Mangrovibacter plantisponsor gen. nov., sp. nov., a nitrogen-fixing bacterium isolated from a mangrove-associated wild rice (Porteresia coarctata Tateoka)

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A facultatively anaerobic, nitrogen-fixing bacterium, strain MSSRF40𝑇, was isolated from roots of mangrove-associated wild rice (Porteresia coarctata Tateoka). On the basis of 16S rRNA gene sequence similarities, strain MSSRF40𝑇 was shown to belong to the family Enterobacteriaceae, most closely related to Cronobacter muytjensii E603𝑇 (97.2 % sequence similarity), Enterobacter cloacae subsp. dissolvens LMG 2683𝑇 (97.1 %), E. radicincitans D5/23𝑇 (97.1 %) and E. ludwigii EN-119𝑇 (97.0 %). Sequence analysis of rpoB, gyrB and hsp60 genes showed that strain MSSRF40𝑇 had relatively low sequence similarity (<91, <84 and <90 %) to recognized species of different genera of the family Enterobacteriaceae and formed an independent phyletic lineage in all phylogenetic analyses using the 16S rRNA, rpoB, gyrB and hsp60 genes, clearly indicating that strain MSSRF40𝑇 could not be affiliated to any of the recognized genera within the family Enterobacteriaceae. The dominant cellular fatty acids were C16:0, C16:1ω7c and/or iso-C15:0 2-OH and C18:1ω7c, similar to those of other members of the Enterobacteriaceae. The DNA G+C content was 50.1 mol%. Phylogenetic distinctiveness and phenotypic differences from its phylogenetic neighbours indicated that strain MSSRF40𝑇 represents a novel species and genus within the family Enterobacteriaceae, for which the name Mangrovibacter plantisponsor gen. nov., sp. nov. is proposed. The type strain of Mangrovibacter plantisponsor is strain MSSRF40𝑇 (=LMG 24236𝑇 =DSM 19579𝑇).

The family Enterobacteriaceae is a large, heterogeneous group of Gram-negative, facultatively anaerobic, rod-shaped bacteria that do not form endospores and are catalase-positive and oxidase-negative (Brenner, 1984). Members of the family are distributed worldwide, with some being saprophytes and others being parasites of plants and animals. Many species of this family are of considerable economic importance due to their pathogenic effects on agriculture and livestock (Janda & Abbott, 2006). Currently, there are more than 35 genera described in this family (Dauga, 2002; Janda, 2006), including the recently described genus Cronobacter (Iversen et al., 2008), which was previously recognized as Farmer’s Enterobacter sakazakii biogroups 1–4, 7, 8, 11 and 13 (Iversen et al., 2007, 2008).

Several studies have shown that members of the Enterobacteriaceae may have beneficial effects on plant development when they are associated with the plants as rhizobacteria (Lodewyckx et al., 2002; Taghavi et al., 2009). They improve plant growth via nitrogen fixation, suppression of plant pathogens and production of phytohormones and enzymes involved in the metabolism of growth regulators such as ethylene, 1-aminocyclopropane 1-carboxylic acid (ACC), auxins and indole-3-acetic acid (IAA) (Gyaneshwar et al., 2001; Kämpfer et al., 2005; Taghavi et al., 2009).

During a study of diazotrophic bacteria from mangrove-associated wild rice, numerous isolates that are able to fix atmospheric nitrogen were isolated. Based on preliminary characterization, most isolates were tentatively identified as members of the genera Swaminathania, Vibrio and Serratia. In the present work, we describe the isolation and taxonomic characterization of a diazotroph, strain MSSRF40𝑇, belonging to the family Enterobacteriaceae. On the basis of our results obtained from a polyphasic

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA, gyrB, rpoB and hsp60 gene sequences of strain MSSRF40𝑇 are EF643377, EU713848, EU713850 and EU713849. Details of PCR primers, additional phylogenetic trees and an electron micrograph of a cell of strain MSSRF40𝑇 are available as supplementary material with the online version of this paper.
approach, it can be concluded that isolate MSSRF40<sup>T</sup> represents a new genus and species in the family Enterobacteriaceae.

Strain MSSRF40<sup>T</sup> was isolated from mangrove-associated wild rice (*Porteresia coarctata* Tateoka) collected from the Pichavaram mangrove forest in India. The plant roots were washed with sterilized distilled water, surface-sterilized with sodium hypochlorite (4%) for 5 min and washed several times with sterile distilled water. One gram of surface-sterilized roots was macerated in a blender and serially diluted, and 100 μl aliquots were inoculated into 30 ml test tubes containing 10 ml semi-solid N-free medium as described by Rameshkumar et al. (2008b) and then on tryptone soya agar (TSA; HiMedia). Isolates were maintained on TSA at 4 °C for 4–5 days. Material from tubes showing a fine subsurface pellicle was transferred to fresh semi-solid N-free medium as described above and observed for pellicle formation. Further purification was done by repeatedly streaking the isolates on plates of NM + Y agar as described by Rameshkumar et al. (2008b) and then on tryptone soya agar (TSA; HiMedia). Isolates were maintained on TSA at 4 °C or stored frozen in tryptone soya broth (TSB; HiMedia) with 15% glycerol at –80 °C.

Genomic DNA was extracted from isolate MSSRF40<sup>T</sup> as described by Ausubel et al. (1987). The 16S rRNA gene was amplified and sequenced with primers as described by Rameshkumar et al. (2008b) and the *rpoB*, *gyrB* and *hsp60* genes were amplified and sequenced as described by Mollet et al. (1997), Dauga (2002) and Iversen et al. (2004). The primer sequences for amplification and sequencing of the 16S rRNA, *rpoB*, *gyrB* and *hsp60* genes are listed in Supplementary Table S1, available in IJSEM Online. For all the above-mentioned genes, PCR amplification was carried out in a total volume of 20 μl containing 2 μl template DNA (50–100 ng), 0.3 μl Taq DNA polymerase (3 U μl<sup>−1</sup>), 2 μl 10 × Taq buffer, 2 μl dNTP mixture (2 mM) and 2 μl each of the forward and reverse primers (30 ng μl<sup>−1</sup>) and brought to a final volume of 20 μl using double-sterilized distilled water. Amplification was carried out in an MJ Research minicycler. In all the reactions, water was used in place of DNA as a negative control. The sequences of these genes were compared with sequences available from GenBank using the **BLAST** program (Altschul et al., 1990) and were aligned using **CLUSTAL_X** software (Thompson et al., 1997). Distances were calculated according to Kimura’s two-parameter correction (Kimura, 1980). Phylogenetic trees were inferred using the neighbour-joining (Saitou & Nei, 1987) and maximum-parsimony (Fitch, 1971) methods and bootstrap analysis was based on 1000 resamplings. The **MEGA3** package (Kumar et al., 2004) was used for all analyses.

An almost-complete 16S rRNA gene sequence of strain MSSRF40<sup>T</sup> comprising 1368 nt was determined and used for phylogenetic analysis. The analysis showed that strain MSSRF40<sup>T</sup> was phylogenetically related to members of the family Enterobacteriaceae. A neighbour-joining tree based on these 16S RNA gene sequences was constructed (Fig. 1) and showed that strain MSSRF40<sup>T</sup> formed an independent phylogenetic lineage that was related most closely to the clade that includes the recently described genus *Cronobacter* (Iversen et al., 2008) and the type strains of two *Enterobacter* species (*Enterobacter helveticus* 513/05<sup>T</sup> and *Enterobacter pulveris* 601/05<sup>T</sup>). Although the stability of the branch was not confirmed by a high bootstrap resampling value (<55%), the branching of the MSSRF40<sup>T</sup> lineage separate from *Cronobacter* or any of the *Enterobacter* clusters was confirmed by maximum-parsimony analysis (Supplementary Fig. S1). Pairwise 16S rRNA gene sequence comparisons revealed that strain MSSRF40<sup>T</sup> exhibited the highest similarity to *Cronobacter muytjensii* E603<sup>T</sup> (97.2%), followed by *Enterobacter cloacae* subsp. *dissolvens* LMG 2683<sup>T</sup> (97.1%), *Enterobacter radicincitans* D5/23<sup>T</sup> (97.1%) and *Enterobacter ludwigi* EN-119<sup>T</sup> (97.0%). Furthermore, relatively high sequence similarity was also found to *Enterobacter cancerogenus* LMG 2693<sup>T</sup>, *Citrobacter farmeri* CDC 2991-81<sup>T</sup> and *Enterobacter cloacae* subsp. *cloacae* ATCC 13047<sup>T</sup>, sharing 96.9% sequence similarity, and *Serratia ureilytica* NIVa 51<sup>T</sup>, sharing 96.8% sequence similarity. These relatively high 16S rRNA gene sequence similarities between members of different genera and the partitioning of genera to several different phyla have been reported in other phylogenetic studies on the *Enterobacteriaceae* (Drancourt et al., 2001; Hoffmann & Roggenkamp, 2003; Rosenblueth et al., 2004; Kämpfer et al., 2005). Overall, no 16S rRNA gene sequence similarities above 97.2% were found with any recognized species of different genera of the family *Enterobacteriaceae*, suggesting that strain MSSRF40<sup>T</sup> could represent a novel genus, as it has been observed in previous studies that 98% 16S rRNA gene sequence similarity is a reasonable cut-off value to delineate different genera in the family *Enterobacteriaceae* (Drancourt et al., 2001; Iversen et al., 2007, 2008).

Since the branches that represent the different genera of the family *Enterobacteriaceae* are not monophyletic and are not supported by high bootstrap values and since the highest similarity values of strain MSSRF40<sup>T</sup> were found with strains of different genera, it can be concluded that, for the family *Enterobacteriaceae*, the similarity levels obtained reflect a high level of homoplasy in the 16S rRNA gene sequences. The results of 16S rRNA gene sequence analysis indicate that strain MSSRF40<sup>T</sup> belongs to the family *Enterobacteriaceae* but, based on these results alone, the novel strain cannot be allocated unequivocally to a lower taxonomic rank.

As the usefulness of *rpoB* (encoding the RNA polymerase beta subunit) gene sequences for identification and species discrimination among members of the family *Enterobacteriaceae* has been reported previously by several authors (Mollet et al., 1997; Drancourt et al., 2001; Li et al., 2004; Kämpfer et al., 2005; Stephan et al., 2007, 2008), this approach was also used to determine the taxonomic position of strain MSSRF40<sup>T</sup>. A 919 bp *rpoB* sequence of
strain MSSRF40T was compared with sequences from the databases. This analysis showed low levels of sequence similarity with different species of the family Enterobacteriaceae. For example, the analysis showed the highest similarity to Citrobacter braakii CDC 80-58 (GenBank accession no. EU010096; 91.2%) and Citrobacter freundii ATCC 11021 (U77434; 89.9%). A neighbour-joining tree based on these rpoB gene sequences was constructed (Supplementary Fig. S2) and showed that strain MSSRF40T formed a long separate branch that did not cluster with any species of the genera Enterobacter, Cronobacter, Citrobacter, Klebsiella, Salmonella or Kluyvera. Only similarities below 91% were found to the rpoB sequences of all other strains shown in Supplementary Fig. S2. Similar results were obtained with the maximum-parsimony algorithm (not shown), supporting the view that strain MSSRF40T does not belong to any existing genus in the family Enterobacteriaceae, taking into account 6% rpoB sequence dissimilarity as a reasonable limit to differentiate genera of the Enterobacteriaceae (Drancourt et al., 2001).

We used sequences of two further protein-encoding genes, gyrB (Dauga, 2002) and hsp60 (Harada & Ishikawa, 1997; Iversen et al., 2004), to describe the phylogenetic relationship of strain MSSRF40T with other members of the Enterobacteriaceae. The results of gyrB sequence analysis showed that strain MSSRF40T shared relatively low similarity (76.0–83.8%) with all strains shown in Supplementary Fig. S3. According to the studies of Dauga (2002), similarities between gyrB nucleotide sequences from all Serratia species ranged from 84.8 to 97.3%, and the range of variation within the genera Klebsiella, Enterobacter and Proteus was similar to that for Serratia. Strain MSSRF40T exhibited gyrB sequence similarities of less than 84% to all its relatives, indicating that this strain does not belong to any existing genus in the family Enterobacteriaceae, supporting the results of rpoB sequence analysis. Furthermore, phylogenetic analysis of gyrB sequences also placed strain MSSRF40T as a separate branch that did not cluster with any of the species of the Enterobacteriaceae (Supplementary Fig. S3), and the same
results were obtained when using the maximum-parsimony algorithm (not shown), indicating that strain MSSRF40\textsuperscript{T} represents a novel genus.

Supporting these findings, the results of hsp60 gene analysis demonstrated that strain MSSRF40\textsuperscript{T} had low sequence similarity (83.4–90.6 %) to the strains shown in Supplementary Fig. S4, and phylogenetic analysis of hsp60 also placed strain MSSRF40\textsuperscript{T} as a separate branch that did not cluster with any of the species of the Enterobacteriaceae (Supplementary Fig. S4). The same results were obtained when using the maximum-parsimony algorithm (not shown).

Thus, based on phylogenetic analysis using 16S rRNA, rpoB, gyrB and hsp60 gene sequences, strain MSSRF40\textsuperscript{T} could not be affiliated to any described genus. We therefore propose that strain MSSRF40\textsuperscript{T} represents a taxonomic unit that deserves genus rank.

DNA base composition was determined by HPLC. Briefly, DNA was isolated after cell disruption with a French pressure cell and purified on hydroxyapatite, according to Cashion et al. (1977). PI hydrolysis and nucleotide dephosphorylation with alkaline phosphatase were done as described by Mesbah et al. (1989). HPLC conditions (LKB equipment with Shimadzu CR-3A integrator) on a Nucleosil 100-5C18 column were chosen according to Tamaoka & Komagata (1984). The DNA G + C content of strain MSSRF40\textsuperscript{T} was 50.1 mol%, within the range given for the family Enterobacteriaceae (38–60 mol%; Farmer, 2006). However, the value was lower than the range given for the genus Cronobacter (56.7–57.0 mol%; Iversen et al., 2007) and slightly lower than the range given for the genus Enterobacter (52–60 mol%; Grimont & Grimont, 2005). The G + C contents of the Enterobacter species most closely related to MSSRF40\textsuperscript{T} are not known except that for E. cloacae subsp. dissolvens, which is 54 mol% (Grimont & Grimont, 2005).

Physiological and biochemical tests were carried out at 28 °C. Conventional biochemical tests were performed according to standard methods (Smibert & Krieg, 1994). API 20E, API 20NE and API 50CH (medium E) strips (bioMérieux) were used according to the manufacturer’s instructions; results were read after 1 and 2 days. Salt tolerance tests were carried out as described by Rameshkumar et al. (2008a). Data for reference type strains were obtained at the DSMZ under the same conditions as for MSSRF40\textsuperscript{T}. Electron microscopy was carried out as described by Rameshkumar & Nair (2007). The results for strain MSSRF40\textsuperscript{T} were in accord with the main phenotypic features of the Enterobacteriaceae: cells were Gram-negative, catalase-positive and oxidase-negative motile rods (peritrichous flagella; Supplementary Fig. S5), facultatively anaerobic, did not form endospores and had no requirement for NaCl for growth (Brenner, 1984). It is virtually impossible to provide genus definitions and a single meaningful table that differentiates the 30 genera in Enterobacteriaceae. The biochemical features that distinguish strain MSSRF40\textsuperscript{T} from its closest phylogenetic neighbours – selected on the basis of 16S rRNA, rpoB, gyrB and hsp60 gene sequence similarity – are presented in Table 1. E. radicicinata, Pantoea stewartii and Citrobacter koseri are the species that are biochemically most similar to MSSRF40\textsuperscript{T} in respect of the tests listed in Table 1. The fact that these species are members of different genera underpins the difficulty of giving clear-cut physiological features for the delineation of genera within the family Enterobacteriaceae at present. The combination of a positive reaction for arginine dihydrolase and a negative reaction for ornithine decarboxylase is shared by E. radicicinata only, which has the capacity for nitrogen fixation and beneficial effects on plants in common with strain MSSRF40\textsuperscript{T}. Detailed phenotypic and biochemical properties of strain MSSRF40\textsuperscript{T} are given in the species description.

Whole-cell fatty acid methyl ester analysis was performed as described by Lang et al. (2003). This analysis showed that strain MSSRF40\textsuperscript{T} exhibited a fatty acid pattern typical of the family Enterobacteriaceae, containing high levels of C\textsubscript{16:0} (28.42 %), C\textsubscript{18:1\text{\textit{v c}}} (28.04 %) and summed feature 3 (C\textsubscript{16:0(\textit{v 7c} and/or iso-C\textsubscript{15:0} 2-OH; 23.65 %)). The acids C\textsubscript{12:0} (0.35 %), C\textsubscript{14:0} (8.63 %), an unidentified fatty acid with an equivalent chain-length of 14.502 (0.72 %), C\textsubscript{15:0} (0.36 %) C\textsubscript{16:0} (0.27 %), C\textsubscript{17:0} (0.18 %), C\textsubscript{17:0} cyclo (1.84 %), C\textsubscript{18:0} (0.23 %) and summed feature 2 (iso-C\textsubscript{16:1} \textit{I and/or C\textsubscript{14:0} 3-OH; 7.32 %) were also detected.

The acetylene reduction assay was used to test for nitrogen fixation by the novel isolate grown on semi-solid (N\textsubscript{M} + Y) medium. The amount of ethylene produced was measured using 10 % (v/v) acetylene according to the method of Li & MacRae (1992) using a Hewlett Packard 4890 GC equipped with a Poropack N column, as described previously (Rameshkumar, 2008; Rameshkumar et al., 2008b). Strain MSSRF40\textsuperscript{T} was able to reduce acetylene to ethylene (32.68 ± 1.42 nmol ethylene ml\textsuperscript{-1} h\textsuperscript{-1}), indicating that the isolate is able to fix atmospheric nitrogen.

In conclusion, based on the phenotypic, chemotaxonomic and phylogenetic data, it was clear that strain MSSRF40\textsuperscript{T} was a member of the family Enterobacteriaceae. However, 16S rRNA gene sequence similarity values between strain MSSRF40\textsuperscript{T} and all other described species within the family Enterobacteriaceae were < 97.2 %. It was stated previously that 16S rRNA gene sequence similarity values between species of Klebsiella and Raoultella and of Cronobacter and Enterobacter are 97–98 % (Drancourt et al., 2001; Iversen et al., 2007, 2008) and that it can be assumed from these values that the threshold for the differentiation of genera within the family Enterobacteriaceae is at < 98 % similarity (Drancourt et al., 2001; Iversen et al., 2007, 2008). Supporting this observation, strain MSSRF40\textsuperscript{T} had very low rpoB gene similarity (< 91 %) to related members of the family Enterobacteriaceae and formed a long, separate branch that did not cluster with any species of the genera...
Enterobacter, Cronobacter, Citrobacter, Klebsiella, Salmonella or Kluyvera (Supplementary Fig. S2), demonstrating clearly that strain MSSRF40\textsuperscript{T} does not belong to any established genus of the family Enterobacteriaceae, taking into account 6% rpoB sequence dissimilarity as a reasonable limit to differentiate genera of the Enterobacteriaceae (Drancourt et al., 2001). Additionally, strain MSSRF40\textsuperscript{T} formed an independent phyletic lineage in all phylogenetic analyses using sequences of the genes gyrB (Supplementary Fig. S3; <84% similarity) and hsp60 (Supplementary Fig. S4; <90% similarity), supporting the conclusion from the 16S rRNA gene and rpoB sequence analyses that it is difficult to allocate strain MSSRF40\textsuperscript{T} to any of the previously described genera in the family Enterobacteriaceae.

Some of the genera in the family Enterobacteriaceae have been distinguished mostly on the basis of differences at the molecular phylogenetic level. For instance, Cronobacter (Iversen et al., 2007, 2008) was delineated from Enterobacter (Farmer et al., 1980) on the basis of 98% 16S rRNA gene sequence similarity and its clinical importance (Iversen et al., 2007, 2008), though members of Cronobacter are phenotypically similar to members of Enterobacter (Iversen et al., 2007, 2008). The genus Raoultella (Drancourt et al., 2001) was delineated from Klebsiella (Orskov, 1984) at the level of 16S rRNA gene and rpoB sequence similarity (98 and 94%), though it exhibited phenotypic differences only with respect to growth at 10°C and utilization of l-sorbose (Drancourt et al., 2001). Brenneria (Hauben et al., 1998) was delineated from Erwinia (Winslow et al., 1917) at the level of 16S rRNA gene and glyceraldehyde-3-phosphate dehydrogenase (gapDH) gene sequence similarity (Brown et al., 2000), though members of Brenneria are biochemically very similar to members of Pantoaea, Erwinia and Pectobacterium in that they fail to produce arginine dehydrogenase and to decarboxylate amino acids such as ornithine and lysine (Lelliott & Dickey, 1984).

Pectobacterium (Brenner et al., 1973) was delineated from Erwinia (Winslow et al., 1917) on the basis of 16S rRNA gene sequence similarity (Hauben et al., 1998) and distinct pathogenic and biochemical properties (Brenner et al., 1973).

Phenotypically, strain MSSRF40\textsuperscript{T} most closely resembles the genera Cronobacter and Enterobacter, but it can be distinguished from species of these genera by biochemical characteristics and G+C content. Strain MSSRF40\textsuperscript{T} differed from the type strains of the genus Cronobacter in negative reactions for the Voges–Proskauer reaction, ornithine decarboxylase, ascorbic acid hydrolysis and growth at 45°C and positive reactions for acid production from sorbitol and the methyl red test. For several genera and species within the family Enterobacteriaceae, it has been decided that they should retain their taxonomic status not only on a genetic basis but also by virtue of their source and functional role. For instance, the genera Escherichia and Shigella are genetically indistinguishable; however, the
genus *Shigella* remains separate from *Escherichia* because of its unique clinical and public-health importance as the cause of bacillary dysentery and shigellosis (Janda, 2006). Similarly, the genera *Pectobacterium* and *Erwinia* are genetically closely related at the 16S rRNA gene sequence level (Hauben et al., 1998); however, the genus *Pectobacterium* remains separate from *Erwinia* on the basis of its distinct pathogenic properties (Brenner et al., 1973). Likewise, sources from which *Cronobacter* strains have been isolated include sterile body sites of children, infants and adults and these strains are involved in clinical disease, which was deemed sufficient to delineate the genus from the genus *Enterobacter* (Iversen et al., 2007, 2008). Strain MSSRF40T is associated with mangrove roots and fixes atmospheric nitrogen, supporting the fact that strain MSSRF40T should not be placed in the genus *Cronobacter*.

Similarly, strain MSSRF40T differs from the description of the genus *Enterobacter* (Grimont & Grimont, 2005) in that most members of the latter genus are negative for the methyl red test and positive for the Voges–Proskauer reaction. Furthermore, strain MSSRF40T differed from the genera *Cronobacter* and *Enterobacter* in its G+C content, which is 50.1 mol% compared with 56.7–57.0 mol% for *Cronobacter* (Iversen et al., 2007) and 52–60 mol% for *Enterobacter* (Grimont & Grimont, 2005).

Thus, based on the combination of phylogenetic information showing the formation of a distinct clade within the family *Enterobacteriaceae* (Fig. 1 and Supplementary Figs S2–S4) and low sequence similarity for the 16S rRNA 

\[ (\leq 97.2 \%) \]

, *rpoB* (<91%), *gyrB* (<84%) and *hsp60* (<90%) genes to related genera and phenotypic characters (Table 1), it is most appropriate to conclude that the diazotrophic strain MSSRF40T represents a novel genus and species of the family *Enterobacteriaceae*, for which the name *Mangrovibacter plantisponsor* gen. nov., sp. nov. is proposed.

**Description of Mangrovibacter plantisponsor gen. nov., sp. nov.**

*Mangrovibacter* (Man.gro’vi.bac’ter. N.L. n. mangro’vu mum mangrove; N.L. masc. n. bac’ter rod; N.L. masc. n. Mangro’vibacter mangrove rod).

Cells are Gram-negative rods (1.0 × 1.2–4.0 μm) with peritrichous flagella, facultatively anaerobic, oxidase-negative and catalase-positive. Phylogenetically, most closely related to members of the genera *Cronobacter*, *Enterobacter* and *Citrobacter*. Phenotypically similar to species of the genus *Cronobacter*, but distinguished by biochemical characteristics such as negative reactions for the Voges–Proskauer reaction, ornithine decarboxylase, ascelin hydrolysis and acid from inositol and positive reactions for acid from sorbitol and the methyl red test. No growth at or above 42 °C. Environmental isolates may be able to fix nitrogen. Major fatty acids are \( C_{16:0}, C_{18:1} \) \( \omega 7c \) and summed feature 3 [\( C_{16:1} \) \( \omega 7c \) and/or \( C_{15:0} \) 2-OH]. The DNA G+C content of the type strain of the type species is 50.1 mol%. The type species is *Mangrovibacter plantisponsor*.

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