>Gliding motility</td>
<td>+</td>
<td>-</td>
</tr>
<tr>
<td>Growth at 39°C</td>
<td>+</td>
<td>-</td>
</tr>
<tr>
<td>H₂S production</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>Degradation of casein and Tween 40</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>Acid production from D-glucose and D-maltose</td>
<td>+</td>
<td>-</td>
</tr>
<tr>
<td>Utilization of L-arabinose, D-glucose and D-mannose</td>
<td>+</td>
<td>-</td>
</tr>
<tr>
<td>Susceptibility to:</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Benzylenicillin</td>
<td>+</td>
<td>-</td>
</tr>
<tr>
<td>Carbencillin and oleandomycin</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>DNA G+C content (mol%)</td>
<td>36·1</td>
<td>32–34</td>
</tr>
</tbody>
</table>

may be also used to differentiate the new isolate from M. algae.

Thus, on basis of the phenotypic, genotypic and molecular distinctiveness of strain KMM 6059T, we suggest that it represents a novel species in the genus Mesonia, for which the name Mesonia mobilis sp. nov. is proposed.

Although bacteria belonging to the genus Mesonia were described as non-motile organisms, gliding motility was observed for cells of strain KMM 6059T. For this reason, and because data on phospholipid composition are now available, we provide an emended description of the genus Mesonia.

Description of Mesonia mobilis sp. nov.

Mesonia mobilis (mo.bi’lis. L. fem. adj. mobilis movable, mobile, referring to the ability to move by gliding).

Cells are Gram-negative, strictly aerobic with respiratory metabolism, chemo-organotrophic, motile by gliding, asporogenic and rod-shaped, ranging from 0·4 to 0·5 μm in width and from 1·0 to 2·1 μm in length. Oxidase-, catalase- and alkaline phosphatase-positive and β-galactosidase-negative. Colonies are circular, convex and shiny with entire edges. Colonies are 1–3 mm in diameter when grown on marine agar. Produces non-diffusible yellow pigments. Flexirubin-type pigments are absent. Grows in the presence of 1–12 % NaCl, at 4–39°C and at pH 6·0–9·5. Optimal growth is observed with 3–4 % NaCl, at 28–30°C and at pH 7·5. Depresses gelatin and Tween 20. Does not hydrolyse agar, casein, starch, cellulose (carboxymethylcellulose and filter paper), chitin, DNA, urea or Tweens 40 or 80. Forms acid from D-glucose and D-maltose, but not from L-arabinose, D-cellubiose, L-fucose, D-galactose, D-lactose, D-melibiose, L-rhamnose, sucrose, L-sorbitol, adonitol, dulcitol, glycerol, inositol, mannitol, malate, fumarate or citrate. Nitrate is not reduced. H₂S, indole and acetoin (Voges–Proskauer reaction) are not produced. Susceptible to ampicillin, benzylpenicillin and lincomycin. Resistant to carbenicillin, gentamicin, kanamycin, neomycin, oleandomycin, polymyxin B, streptomycin and tetracycline. The predominant cellular fatty acids are straight-chain unsaturated, branched-chain unsaturated and saturated, namely iso-C₁₅:₀ (9·7 %), anteiso-C₁₅:₀ (4 %), C₁₅:₀ (7·6 %), iso-C₁₅:₁ (38·3 %), C₁₆:₁ω₇ (8·1 %), iso-C₁₇:₁ (6·2 %) and iso-C₁₅:₂ 2-OH (8·3 %). The G+C content of the DNA is 36·1 mol%.

The type strain, KMM 6059T (= KCTC 12708T = LMG 23670T), was isolated from seawater collected in Troitsa Bay, Gulf of Peter the Great, East Sea (also known as the Sea of Japan).

Emended description of the genus Mesonia

Nedashkovskaya et al. 2003

The description is as given by Nedashkovskaya et al. (2003), with the following changes. Cells may be motile by means of gliding. Phosphatidylethanolamine is the only phospholipid identified. The G+C content of the DNA is in the range 32–37 mol%. The type species is Mesonia algae.
Acknowledgements

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References


