The draft genome sequence of Mangrovibacter sp. strain MP23, an endophyte isolated from the roots of Phragmites karka

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Abstract

To date, only one draft genome has been reported within the genus Mangrovibacter. Here, we report the second draft genome shotgun sequence of a Mangrovibacter sp. strain MP23 that was isolated from the roots of Phragmites karka (P. karka), an invasive weed growing in the Chilika Lagoon, Odisha, India. Strain MP23 is a facultative anaerobic, nitrogen-fixing endophytic bacterium that grows optimally at 37°C, 7.0 pH, and 1% NaCl concentration. The draft genome sequence of strain MP23 contains 4,947,475 bp with an estimated G + C content of 49.9% and total 4392 protein coding genes. The genome sequence has provided information on putative genes that code for proteins involved in oxidative stress, uptake of nutrients, and nitrogen fixation. The draft genome sequence and annotation have been deposited at DDBJ/EMBL/GenBank under the accession number LYRP00000000.

Keywords:
Mangrovibacter sp., Phragmites karka, Draft genome, Chilika Lagoon, Endophyte

1. Direct link to deposited data
http://www.ncbi.nlm.nih.gov/nuccore/LYRP00000000

2. Experimental design, materials, and methods

Members of the genus Mangrovibacter are facultative anaerobic and nitrogen fixing bacteria [1]. To date only two species, Mangrovibacter plantisponsor DSM 19579 [1] and Mangrovibacter yixingensis KCTC 42181 [2] have been described under the genus Mangrovibacter (http://www.bacterio.net/mangrovibacter.html). The draft genome of Mangrovibacter sp. strain MFB070, isolated from an aquaculture farm in India has been described recently [3] which is the only available genome sequence within genus Mangrovibacter. Members of the genus Mangrovibacter have been shown to possess plant growth promoting features such as nitrogen fixation [1] and may provide niche-specific advantage to the plant. In context to invasive weeds, this could provide a better ecological fitness in an invaded territory compared to native vegetation. Thus, understanding the microbiota and role they may play during plant invasion could lead to more directed and sustainable management of weeds.

Chilika Lagoon (19°28′-19°54′N; 85°06′-85°35′E) is a brackish water lagoon located in the Odisha State of India [4]. An invasive weed P. karka (Retz.) Trin. ex Steud is extensively spreading and threatening the ecological health of lagoon. P. karka is a large perennial grass of the family Poaceae and occupy most of the northern shoreline of lagoon. In order to understand the microbial basis of the invasive success of this weed, a study was undertaken to investigate the culturable diversity of rhizosphere microbiota associated with P. karka. During this study, a gamma-proteobacterium, facultative anaerobic, endophytic nitrogen fixing Mangrovibacter sp. strain MP23 was isolated from the roots of P. karka. Strain MP23 grew at temperatures between 20 °C and 40 °C with an
optimum at 37 °C in presence of 1% NaCl. The 16S rRNA gene phylogenetic analysis showed that strain MP23 was most closely (99.71% similarity) related to *M. yixingensis* KCTC 42181 and *M. plantisponsor* DSM 19579 indicating that it belong to genus *Mangrovibacter*. Here, we described the draft whole genome shotgun sequence of strain *Mangrovibacter* sp. strain MP23 (DSM 100250T = KCTC 42580T), which will provide genetic insights into the nitrogen fixation, stress tolerance, plant niche adaptation, and comparative evolution of this species.

The genome of *Mangrovibacter* sp. strain MP23 was sequenced by a shotgun sequencing method using the Illumina MiSeq sequencing system with a paired-end module. The NGS QC Toolkit v 2.3 [5] was used to filter the data for high-quality (HQ) vector- and adapter-free reads for genome assembly. A total of 6,895,374 paired end reads were generated out of which 6,702,332 high quality vector-free reads were considered, representing approximately 310 fold coverage of the genome. These reads were assembled using MaSuRCA v. 3.1.3 [6] and resulted into 50 contigs with a total size of 4,947,475 bp and an N50 contig length of 428,946 bp. The largest assembled contig measured 1,277,690 bp. Annotations of protein-coding genes, as well as other functional genome units were carried out through NCBI Prokaryotic Genome Annotation Pipeline (PGAP) [7]. The genome contained a total of 4592 genes and 4392 protein-coding genes with predicted function.

The complete genome of strain MP23 was 4,947,475 bp in length with an estimated G + C content of 49.9% and consists of 77 tRNA genes and 28 rRNA (8 = 5S, 5 = 16S, 15 = 23S) genes (Table 1).

### Table 1
General features of *Mangrovibacter* sp. strain MP23 draft genome.

| Attributes          | Values          |
|---------------------|-----------------|
| Assembly size (bp)  | 4,947,475       |
| Contigs             | 50              |
| G + C content (%)   | 49.9            |
| Total genes         | 4592            |
| tRNA genes          | 77              |
| rRNA genes          | 28              |
| Protein coding genes| 4392            |
| Fold coverage       | 310×            |

### 3. Nucleotide sequence accession number

This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number LYPRP000000000. The version described in this paper is version LYPRP01000000.

### Conflict of interest

The authors declare that there is no conflict of interests with respect to the work published in this paper.

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