Methylobacterium salsuginis sp. nov., isolated from seawater

Xun Wang, Foday Sahr, Ting Xue and Baolin Sun

Hefei National Laboratory for Physical Sciences at Microscale and School of Life Sciences, University of Science and Technology of China, Hefei, Anhui 230027, People’s Republic of China

Three pink-pigmented, facultatively methylotrophic strains, designated MP1, MP2 and MR\textsuperscript{T}, were isolated from seawater from southern China and characterized. Analysis of their complete 16S rRNA gene sequences revealed that they constituted three separate phylogenetic groups, showing the highest levels of similarity with respect to some members of the genus Methylobacterium. PCR amplification also showed the gene coding for the \(\alpha\)-subunit of methanol dehydrogenase (\(mxaF\)) to be present in all strains, indicating a methylotrophic metabolism. All three strains utilized \(\delta\)-fructose, ethanol and nutrient agar as carbon sources, but did not utilize sucrose, citrate, acetate or formaldehyde. On the basis of the phenotypic, phylogenetic and genotypic analyses, strain MR\textsuperscript{T} represents a novel species, for which the name Methylobacterium salsuginis sp. nov. is proposed, with MR\textsuperscript{T} (=CGMCC 1.6474\textsuperscript{T} =NCCB 100140\textsuperscript{T}) as the type strain. Strains MP1 and MP2 respectively represent novel strains of the species Methylobacterium oryzae and Methylobacterium lusitanum.

Species of the genus Methylobacterium are strictly aerobic, facultatively methylotrophic, Gram-negative, rod-shaped bacteria that can grow on single-carbon compounds such as formate, formaldehyde and methanol as the sole source of carbon and energy, as well as on a wide range of multi-carbon growth substrates (Green, 2006).

The genus Methylobacterium was initially proposed by Patt et al. (1976) with the type species Methylobacterium organophilum. The genus Methylobacterium belongs to the \(\beta\)-2 subgroup of the Proteobacteria and consists of 23 species at the time of writing: Methylobacterium aminovorans (Uarakami et al., 1993), Mtb. aquaticum (Gallego et al., 2005a), Mtb. chloromethanicum (McDonald et al., 2001), Mtb. dichloromethanicum (Doronina et al., 2000), Mtb. extorquens (Bousfield & Green, 1985), Mtb. fujisawaense (Green et al., 1988), Mtb. hispanicum (Gallego et al., 2005a), Mtb. lusitanum (Doronina et al., 2002), Mtb. mesophilicum (Green & Bousfield, 1983), Mtb. nodulans (Jourand et al., 2004), Mtb. organophilum (Patt et al., 1976), Mtb. podarium (Anesti et al., 2004), Mtb. populi (Van Aken et al., 2004), Mtb. radotolerans (Green & Bousfield, 1983), Mtb. rhodanum (Green et al., 1988), Mtb. rhodinum (Green & Bousfield, 1983), Mtb. suomiense (Doronina et al., 2002), Mtb. thiocyanatum (Wood et al., 1998), Mtb. zatmanii (Green et al., 1988), Mtb. variabile (Gallego et al., 2005b), Mtb. ibisiense (Gallego et al., 2005c), Mtb. adhaesivum (Gallego et al., 2006) and Mtb. oryzae (Madhaiyan et al., 2007).

Several studies have reported the isolation of members of this genus from various natural environments (Green & Bousfield, 1981, 1983), including soil, freshwater, tap-water systems, lake sediments and as contaminants in various products and processes. Their existence in tap-water systems has been attributed to their acquired resistance to chlorination (Hiraishi et al., 1995). More recently, strains of Methylobacterium have been associated with opportunistic urinary tract infection in immunocompromised persons (Lee et al., 2004). Here we report the isolation and characterization of a novel species and two novel strains of Methylobacterium isolated from seawater off the coast of southern China.

The methods used for enrichment and isolation were as described by Bodrossy et al. (1995) but with slight modifications. One litre of seawater obtained off the coast near Xiamen (Fujian Province) was concentrated using a polysulfone-fibre membrane with pore size of 0.22 \(\mu\)m. Aliquots (20 \(\mu\)l) of the concentrated samples were added to 250 ml flasks containing 50 ml sterile mineral medium and were then incubated at 30 \(^\circ\)C for 7 days. Serial dilutions of the active cultures were then spread onto 0.1 M methanol mineral medium agar plates and incubated at 30 \(^\circ\)C for 5–7 days. Individual colonies were isolated and purified by streaking several times onto similar agar plates. Only those cultures with a single type of morphology (as observed under light microscopy) were considered to be pure.
Morphological characterization of the isolates included culture characterization on mineral salts media, Gram-staining and negative-staining for transmission electron microscopy. Cell growth at different pH values (5.0–10.0) and NaCl concentrations (0.1–10.0 %) was determined by measuring the OD$_{600}$ using a spectrophotometer. Growth of the isolates at 4, 28, 30, 32 and 40 °C was also measured. Carbon-source utilization tests involving 12 carbon sources were performed by using a standard protocol described by Green & Bousfield (1982). Biochemical characterization of the isolates included catalase, urease, indole, methyl red and Voges–Proskauer tests. Hydrolysis of starch and gelatin, hydrogen sulfide production, the Simmons’ citrate test and nitrate-reduction tests were also performed using standard protocols.

Genomic DNA from the three strains was extracted and purified according to the methods described by Möller et al. (1992), with slight modifications. Primers 5'-AGAGTTTGATCTCAG-3' and 5'-AAGGAGGTGATCAGCC-3', designed on the basis of previously published sequences of methanotrophic bacteria and synthesized by Invitrogen (Shanghai), were used as the forward and reverse primer, respectively, for 16S rRNA gene amplification. The mxaF gene, encoding the methanol dehydrogenase required for methanol utilization, was detected by PCRs in these three strains, using primers 1003f (5'-GGGCGACCAAACGGGCCTGT-3') and 1561r (5'-GGCCAGCATGAAGGCTTCCC-3') as described by Heyer et al. (2002).

PCR products of the 16S rRNA and mxaF genes were cloned in the pCR2.1 vector (Invitrogen) and submitted to Invitrogen for sequencing. The 16S rRNA gene sequences were aligned with reference sequences available for known species, and the 16S rRNA gene sequences determined for our isolates were aligned, using RDP II (http://rdp.cme.msu.edu), with 16S rRNA gene sequences cloned in the pCR2.1 vector (Invitrogen) and submitted to GenBank for sequencing. A phylogenetic tree was inferred by using the neighbour-joining (Saitou & Nei, 1987) method with MEGA (version 3.1) software.

On the basis of the criteria of Bodrossy et al. (1995), three pure colonies were isolated and labelled MP1, MP2 and MR$^T$. On mineral medium agar plates, the three isolates produced pink, circular colonies, 1–4 mm in diameter. Gram-staining established them as Gram-negative rods that occurred as single cells or in rosettes. Negative staining followed by transmission electron microscopy showed that all three isolates had a rod-shaped morphology. Their cells were strictly aerobic, catalase-positive, motile, lacked flagella and were able to produce urease. Indole and H$_2$S were not produced and the methyl red and Voges–Proskauer tests gave negative results. Further biochemical analysis showed the strains to be capable of hydrolysing starch but not gelatin. The results of Simmons’ citrate tests and nitrate-reduction tests were also positive. Growth occurred at 28, 30 and 32 °C, but not at 4 or 40 °C. For strains MP1 and MP2, optimal growth occurred at pH 7, whilst that for MR$^T$ occurred at pH 6. For strains MP1 and MR$^T$, no growth occurred in the presence of ≥1.5 % NaCl; for MP2, growth inhibition occurred at ≥2 % NaCl.

Analysis of the 16S rRNA gene sequences identified our isolates as three distinct strains of the genus Methylobacterium. Strains MP1 and MP2 were identified as novel strains of two previously characterized species of the genus, *Mtb. oryzae* and *Mtb. lusitanum*, respectively, whereas strain MR$^T$ appeared to represent a novel species of this genus (Fig. 2). Because of the chemotaxonomic homogeneity of the genus *Methylobacterium*, phylogenetic analyses constitute a critical tool in species identification (Green & Bousfield, 1982; Doronina et al., 2002). Strain MP1 had 96.3 % 16S rRNA gene sequence similarity with respect to a previously characterized strain of *Mtb. oryzae*, whereas strain MP2 shared 98 % sequence similarity with respect to a previously characterized strain of *Mtb. lusitanum*. Strain MR$^T$ was found to be most closely related to *Mtb. suomiense* F20$^T$; however, the level of sequence similarity was only 93.1 %, suggesting that this strain represents a novel species of the genus *Methylobacterium*.

The gene for the $\alpha$-subunit of methanol dehydrogenase (mxaF) was amplified from strains MP1, MP2 and MR$^T$ and then sequenced. A comparison of the mxaF gene sequences of the three isolates showed varying levels of similarity. Strain MP1 showed mxaF gene sequence similarities of 92.6 and 93.2 % with respect to strain MP2 and strain MR$^T$, respectively, while strain MP2 showed 96.9 % mxaF gene sequence similarity with respect to strain MR$^T$. When compared with representative *Methylobacterium* strains from the database, strain MP1 was most closely related to *Mtb. organophilum*, with 93 % mxaF gene sequence similarity. Strains MP2 and MR$^T$ were most closely related to *Mtb. podarium*, with 97 and 96 % sequence similarity, respectively. Analysis of the mxaF
genes of our three strains confirmed the 16S rRNA gene sequencing results, indicating that MP1, MP2 and MRT belong to the genus *Methylobacterium*, exhibiting varying sequence similarity with respect to a number of previously characterized members of the genus (Table 1).

Three carbon sources, D-fructose, ethanol and nutrient agar, were utilized by all three strains. In comparisons between the carbon-source utilization profiles of previously characterized strains, strain MP1 and a previously characterized strain of *Mtb. oryzae* were both able to utilize D-glucose, D-xylose, L-arabinose, fructose, ethanol and nutrient agar, but MP1 differed from its relative by not utilizing citrate or acetate as carbon sources. Strain MP2 and a previously characterized strain of *Mtb. lusitanum* also showed the ability to utilize D-fructose and ethanol. Strain MP2 was also able to utilize betaine, but was unable to utilize acetate, unlike the previously characterized strain of *Mtb. lusitanum*, which utilized acetate but not betaine. Strain MRT and its closest relative, *Mtb. suomiense*, were both able to utilize D-glucose, D-fructose, betaine and ethanol. Strain MRT failed to utilize acetate, whilst its relative, *Mtb. suomiense*, was able to utilize acetate as an energy source.

The phylogenetic data and several phenotypic features indicate that strain MRT represents a novel species and that strains MP1 and MP2 represent novel strains of *Methylobacterium oryzae* and *Methylobacterium lusitanum*, respectively. Strain MRT represents a novel species of the genus *Methylobacterium*, for which we propose the name *Methylobacterium salsuginis* sp. nov.

**Description of *Methylobacterium salsuginis* sp. nov.**

*Methylobacterium salsuginis* (sal.sugi.nis. L. gen. n. salsuginis of brine, seawater).

Cells are Gram-negative rods, 1.0–1.5×4.0–8.0 μm, occurring singly or in aggregates, and are strictly aerobic. Colonies are circular, regular in shape, pink to red, slow-growing and 1–2 mm in diameter after 3–4 days at 30 °C on methanol mineral medium agar plates. The pink pigment is water-insoluble. Catalase- and urease-positive, but negative for indole and in methyl red and Voges-Proskauer reactions. Simmons’ citrate test is positive. Starch is hydrolysed, but gelatin is not. Hydrogen sulfide is
Table 1. Differential phenotypic characteristics of strain MR<sup>T</sup>, strains MP1 and MP2 and type strains of related Methylobacterium species

<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>
<th>8</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cell arrangement</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>Pairs</td>
<td>+</td>
<td>Rarely</td>
<td>Rarely</td>
<td>Rarely</td>
<td>Rarely</td>
<td>Rarely</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>Aggregates/rosettes</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>Cell size</td>
<td>4.0–8.0</td>
<td>1.0–4.0</td>
<td>2.0–3.0</td>
<td>1.5–4.0</td>
<td>1.2–2.5</td>
<td>1.0–2.0</td>
<td>2.0</td>
<td>2.5–3.5</td>
</tr>
<tr>
<td>Width (μm)</td>
<td>1.0–1.5</td>
<td>1.0–1.5</td>
<td>0.8–1.0</td>
<td>0.8–1.0</td>
<td>0.8–1.0</td>
<td>0.8–1.0</td>
<td>0.8</td>
<td>0.8–1.0</td>
</tr>
<tr>
<td>Pigmentation</td>
<td>Pink to red</td>
<td>Pink</td>
<td>Pink</td>
<td>Pink to red</td>
<td>Pink</td>
<td>Pink</td>
<td>Pink</td>
<td>Pink</td>
</tr>
<tr>
<td>Colony diameter (mm)</td>
<td>1–2</td>
<td>2–4</td>
<td>1–2</td>
<td>1–3</td>
<td>0.5–1</td>
<td>1–3</td>
<td>1.5</td>
<td>ND</td>
</tr>
<tr>
<td>Growth on:</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>D-Glucose</td>
<td>+</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>+</td>
<td>–</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>D-Xylose</td>
<td>–</td>
<td>–</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>L-Arabinose</td>
<td>–</td>
<td>–</td>
<td>+</td>
<td>–</td>
<td>ND</td>
<td>–</td>
<td>ND</td>
<td>w</td>
</tr>
<tr>
<td>D-Fructose</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>ND</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>Sucrose</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>Citrate</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Acetate</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Betaine</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>ND</td>
<td>+</td>
</tr>
<tr>
<td>Ethanol</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>ND</td>
<td>+</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>Formaldehyde</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>Formate</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>Nutrient agar</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>ND</td>
<td>–</td>
<td>–</td>
<td>ND</td>
<td>+</td>
</tr>
</tbody>
</table>

not produced. Nitrate is reduced to nitrite. Carbon sources utilized include D-fructose, D-glucose, methanol, ethanol, formate, betaine and nutrient agar. Does not utilize D-xylose, L-arabinose, sucrose, citrate, acetate or formaldehyde. Nitrogen sources utilized include ammonium and nitrate. Growth occurs at 28, 30 and 32°C (optimum, pH 7.0). No growth occurs in the presence of 30 °C but not at 4 or 40 °C. Growth occurs at pH 5.0–8.0 (optimum, pH 7.0). No growth occurs in the presence of ≥1.5 % NaCl.

The type strain, MR<sup>T</sup> (=CGMCC 1.6474<sup>T</sup> =NCCB 100140<sup>T</sup>), was isolated from seawater collected off the coast of southern China, near Xiamen (Fujian Province).

Acknowledgements

The authors wish to thank Liang Tao for collecting the seawater sample and Yonglong Zhuang for his assistance with the transmission electron microscopy. This research was supported by the One Hundred Talent Project of the Chinese Academy of Sciences.

References


