



Short Communication

Genome sequence announcement of potential phthalic acid degrader *Pseudomonas aeruginosa* HNYM 41 and *Bacillus cereus* BVC 11 isolated from plastic dumping ground area

Chaitanya Raorane¹, Dhananjay Desai^{1*}, Girish Kukreja², Sameer Desai², Chittaranjan Nadkarni²¹Dept. of Microbiology Kankavli College India.²Dept. of Microbiology New Arts Commerce and Science College, Ahmednagar, Maharashtra, India.

Received: 6/21/2017; Accepted: 6/29/2017

Available online: 1st July 2017

Abstract: Putative phthalic acid degrader *Pseudomonas aeruginosa* HNYM 41 and *Bacillus cereus* BVC 11 isolated from plastic dumping ground area of Ahmednagar city. Here we report the genome sequence of HNYM 41 and BVC 11, which have capacity to degradation capacity up to 1500 and 3000 ppm in absent of other carbon source.

Keywords: phthalic acid, *Pseudomonas aeruginosa*, *Bacillus cereus*, Ahmednagar

Introduction

Bioremediation is the economical and environment friendly process of degradation and detoxification of organic contamination by using microbes. Phthalic acid is an important precursor in production of plasticizers as well as cosmetic and nutrition products. Phthalate esters, which can make up 40% weight of some plastic materials. Phthalates have been shown to be nervous system depressants and stimulator, teratogenic and estrogenic mimics [1, 2].

The bacterial strains HNYM 41 and BVC 11 have been isolated from dumping ground area of Ahmednagar [19.0952° N, 74.7496° E], India. Both the isolates showed degradation capacity up to 1500 and 3000 ppm of Phthalic acid in presence of only Phthalic acid is a sole source of carbon. Both the isolate was initially identified as strain of *Pseudomonas aeruginosa* and *Bacillus cereus* respectively based on 16S rRNA gene sequence as well as Polyphasic approach of bacterial identification. 16s rRNA sequencing was performed using a standard protocol by NCCS Pune (MS India) [3, 4, 5] the raw sequence data obtained were used to construct NJ using MEGA5 software. The NCBI BLAST analysis revealed that this isolate shared 100% identity with strains JQ579643.1 and JQ518346.1 [6]. The sequence alignments and phylogenetic analysis revealed that the bacterial strain belongs to *Pseudomonas aeruginosa* HNYM 41 and *Bacillus cereus* BVC 11 respectively. This is the report of a 16 S rRNA genome of potential Phthalic acid degrader microbes. And they showed pronounced Phthalic acid degradation and may be promising candidate for development of new bioremediation system.

Accession numbers

The 16S rRNA genome sequence of the *Pseudomonas aeruginosa* HNYM 41 and *Bacillus cereus* BVC 11 isolate has been deposited in NCBI GenBank under the accession number KX886787 and KX886788. The version described in this report is the first version, KX886787.1 and KX886788.1.

Acknowledgment

We thank the Principal, New Arts Commerce and Science College Ahmednagar, MS, India, for providing necessary facilities for conducting this study. Authors also thankful to Director NCCS Pune, MS, India for genome sequencing Facility.

References

- Feidieker, D., P. Karemper & W. Dott. (1994) "Microbiological and chemical evaluation of a site contaminated with chlorinated aromatic and hexachlorocyclohexanes". *FEMS. Microbiol. Ecol* 15; 265-78.
- Harris, C.A., P. Henttu, M.G. Parker & J.P. Sumpter. (1997) "The estrogenic activity of phthalate esters -In vitro". *Environ. Health Perspect* 105; 802-10.
- Desai, D. A., Kukreja, G. P., Raorane, C. J., Patil, S. B. (2016) Partial Sequencing of Serendipitously Isolated Antifungal Producer, *Pseudomonas tolaasii* Strain GD76 16s Ribosomal RNA Gene. *Int J Curr Microbiol App Sci* 5:1;455-458. <http://dx.doi.org/10.20546/ijcmas.2016.5.11.052>

*Corresponding Author:

Dhananjay Desai,
 Dept. of Microbiology,
 Kankavli College, Kankavali,
 Maharashtra India.

E-mail: dhananjayashokdesai@gmail.com



4. Gauthier, J., Charette, S. J., Derome, N. (2017) Draft Genome Sequence of *Pseudomonas fluorescens* ML11A, an Endogenous Strain from Brook Charr with Antagonistic Properties against *Aeromonas salmonicida* subsp. *Salmonicida*. 5:9; doi:10.1128/genome.A.01716-16.
5. Harris, C.A., P. Henttu, M.G. Parker & J.P. Sumpter. (1997) "The estrogenic activity of phthalateesters -In vitro". *Environ. Health Perspect* 105; 802-10.
6. Raorane, C. J., Gavimath, C. C., Kukreja, G. P., Kalsekar, D. P., Kulkarni, S. M., Ravishankar, B. E., Hooli, R. S. (2012)

Isolation, Identification & Phylogenetic Analysis OF Phthalic Acid Degrading Bacteria. *Int J Adv Biotechnol and Res.* 3:4; 804-809. ISSN 2278-599X.

Cite this article as:

Chaitanya Raorane, Dhananjay Desai, Girish Kukreja, Sameer Desai, Chittaranjan Nadkarni. Genome sequence announcement of potential phthalic acid degrader *Pseudomonas aeruginosa* HNYM 41 and *Bacillus cereus* BVC 11 isolated from plastic dumping ground area. *International Journal of Bioassays* 6.7 (2017) pp. 5444-5445.

DOI: <http://dx.doi.org/10.21746/ijbio.2017.07.004>

Source of support: Nil.

Conflict of interest: None Declared