



## Letter to the Editor

## Complete genome sequence of plant growth promoting *Pseudomonas aeruginosa* AJ D 2 an isolate from monocrop cotton rhizosphere

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## ABSTRACT

A plant growth promoting *Pseudomonas aeruginosa* AJD 2 was isolated from monocrop cotton rhizosphere of Maharashtra state, India. The strain was identified as per physiological, biochemical and 16S rRNA gene sequencing (Accession number MG234531). The strain possess multiple functional plant growth promoting traits and antifungal activity. The genome was extracted, purified and library of avg.515 bp was prepared and sequenced by over Illumina platform. The sequenced genome was studied by using CLC workbench and NCBI pipeline using *Pseudomonas aeruginosa* PAO1 and *Pseudomonas aeruginosa* YL84 as reference assembler. The size of the genome is 6.1 Mb with 5802 genes within it. The study over strain may give an insight into its plant growth promotion mechanism.

## 1. Introduction

*Pseudomonas aeruginosa* AJ D2 a plant growth promoting strain was isolated from monocrop cotton rhizosphere of Maharashtra state, India. The isolate possess antifungal and plant growth promotion activity [1,2]. The isolate was able to possess the genes for pyocyanin-production, phosphate solubilisation-exopolyphosphatase, zinc tolerance, Polyhydroxy alkanonate (PHA) synthetase, urease, siderophore producing genes. The rhizosphere isolate also possess genes for multi-drug efflux, haemagglutinin and neuraminidase surface producing genes with type VI secretion system.

The sequencing of isolate was performed using Illumina platform with 2 × 150 paired-end chemistry. The high quality reads were aligned to *Pseudomonas aeruginosa* PAO1 and *Pseudomonas aeruginosa* YL84 reference genome using CLC genomics workbench 7 [3,4]. In total, 93.56% of reads were mapped to the *Pseudomonas aeruginosa* PAO1 and 93.21% of reads were mapped to the *Pseudomonas aeruginosa* YL84 reference genome, resulting in a genome-wide coverage of ~97% on *Pseudomonas aeruginosa* PAO1 and 94% on *Pseudomonas aeruginosa* YL84. A total of 5572 gene sequences were extracted from consensus file of *Pseudomonas aeruginosa* PAO1 and 5998 gene sequences were extracted from consensus file of *Pseudomonas aeruginosa* YL84 for AJD2 sample. The GO distribution was carried out using Blast2GO command line 1.4.1. A total of 1650 GO terms were assigned to Biological Process, 1077 GO terms to Cellular Component and 1702 GO terms to Molecular Function in *Pseudomonas aeruginosa* PAO1 and a total of 1758 GO terms were assigned to Biological Process, 1138 GO terms to Cellular Component and 1814 GO terms to Molecular Function in *Pseudomonas aeruginosa* YL84. In total of 28,814 SNPs were found using *Pseudomonas aeruginosa* PAO1 and 28,901 SNPs were found using *Pseudomonas aeruginosa* YL84.

The genome is available over NCBI with accession number CP038661.1. [5,6]The NCBI pipeline shows total 5882 genes, out of

5702 were coding genes and 100 were pseudogenes. Out of the 80 RNA genes isolate contain 64 genes for tRNA, 12 genes for rRNA and 4 genes for ncRNA.

The genome study over *Pseudomonas aeruginosa* AJ D2 may give an insight over the plant growth promotion and virulence activity of strain.

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