Marinobacterium halophilum sp. nov., a marine bacterium isolated from the Yellow Sea

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A moderately halophilic, aerobic, Gram-negative bacterium was isolated from a tidal flat area of Dae-Chun, Chung-Nam, Korea. The strain, designated mano11T, comprised rod-shaped cells that were motile by means of polar flagella. It grew with 3–12 % NaCl and at 4–37 °C and pH 5.3–9.3. The predominant menaquinone present in this strain was MK-7 and diaminopimelic acid was not found in the cell-wall peptidoglycan. A phylogenetic analysis based on 16S rRNA gene sequences showed that strain mano11T belongs to the genus Marinobacterium. Strain mano11T exhibited 92.8–98.3 % 16S rRNA gene sequence similarity when compared with the type strains of three other species of the genus Marinobacterium. DNA–DNA hybridization between strain mano11T and Marinobacterium georgiense DSM 11526T, its closest relative in terms of 16S rRNA gene sequence similarity, was 13 %. On the basis of the phenotypic, genetic and phylogenetic data, strain mano11T represents a novel species of the genus Marinobacterium, for which the name Marinobacterium halophilum sp. nov. is proposed. The type strain is mano11T (=KCTC 12240T = DSM 17586T).

Halophilic bacteria can be found in habitats representing a wide range of salt concentrations, from marine biotopes to hypersaline environments (Ollivier et al., 1994). The western and south-western coasts of the Korean peninsula consist primarily of tidal flats, which are also known as getbol (Kim et al., 2004). Getbol are unique among other marine sediments as they are alternately undergoing flooding with seawater and exposure to the atmosphere (Kim et al., 2005). Recently, a variety of bacterial species were isolated from Korean getbol and identified as phylogenetically novel micro-organisms (Baik et al., 2005; Yi et al., 2003; Yi & Chun, 2004; Yoon et al., 2004). To elucidate the bacterial diversity of Korean getbol, we have searched for novel micro-organisms in these sediments. Among the different isolates obtained was a novel Marinobacterium-like strain, designated mano11T. In this study, the taxonomic position of this novel strain was determined using phenotypic, genetic and chemotaxonomic analyses.

Strain mano11T was isolated from a tidal flat area of Dae-Chun, Chung-Nam, Korea (36° 17′ 45.2″ N 126° 31′ 9.5″ E), using the dilution plating technique. It was grown at 25 °C for 3 days on marine agar (Difco) plates or marine salts basal medium (MB; Baumann & Baumann, 1981) supplemented with various carbon sources. Its closest relative in terms of 16S rRNA gene sequence similarity, Marinobacterium georgiense DSM 11526T, which was used as a reference strain, was obtained from the Deutsche Sammlung von Mikroorganismen und Zellkulturen (Braunschweig, Germany) and grown under the same conditions. All phenotypic growth tests were carried out with the novel isolate and M. georgiense DSM 11526T. Bacterial cultures of the isolate and the reference strain were stored at -20 °C on MB containing 20 % glycerol. For morphological and physiological characterization, strain mano11T and the reference strain were generally cultivated in MB at 25 °C with shaking. API 20E, API 20NE and API ZYM test strips (bioMérieux) were used to analyse these bacterial strains biochemically and physiologically and other biochemical tests were performed using the methods and media described by Gordon et al. (1973). The ability to grow on various carbon sources was tested as described by Gonzalez et al. (1997). Catalase activity was determined by means of bubble production in a 3 % (v/v) H2O2 solution. Oxidase activity was determined using an oxidase reagent.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain mano11T is AY563030.
Growth under anaerobic conditions was determined after incubation for 7 days in anaerobic GasPak jars (BBL) containing an atmosphere comprising N₂/CO₂/H₂ (80:10:10). Growth at various NaCl concentrations, temperatures and pH values was measured in MB. Cellular morphology and sporulation were investigated using microscopy (E600; Nikon). Cellular motility was observed for the novel isolate in fresh wet mounts of young bacterial cultures (grown in MB) by means of the hanging drop method. For observation using transmission electron microscopy, cells from exponentially growing cultures were negatively stained with 1% (w/v) phosphotungstic acid. After being air-dried, the grid was examined using a transmission electron microscope (H-7600; Hitachi). Isoprenoid quinones of the mano11T strain were extracted from 100 mg aliquots of freeze-dried cells according to methods described previously (Collins & Jones, 1981); they were then purified via preparative TLC (silica gel F254; Merck). The ubiquinone fraction was also analysed by HPLC (L-5000; Hitachi) using a reversed-phase column (YMC pack ODS-AM; YMC), as described previously (Shin et al., 1996). Bacterial strains grown on marine agar for 3 days at 25°C were used for the analysis of fatty acid methyl esters, which were extracted and prepared according to standard protocols provided by the MIDI/Hewlett Packard Microbial Identification System (Sasser, 1990). Chromosomal DNA was extracted and purified as described by Sambrook et al. (1989). The 16S rRNA gene was amplified by a PCR using two universal primers, as previously described (Stackebrandt et al., 1993). Sequencing of the amplified 16S rRNA gene and phylogenetic analysis were performed according to the methods described by Yoon et al. (1998). DNA–DNA hybridization was performed according to previously described methods (Ezaki et al., 1989). The 16S rRNA gene sequence of mano11T was aligned with 13 reference sequences from the Ribosomal Database Project (Fig. 1), using the multiple sequence-alignment program CLUSTAL_X (1.8) (Thompson et al., 1997). Phylogenetic relationships between representatives of the genus Marinobacterium were determined using MEGA, version 2.1. Distance matrices were determined according to the assumptions described by Kimura (1980). These matrices were used to elaborate dendrograms using the neighbour-joining method (Saitou & Nei, 1987). To investigate the stability of the trees, a bootstrap analysis was performed. The consensus tree obtained was based on 1000 randomly generated trees.

The morphological, cultural, physiological and biochemical characteristics of strain mano11T and related species are shown in Table 1 and are provided in the species description (below). Strain mano11T grew at temperatures from 4 to 37°C, but not at temperatures below 4°C or above 37°C; it grew at pH 5.3–8.8 but not at pH values below 4.1 or above 9.3. Growth was observed in the presence of 3–12 % NaCl and very weak growth was observed at NaCl concentrations of 1–2 %. No growth was detected at NaCl concentrations below 1 % or above 15 %. However, growth of M. georgiense DSM 11526T occurred at NaCl concentrations from 0.5 to 11.4 % (Gonzalez et al., 1997). The novel isolate did not

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**Fig. 1.** Consensus phylogenetic tree, based on 16S rRNA gene sequences, showing the relationship between strain mano11T, type strains of different *Marinobacterium* species and representatives of related genera. The tree was constructed using the neighbour-joining method and p-distance. Bootstrap analyses were performed with 1000 repetitions and only values >50% are shown. GenBank accession numbers are shown in parentheses. Bar, 0.02 substitutions per nucleotide position.
Taxa: 1. *M. georgiense* DSM 11526T; 2. *M. jannaschii* DSM 6296T (data from Bowditch et al., 1984); 3. *M. stanieri* DSM 7027T (Baumann et al., 1983); 4. *M. halophilum* sp. nov. mano11T. Data for *M. georgiense* and strain mano11T are from this study. +, Positive reaction; −, negative reaction; ND, not determined. All of the taxa are motile by means of single polar flagellum, rod-shaped, aerobic, oxidase-positive, catalase-positive, unable to reduce nitrate, utilize citrate and possess quinone type Q-8.

<table>
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<tr>
<th>Characteristic</th>
<th>1</th>
<th>2</th>
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<td>Growth at 35 °C</td>
<td>+</td>
<td>–</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Arginine dihydrolase</td>
<td>+</td>
<td>+</td>
<td>–</td>
<td>–</td>
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</table>

Growth under anaerobic conditions, gave a negative Voges–Proskauer test and showed catalase, oxidase and urease activities. Although *Marinobacterium jannaschii* DSM 6295T and *Marinobacterium stanieri* DSM 7027T were able to reduce nitrate to nitrite, strain mano11T could not. Colonies of strain mano11T were pale orange to yellow, whereas those of *M. georgiense* DSM 11526T were translucent. Strain mano11T grew on the following carbon sources: glucose, rhamnose, lactose, glucose, maltose and trehalose. Acid is not produced from dulcitol, galactose, inulin, D-arabitol, rhamnose, arabinose, sorbitol or D-xylene. Using the API ZYM system, activity is detected for alkaline phosphatase, esterase (C4), esterase lipase (C8), leucine arylamidase, acid phosphatase and naphthol-AS-BI-phosphohydrolase. No activity is detected for lipase (C14), valine arylamidase, cystine arylamidase, trypsin, z-chymotrypsin, z-galactosidase, β-galactosidase, β-glucuronidase, β-glucosidase, x-glucosidase, β-glucosidase, N-acetyl-β-glucosaminidase, x-mannosidase or x-fucosidase. Diaminopimelic acid is not present in the cell-wall peptidoglycan and the predominant quinone is Q-8. The predominant fatty acids are C16:1ω7c and C16:0 (43.2 and 21.9 %, respectively).

The type strain, strain mano11T (=KCTC 12240T=DSM 17586T), was isolated from a tidal flat area of Dae-Chun, Chung-Nam, Korea.

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