Mangrovibacter phragmitis sp. nov., an endophyte isolated from the roots of Phragmites karka

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Abstract

A facultatively anaerobic, Gram-stain-negative, rod-shaped, nitrogen-fixing, endophytic bacterial strain designated MP23T was isolated from the roots of Phragmites karka growing in Chilika Lagoon, Odisha, India. Strain MP23T was slightly halophilic, and the optimal NaCl concentration and temperature for growth were 1% and 30 °C, respectively. On the basis of 16S rRNA gene sequence similarities, strain MP23T was affiliated to the family Enterobacteriaceae and most closely related to Mangrovibacter yixingensis KCTC 42181T and Mangrovibacter plantisponsor DSM 19579T with 99.71% similarity, followed by Salmonella enterica subsp. salamae DSM 9220T (97.22%), Cronobacter condimenti LMG 26250T (97.14%) and Salmonella enterica subsp. diarizonae DSM 14847T (97%). Sequence analysis of 16S RNA, hsp60, gyrB and rpoB genes showed that strain MP23T formed a phylogenetic cluster with M. yixingensis KCTC 42181T and M. plantisponsor DSM 19579T indicating that it belongs to the genus Mangrovibacter. The major cellular fatty acids were C16:0, C18:1ω6c and/or C18:1ω7c, C16:1ω5c and/or C16:1ω7c, C14:0 3-OH and/or iso-C15:0 1I and C17:0 cyclo. Polar lipids of strain MP23T consisted of phosphatidylglycerol, diphosphatidylglycerol and phosphatidylethanolamine. The DNA G+C content was 50.3 mol%. Based on experimental DNA–DNA hybridization values and average nucleotide identity derived from in silico comparison of whole-genome sequences, strain MP23T could be distinguished from its closest neighbours. We therefore conclude that strain MP23T represents a novel species of the genus Mangrovibacter for which the name Mangrovibacter phragmitis sp. nov. is proposed. The type strain is MP23T (=DSM 100250T=KCTC 42580T).

The family Enterobacteriaceae consists of non-spore-forming, Gram-stain-negative, facultatively anaerobic and rod-shaped bacteria that are widely associated with plants, water and soil environments [1]. Many species of this family have been isolated from plant tissues [2–4], and some of them have been recognized as plant-growth-promoting rhizobacteria [1, 5]. The genus Mangrovibacter of the family Enterobacteriaceae includes two species, Mangrovibacter yixingensis and Mangrovibacter plantisponsor, at the time of submission of this manuscript (www.bacterio.net/mangrovibacter.html). M. yixingensis KCTC 42181T was isolated from a farmland soil in China [6] while M. plantisponsor DSM 19579T was isolated from mangrove-associated wild rice plants (Porteresia coarctata Tateoka) of the Pichavaram mangrove forest in India [7]. Both of these type strains have been shown to possess a nitrogen-fixing property, which is considered a plant-growth-promoting characteristic.

Phragmites karka plants occupy most of the northern shoreline (19.52°N 85.24°E) of Chilika, a brackish water lagoon on the East coast of India in the Odisha state [8]. The northern shoreline of the lagoon is the shallowest part and has average salinity <5 g l−1, which is significantly lower than other parts of lagoon in which salinity varies between 10 and 30 g l−1 [9]. In general, Phragmites is a large perennial weed that grows as an emergent macrophyte on the shorelines of wetlands [10]. This invasive

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Keywords: Phragmites karka; Mangrovibacter phragmitis sp. nov.; Polyphasic taxonomy; Chilika Lagoon.
Abbreviations: ANI, average nucleotide identity; DDH, DNA–DNA hybridization.
Present address: State Project Management Unit, Integrated Coastal Zone Management Project, Bhubaneswar, Odisha 752003, India. The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA, hsp60, gyrB, rpoB and whole-genome sequences of strain MP23T are KP319034, KT922227, KT922225, KT922226, KU895549 and LYRP00000000, respectively.
Seven supplementary figures and two supplementary tables are available with the online Supplementary Material.

NOTE
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Phragmites karka plants were collected randomly in January 2014 from the northern shoreline of Chilika Lagoon. Root portions of Phragmites karka were excised using a sterile knife, put into plastic bags and transported to the laboratory on ice. The sediment attached to the root surfaces was washed completely under the running tap water. After this, root samples were thoroughly rinsed several times with sterile water followed by a three-step surface sterilization procedure: (i) 30 s rinse in 99 % ethanol, (ii) 5 min wash in 4 % sodium hypochlorite and (iii) final rinse in sterile water [12]. To evaluate the efficacy of the surface sterilization procedure, an aliquot of the last washate was inoculated on Luria–Bertani (LB) agar, which did not yield any colonies even after 3 days of incubation at 30 °C. Root samples were cut into small pieces and macerated in 0.85 % (w/v) NaCl solution with a sterile mortar and pestle. Tissue homogenate was serially diluted and plated on LB agar to recover bacterial endophytes of root tissue. Strain MP23 was picked randomly from a LB agar plate after 48 h of incubation at 30 °C and characterized using a polyphasic taxonomic approach.

The colony morphology of strain MP23 was investigated using light microscopy at ×100 magnification (BX53, Olympus) after growth on LB agar at 30 °C after 48 h of incubation. For scanning electron microscopy, cells were coated with gold-palladium in a Q150R ES sputter coater (Quorum Technologies) and examined under a Zeiss SUPRA55VP FESEM (Carl Zeiss) microscope. Gram staining was carried out using a kit as per the manufacturer’s protocol (HiMedia), and stained cells were observed under a light microscope.

Physiological and biochemical tests were carried out at 30 °C in LB broth unless otherwise stated. Salt tolerance tests were carried out in LB broth (10 g tryptone $^1$ and 5 g yeast extract $^1$) supplemented with different NaCl concentrations (0, 1, 3, 5, 7, 8, 9 and 10 %, w/v) at pH 7.0. Growth at pH 4–11 (in 1 pH unit intervals) was checked in LB broth. Growth at different temperatures (10, 15, 20, 30, 40 and 45 °C) was conducted in LB broth with 1 % NaCl concentration at pH 7.0. The growth of the strain was measured by taking absorbance at 600 nm at every 2 h interval. Citrate hydrolysis was checked on Simmons’ citrate agar (HiMedia) [13]. Motility, indole production and H₂S production were examined by observing growth on sulfide-indole-motility medium [14]. Catalase activity was determined by bubble production in 3 % (v/v) H₂O₂ [15]. Acid production from the fermentation of various carbohydrates was tested using Carbohydrates Differentiation discs (HiMedia) on sugar-free purple agar base medium (HiMedia). Sterile agar plates were inoculated with the novel strain, and the discs were placed aseptically. Results were recorded after 24 h. Change in colour from purple to yellow around the disc was due to the acid production after fermentation and was considered as positive. Various biochemical tests such as reduction of nitrate, arginine dihydrolase activity and urease activity were performed as described by Smibert and Krieg [16]. Oxidase activity was determined by the change in colour of an oxilase disc (HiMedia). Endospore formation was checked by the Schaeffer–Fulton staining method [17]. Nitrogen fixing ability of strain MP23 was determined by streaking on a semi-solid N-free medium (NFM) containing the sugars glucose and mannitol [18], and a change in the colour of the medium from blue to yellow was observed. The quantification of nitrogen-fixing ability of strain MP23 was carried out by estimation of the amount of total nitrogen fixed after 5 days of growth in NFM broth at 30 °C using the Kjeldahl digestion method [19]. Oxygen requirement of strain MP23 was determined on thiglycollate broth (HiMedia). Antibiotic susceptibility discs (HiMedia) were used for testing the sensitivity of bacterial strains in LB agar to the following antibiotics (µg per disc): bacitracin (10), streptomycin (10), chloramphenicol (30), nalidixic acid (30), carbencillin (100), ofloxacin (5), nitrofurantoin (300), erythromycin (10), sulphamethizole (300), kanamycin (30), tetracycline (30), neomycin (10), ampicillin (10), rifampicin (30), gentamicin (30), co-trimoxazole (25), amikacin (10), ciprofloxacin (30), furazolidone (50), amoxycillin (30) and norfloxacin (10).

For fatty acid analysis, strain MP23 and the two other type strains, M. xingensis KCTC 42181T and M. plantisponsor DSM 19579T, were cultured on tryptic soy broth agar (TSBA; HiMedia) at 30 °C for 24–48 h, and aged cell biomass was collected for analysis. According to the MIDI protocols for gas chromatography with a flame ionization detector (GC-FID), cellular fatty acids were analysed as described by Sasser [20] and the peaks for fatty acids were identified using the Microbial Identification Software (Sherlock version 6.1; MIDI). For polar lipids extraction, the cultures were harvested at exponential phase and the cell pellet was freeze dried. Extraction was done with methanol/chloroform/saline (2 : 1 : 0.8, by vol) as described by Bligh and Dyer [21]. Lipids were separated using silica gel in TLC (Kieselgel 60 F254; Merck) by two-dimensional chromatography using
chloroform/methanol/water (65:25:4, by vol.) in the first dimension and chloroform/acetic acid/methanol/water (40:7.5:6:2, by vol.) in the second dimension [22]. The dried plates were subjected to spraying with 5% ethanolic molybdophosphoric acid for total lipids and further characterized by spraying with ninhydrin (specific for amino groups), molybdenum blue (specific for phosphates), Dragendorff reagent (quaternary nitrogen) or α-naphthol (specific for sugars).

Using the fluorimetric method, the G+C content of genomic DNA was determined in triplicates as described by Gonzalez and Saiz-Jimenez [23]. Genomic DNA was extracted and purified according to the method of Marmur [24] for DNA–DNA hybridization experiments. The analysis was done by fluorometry using a Step One Plus Real-Time PCR system (Applied Biosystems) fitted with a 96-well thermal cycling block in 96-well plates [25]. DNA suspended in the 2× saline sodium citrate (SSC) was used for the analysis, and results were expressed as the mean of triplicates. The re-association of DNA was carried out at optimum re-association temperature of 70 °C according to De Ley et al. [26] and Gillis et al. [27].

Whole-genome shotgun sequencing of strain MP23T was performed on an Illumina MiSeq platform with a paired-end module as described previously [28]. ANI and digital DNA–DNA hybridization (DDH) analysis was done in accordance with the methods proposed by Goris et al. [29] and Richter and Rosselló-Móra [30]. For ANI analysis, whole-genome sequences of S. enterica subsp. salamae DSM 9220T [31], C. condimenti LMG 26250T [32] and S. enterica subsp. diarizonae DSM 14847T [33] were obtained from the public databases. An ANI value of 95–96% corresponds to a DDH value of 70% and can be used as a substitute for experimental DDH for the description of novel species [30].

Genomic DNA was extracted from strain MP23 using a microbial DNA isolation kit (FastDNA SPIN Kit; MP Biomedicals). PCR amplification of 16S rRNA, hsp60, gyrB, rpoB and nifH genes was carried out with the primers described by Rastogi et al. [34], Iversen et al. [35], Dauga [36], Mollet et al. [37] and Poly et al. [38], respectively. PCR was carried out using an S1000 Thermal Cycler (Bio-Rad) with the following conditions: initial denaturation at 95 °C for 1 min, 35 cycles of denaturation at 95 °C for 30 s, annealing at 55 °C for 30 s, extension at 72 °C for 1 min 30 s and final extension at 72 °C for 10 min. PCR products were purified with a QIAquick PCR purification kit (Qiagen) and sequenced using a BigDye Terminator v3.1 Cycle Sequencing kit (Applied Biosystems) in an ABI Prism 3700 DNA analyzer (Applied Biosystems). The gene sequences were compared with GenBank database sequences using the BLASTn [39] and EzTaxon-e programs [40], and closely related sequences were aligned using CLUSTAL X software [41]. The BioEdit Sequence Alignment Editor, version 7.1.3 [42], was used for editing the sequence alignment. The MEGA V 6.0 package was used for phylogenetic analyses [43]. Phylogenetic trees were inferred using the neighbour-joining [44], maximum-likelihood [45] and maximum-parsimony [46] methods, and bootstrap analysis was based on 1000 re-samplings [47].

The cells of strain MP23T were Gram-stain-negative, rod shaped and motile (Fig. S1, available in the online Supplementary Material). The colonies were white in colour, circular and smooth when grown on LB agar plates. Strain MP23T could grow within a temperature range of 20–40 °C, with 0–8% NaCl concentration and at pH 5–10. The optimum temperature and pH for growth of strain MP23T were 30 °C and pH 7.0. The optimum growth of strain MP23T was recorded with 1% NaCl concentration, and it was classified as slightly halophilic [48]. The differential biochemical properties of strain MP23T and its closest phylogenetic relatives, M. yixingensis KCTC 42181T and M. plantisponsor DSM 19579T, are shown in Table 1, and the similar characteristics are shown in Table S1. Comparison of the biochemical data indicated that strain MP23T differed from M. yixingensis KCTC 42181T and M. plantisponsor DSM 19579T in various biochemical properties. The cells of strain MP23T were oxidase negative and facultatively anaerobic. Strain MP23T was a nitrogen-fixing strain as evidenced from growth on NFM agar and production of total nitrogen (0.294 mg per ml of broth) in the culture broth after 5 days of growth at 30 °C. Considering the theoretical ratio that 3 moles ethylene reduced is equivalent to 1 mole N2 [49], the amount of nitrogen fixed by strain MP23T equates to 262.3744 nmol ethylene reduced ml−1 h−1, which was much

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Strain MP23T</th>
<th>M. yixingensis KCTC 42181T</th>
<th>M. plantisponsor DSM 19579T</th>
</tr>
</thead>
<tbody>
<tr>
<td>Arginine dihydrolyase</td>
<td>−</td>
<td>−</td>
<td>+</td>
</tr>
<tr>
<td>Voges-Proskauer reaction</td>
<td>−</td>
<td>+</td>
<td>−</td>
</tr>
<tr>
<td>Methyl red test</td>
<td>+</td>
<td>−</td>
<td>+</td>
</tr>
<tr>
<td>Hydrolysis of Tween 80</td>
<td>+</td>
<td>−</td>
<td>+</td>
</tr>
<tr>
<td>Acid production from:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>D-Arabinose</td>
<td>+</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>Adonitol</td>
<td>+</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
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<td>−</td>
<td>−</td>
</tr>
<tr>
<td>Dulcitol</td>
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<td>−</td>
<td>−</td>
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<tr>
<td>Inositol</td>
<td>+</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>Inulin</td>
<td>+</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>Lactose</td>
<td>+</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>NaCl tolerance</td>
<td>0–8%</td>
<td>0–6%</td>
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<td>Temperature for growth</td>
<td>20–40 °C</td>
<td>15–42 °C</td>
<td>15–40 °C</td>
</tr>
<tr>
<td>Antibiotic susceptibility test</td>
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<td></td>
<td></td>
</tr>
<tr>
<td>Streptomycin</td>
<td>Resistant</td>
<td>Sensitive</td>
<td>Resistant</td>
</tr>
<tr>
<td>Erythromycin</td>
<td>Sensitive</td>
<td>Resistant</td>
<td>Resistant</td>
</tr>
</tbody>
</table>

All data are from this study. +, Positive; −, negative.
higher than the amount reduced by M. yixingensis KCTC 42181T (15.57 nmol ethylene ml⁻¹ h⁻¹) [6] and M. plantisponsor DSM 19579T (32.68±1.42 nmol ethylene ml⁻¹ h⁻¹) [7]. At the molecular level, the presence of nif genes in the whole-genome sequence [28] and positive PCR amplification of the nifH gene from the DNA of strain MP23T further confirmed the nitrogen-fixing ability of strain MP23T. Strain MP23T was resistant to bacitracin and streptomycin. Strain MP23T was sensitive to chloramphenicol, nalidixic acid, carbenicillin, ofloxacin, nitrofurantoin, erythromycin, sulphamethizole, kanamycin, tetracycline, neomycin, ampicillin, rifampicin, gentamicin, co-trimoxazole, amikacin, ciprofloxacin, furazolidone, amoxyccillin and norfloxacin.

Strain MP23T was different from M. yixingensis KCTC 42181T and M. plantisponsor DSM 19579T in acid production from D-arabinose, adonitol, L-xylene, dulcitol, inositol and inulin (Table 1) and was sensitive to erythromycin. Strain MP23T differed from M. yixingensis KCTC 42181T in the hydrolisis of Tween 80, Voges–Proskauer reaction, methyl red test and sensitivity to streptomycin. Strain MP23T was different from M. plantisponsor DSM 19579T in the production of the enzyme arginine dihydrolase and in acid production from lactose.

Whole-cell fatty acid analysis showed that strain MP23T exhibited a pattern typical of the genus Mangrovibacter, containing high levels (>10 %) of C₁₆:0 (30.6 %), summed feature 8 (C₁₈:1ωc and/or C₁₈:1ω7c; 18.3 %), summed feature 3 (C₁₆:1ωc/C₁₆:1ω7c; 18.0 %) and C₁₄:0 (15.3 %) (Table 2). The fatty acids summed feature 2 (C₁₄:0 3-OH/iso-C₁₆:1 I; 8.3 %), C₁₇:0 cyclo (7.9 %), C₁₂:0 (1.0 %) and C₁₉:0 cyclo ω8c (0.7 %) were also detected. The detailed differences in fatty acid composition between MP23T, M. yixingensis KCTC 42181T and M. plantisponsor DSM 19579T are presented in Table 2. The polar lipid pattern of strain MP23T consisted of phosphatidylglycerol, diphosphatidylglycerol, phosphatidylethanolamine, an unknown aminolipid, an unknown phospholipid and an unknown lipid (Fig. S2).

The DNA G+C content of strain MP23T was 50.3 mol%, which was in good agreement with those of the two most closely related strains, i.e. M. yixingensis KCTC 42181T (52 mol%) and M. plantisponsor DSM 19579T (50.1 mol%). The DNA–DNA relatedness among strain MP23T and its closest phylogenetic neighbours M. yixingensis KCTC 42181T and M. plantisponsor DSM 19579T was 63.6 % and 27.4 %, respectively. Strain MP23T showed ANI values of 72±1 % with the genomes of S. enterica subsp. salamae DSM 9220T, C. condimenti LMG 26250T and S. enterica subsp. diarizonae DSM 14847T (Table S2). These values are well below the 70 % (for DDH) and 95 % (for ANI) cut-off points recommended for the delineation of bacterial species. Considering the threshold value of DNA–DNA relatedness lower than 70 % [50] for delineation of a novel bacterial species, strain MP23T is thus a representative of a novel species within the genus Mangrovibacter.

The almost complete (1367 nt) 16S rRNA gene sequence of strain MP23T was determined (KP319034) and compared with those of other closely related strains through BLASTN and EzTaxon-e searches. Strain MP23T showed 99.71 % sequence similarity with both Mangrovibacter yixingensis KCTC 42181T and Mangrovibacter plantisponsor DSM 19579T. Strain MP23T was also closely related to S. enterica subsp. salamae DSM 9220T (97.22 % sequence similarity), C. condimenti LMG 26250T (97.14 %) and S. enterica subsp. diarizonae DSM 14847T (97 %). Neighbour-joining phylogenetic analysis showed that strain MP23T belonged to the genus Mangrovibacter within the family Enterobacteriaceae and formed a monophyletic cluster with M. yixingensis KCTC 42181T (Fig. 1). The maximum-likelihood and maximum parsimony methods also demonstrated similar phylogenetic placement of strain MP23T (Figs S3 and S4). Phylogenetic analysis of the housekeeping genes hsp60, gyrB and rpoB based on the neighbour-joining method further confirmed the phylogenetic affiliation of strain MP23T to the genus Mangrovibacter (Figs S5, S6 and S7). The hsp60 nucleotide sequence showed 97 % similarity with that of M. yixingensis KCTC 42181T and 93 % with that of M. plantisponsor DSM 19579T. The gyrB nucleotide sequence showed 97 and 94 % similarity with those of M. yixingensis KCTC 42181T and M. plantisponsor DSM 19579T, respectively. The rpoB nucleotide sequence showed 99 and 95 % similarity with those of M. yixingensis KCTC 42181T and M. plantisponsor DSM 19579T, respectively.

Strain MP23T has to be regarded a representative of a novel species of the genus Mangrovibacter based on the biochemical and genetic differences. Although there was a

<table>
<thead>
<tr>
<th>Fatty acid</th>
<th>Strain MP23T</th>
<th>M. yixingensis KCTC 42181T</th>
<th>M. plantisponsor DSM 19579T</th>
</tr>
</thead>
<tbody>
<tr>
<td>C₁₂:0</td>
<td>1.0</td>
<td>0.5</td>
<td>0.6</td>
</tr>
<tr>
<td>C₁₄:0</td>
<td>15.3</td>
<td>13.0</td>
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<tr>
<td>Summed feature 2*</td>
<td>8.3</td>
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<td>3.2</td>
</tr>
<tr>
<td>iso-C₁₆:0</td>
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<td>0.76</td>
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<td>18.0</td>
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<td>10.8</td>
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<tr>
<td>C₁₆:0</td>
<td>30.6</td>
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<td>38.0</td>
</tr>
<tr>
<td>C₁₇:0 cyclo</td>
<td>7.9</td>
<td>11.5</td>
<td>14.3</td>
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<tr>
<td>Summed feature 8*</td>
<td>18.3</td>
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<tr>
<td>C₁₉:0 cyclo ω8c</td>
<td>0.7</td>
<td>1.5</td>
<td>3.7</td>
</tr>
</tbody>
</table>

*Summed feature 2 comprises C₁₄:0 3-OH/iso-C₁₆:1 I; summed feature 3 comprises C₁₆:1ωc/C₁₆:1ω7c; summed feature 8 comprises C₁₈:1ωc and/or C₁₈:1ω7c.
high 16S rRNA gene sequence similarity (99.71 %) of strain MP23<sup>T</sup> with <i>M. yixingensis</i> KCTC 42181<sup>T</sup> and <i>M. plantisponsor</i> DSM 19579<sup>T</sup>, it differed in the biochemical and genotypic properties. Table 1 shows the main features that distinguished strain MP23<sup>T</sup> from its phylogenetic neighbours: <i>M. yixingensis</i> KCTC 42181<sup>T</sup> and <i>M. plantisponsor</i> DSM 19579<sup>T</sup>. Therefore, from the evidence gathered in this polyphasic study it is concluded that strain MP23<sup>T</sup> represents a novel species of the genus Mangrovibacter, for which the name <i>Mangrovibacter phragmitis</i> sp. nov. is proposed.

**DESCRIPTION OF MANGROVIBACTER PHRAGMITIS SP. NOV.**

<i>Mangrovibacter phragmitis</i> (phrag‘mi.tis. L. fem. gen. n. phragmitis of Phragmites, the source of isolation).

Cells are facultatively anaerobic, Gram-stain-negative rods. Colonies on LB are circular and smooth. Can grow with between 0 and 8 % NaCl and at a temperature of 20–40 °C. The optimum conditions for growth are 1 % (w/v) NaCl, pH 7.0 and 30 °C. Positive for catalase, nitrate reduction, methyl red test and citrate utilization. Negative for H<sub>2</sub>S production, indole production and Voges–Proskauer reaction. Cannot hydrolyse casein, gelatin, Tween 80 or starch. Can produce acid from sorbitol, L-xylene, galactose, mannose, fructose, xylose, galactose, mannose, fructose, mannitol, maltose, melibiose, salicin, trehalose, dextrose, adonitol, cellobiose and dulcitol. It is a nitrogen fixing bacterium, negative for the oxidase test and citrate utilization. Negative for H<sub>2</sub>SO<sub>4</sub>. Proskauer reaction. Cannot produce indole from L-tryptophan, L-arabinose, raffinose, lactose, inositol, inulin, mannitol, maltose, melibiose, salicin, trehalose, dextrose, adonitol, cellobiose and dulcitol. It is a nitrogen fixing bacterium, negative for the oxidase test and citrate utilization.

The major cellular fatty acids are C<sub>16:0</sub>, C<sub>18:1ω6c</sub> and/or C<sub>18:1ω7c</sub>, C<sub>16:1ω6c</sub> and/or C<sub>16:1ω7c</sub>, C<sub>14:0</sub>, C<sub>14:0</sub> 3-OH and/or iso-C<sub>15:0</sub> 1 and/or C<sub>17:0</sub> cyclo. The type strain MP23<sup>T</sup> (=DSM 100250<sup>≡</sup>=KCTC 42580<sup>T</sup>) is an endophyte isolated from the roots of <i>Phragmites karka</i>
from the Chilika Lagoon, Odisha, India. The DNA G+C content of strain MP23\textsuperscript{T} is 50.3 mol%.

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**Conflicts of interest**
The authors declare that there are no conflicts of interest.

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