Data in Brief

**Genome sequence of Ochrobactrum anthropi strain SUBG007, a plant pathogen and potential xenobiotic compounds degradation bacterium**

Kiran S. Chudasama, Vrinda S. Thaker *

Centre for Advanced Studies in Plant Biotechnology and Genetic Engineering, Department of Biosciences, Saurashtra University, Rajkot 360 005, Gujarat, India

**A B S T R A C T**

Ochrobactrum anthropi SUBG007 was isolated from the fruit of Prunus dulcis in Rajkot (22.30°N, 70.78°E), Gujarat, India. Here we present the 4.37 Mb genome sequence strain SUBG007, which may provide the genetic information for the application in environment pollution degradation and agriculture field. The strain also passes many genes cluster which involved in production of important secondary metabolites. The nucleotide sequence of this genome was deposited into NCBI GenBank under the accession LUAY00000000.

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**Keywords:**

*O. anthropi*
Plant pathogen
Xenobiotic compounds
Secondary metabolites

1. Direct link to deposited data

   https://www.ncbi.nlm.nih.gov/nuccore/LUAY00000000

   *Ochrobactrum anthropi* is a gram–negative, aerobic, non-fermentative bacterium from the family Brucellaceae belonging to alphaproteobacterial, order Rhizobiales [1]. This organism strains are broadly distributed from diverse habitats including soil, plant and their rhizosphere, environment, waste water, animals and humans [2,3]. *O. anthropi* is known to produce important enzymes that degrade the pesticides, petroleum waste and pollutant [4]. The complete genome sequence of *O. anthropi* strain SUBG007 is reported here and will provide genomic information on the specific properties of this strain.

2. Experimental design, materials and method

   *O. anthropi* SUBG007 strain was isolated from infected fruit of *Prunus dulcis*. Genomic DNA was extracted from the strain *Ochrobactrum anthropi* SUBG007 according to [5]. Whole-genome shotgun sequencing of *O. anthropi* SUBG007 was performed using a high throughput ion torrent personal genome machine with ion torrent server (torrent suite v3.2), and with 50× coverage was obtained. De novo assembly was performed using Velvet assembler (v. 1.2.10). The annotation of the genome was performed using the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP) (http://www.ncbi.nlm.nih.gov/genome/annotation_prok/) utilizing GeneMark, Glimmer, and tRNAscan-SE tools [6] and functional annotation was carried out using the Rapid Annotations using subsystems Technology (RAST) server with the seed database [7]. Preliminary reference-based annotation using PATRIC was carried out to identify conserved pathways [8].

3. Data description

   The total length of genome was estimated to be 4.37595 bp and contained 21 tRNA, 7rRNA and 5 ncRNA. Fig. 1 presents an overview of the count of each subsystem feature and the subsystem coverage of RAST server annotation. According to RAST annotated, *O. santhrophi* having very important Type I and Type IV secretion system (T4SS), which are essential for the pathogenicity. Type IV systems are multi-component, transenvelope complexes that translocate proteins and nucleoprotein complexes from donor cells to recipient cells in processes related to bacterial conjugation.

   The annotation revealed that genome of strain SUBG007 contains a large number of genes responsible for the degradation of xenobiotic compounds.
of xenobiotic compounds. The xenobiotic compound are involved gamma-Hexachlorocyclohexane, 1,1,1-Trichloro-2,2-bis(4-chlorophenyl)ethane (DDT) degradation, benzoate degradation via hydroxylation, bisphenol, biphenyl, toluene and xylene, 1-2-methylnaphthalene, tetrachloroethene, naphthalene, anthracene, 1,4 Dichlorobenzene, ethylbenzene, styrene and caprolactam. The genome SUBG007 was contained the gene cluster related with the biosynthesis of some secondary metabolites like pucimycin, novo-biocin, vancomycin, penicillin, puroycin, cephalosporium, flavonoid, phenyl propanoid and isoquinoline alkaloid. Interestingly genome also posses the key genes involved, IAA secretion and nitrogen metabolism genes.

Availability of the genome sequence SUBG007 provides opportunities for biotechnological exploitation of genome features related to the biosynthetic studies of some important secondary metabolite and provide promising application in bioremediation. This sequence will lead to a better understanding of its evolution and the development of biotechnological applications and the mechanisms of pathogenicity.

4. Nucleotide sequence accession number

The SUBG007 draft genome sequence has been deposited at GenBank under the accession LUAY00000000.

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