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SHORT COMMUNICATION

Draft Genome Sequence of the Endophytic Bacterium *Enterobacter* spp. MR1, Isolated from Drought Tolerant Plant (*Butea monosperma*)

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Abstract *Enterobacter* sp. MR1 an endophytic plant growth promoting bacterium was isolated from the roots of *Butea monosperma*, a drought tolerant plant. Genome sequencing of *Enterobacter* spp. MR1 was carried out in Ion Torrent (PGM), Next Generation Sequencer. The data obtained revealed 640 contigs with genome size of 4.58 Mb and G+C content of 52.8 %. This bacterium may contain genes responsible for inducing drought tolerance in plant, including genes for phosphate solubilization, growth hormones and other useful genes for plant growth.

Keywords *Butea monosperma* · Drought tolerant · Endophytes · Phosphate solubilization · Plant growth promoting endophytic bacteria · Whole genome sequencing

Endophytic bacteria reside inside living tissues like stem, root and leaf of living plant without harming it. They promote the growth, health and development of their host plant by providing protection to the host against biotic (diseases) and abiotic (drought and salinity) stresses [1]. Beneficial effects of plant growth promoting endophytic bacteria on plant drought tolerance is caused by changes in hormonal content, mainly that of abscisic acid, ethylene and cytokinins [2, 3]. These bacteria are expected to have genes responsible for imparting tolerance to host against drought. In the present study, a total of 100 different bacteria were isolated from the root and stem of drought tolerant plant *Butea monosperma*. They were differentiated based on their morphological characteristics and the bacterium MR1 was selected, based on its highly efficient plant growth promoting activities, for whole genome sequencing.

Genomic DNA was extracted from selected bacterium culture using the DNA extraction kit (Invitrogen). Whole genome sequencing of *Enterobacter* spp. MR1 was done using Ion Torrent (PGM), next generation sequencer (NGS) (Life technologies) at Department of Biotechnology, Junagadh Agricultural University, Junagadh according to the manufacturer's recommended protocol to generate 16-fold coverage. A 314 chip with 260 bp enriched library was used in the Ion Torrent machine to generate sequence data.

A total of 82.10 Mb data with 505,210 reads was obtained. The MIRA assembler v3.4.1.0 (Bastien Chevreux, Rheinfelden) [4] was used for assembling the data which resulted in 640 contigs, with the largest contig size of 59,767 bp and GC content of 52.8 %. The assembled contigs sequences were submitted to Rapid Annotations using Subsystems Technology (RAST) system (The Computation Institute, Chicago) [5], RNAmmer 1.2 (Center for Biological Sequence Analysis, Lyngby) [6], and ARAGORN software (Murdoch University, Perth) [7] for further analysis. Based on analysis obtained from the said softwares, 12 different metabolic pathways which were different from the other *Enterobacter* sp. were identified. These pathways may be responsible for imparting drought tolerance to the plant. A total of 80 RNA sequence were identified, of which eight genes were responsible for 5S rRNA synthesis, one gene for 16S rRNA synthesis and one gene for 23S rRNA synthesis. The genome size of *Enterobacter* sp. MR1 was found to be 4.58 Mb and its closest

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neighbors were *Enterobacter* sp. 638 (Genome ID: 399742.10) and *Enterobacter cloacae* subsp. cloacae ATCC 13047 (Genome ID: 716441.4). We have also reconfirmed the 16S rRNA gene sequence by Sanger's sequencing and found 98 % identity with *Enterobacter aerogenes* KCTC 2190 strain and 100 % identity was found with 16S rRNA sequence obtained from whole genome sequence by using RNAmmer-predicted 16S rRNA sequence. All the contigs were submitted to the Gene bank and NCBI has published sequence data in April 2013. The further analysis is going on.

Nucleotide sequence accession numbers This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession ARPV00000000. The version described in this paper is the first version, NZ_ARPV00000000.1 GI: 499134312. Bioproject registered under accession: PRJNA203094 ID: 203094.

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