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Short communication

Draft genome sequence of phenol degrading *Acinetobacter* sp. Strain V2, isolated from oil contaminated soil

*Vikas Sharma, Johnson Lin**

University of KwaZulu-Natal (Westville), School of Life Sciences, Department of Microbiology, Durban, South Africa

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ABSTRACT

We report here the draft genome sequence of *Acinetobacter* sp. Strain V2 isolated from the oil contaminated soil collected from ENGEN, Amanzimtoti, South Africa. Degradation of phenolic compounds such as phenol, toluene, aniline etc. at 400 ppm in 24 h and oil degrading capability makes this organism an efficient multifunctional bioremediator. Genome sequencing of *Acinetobacter* spp. V2 was carried out on Illumina HiSeq 2000 platform (performed by the Beijing Genomics Institute [BGI], Shenzhen, China). The data obtained revealed 643 contigs with genome size of 4.0 Mb and G + C content of 38.59%.

Genome announcement

Acinetobacter spp. have been involved in bioremediation of various pollutants such as phenols, benzoate, crude oil, acetonitrile etc.[1,2] and biotechnological applications like production of extra-and-intracellular lipases, proteases, bioemulsifiers and various types of biopolymers.[3,4] Physiological and genetic characterisation of large number of phenol-degrading bacteria isolated from various sources have been done,[5,6] however, little information on bacteria with a high phenol tolerance and high metabolising activity is available.[7] Substrate inhibition and low degradation rate are the key factors which limits their applications.[8] *Acinetobacter* sp. V2 strain is able to degrade 400 ppm of phenol within 24 h.[9] Presence of commercially important proteins apart from its ability to degrade diesel and engine oil makes this organism unique and thus genome sequencing.

Whole-genome sequencing was carried using Illumina HiSeq 2000 platform (Beijing Genomics Institute [BGI], Shenzhen, China) by generating paired-end libraries with an average insert size of 500 bp following the manufacturer's instructions. The reads were then aligned with the reference sequence using SOAPaligner (version 2.21) software to calculate average depth and coverage ratio (http://soap.genomics.org.cn/soapaligner.html, version 2.21).[10] The filtered short reads were first de novo assembled using SOAPdenovo v 2.04 according to the method described previously (http://soap.genomics.org.cn/soapdenovo.html),[11] and then contigs were manually connected according to their 500 bp paired-end relationships. The draft genome sequence of *Acinetobacter* sp. V2 strain comprised of 643 contigs and

* *Corresponding author at*: Microbiology Discipline, School of Life Sciences, University of KwaZulu-Natal (Westville), Private Bag X54001, Durban 4000, South Africa.
E-mail: linj@ukzn.ac.za (J. Lin).

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Table 1 – General features of the *Acinetobacter* sp. Strain V2 genome.

Sl. No.	Features	Values
1	Genome Size (bp)	4,007,850
2	DNA G + C content (%)	38.59
3	Total contigs	643
4	Total genes (CDS)	3717
5	rRNA	14
6	tRNA	71
7	Genes with predicted function	2971

16 scaffolds with the maximum contig size of 910,143 bp and scaffold size of 1,913,879 bp (Table 1). The genome size was 4,007,850 bp at 109.2 × coverage, with N50 of 466,223 bp and N_{90} of 97,271 bp and G + C content was 38.59%. A total of 3717 coding sequences (CDSs) or ORFs were predicted using Glimmer v3.02,[12] and homologous comparison to a non-redundant public database was performed by BLAST for function annotation. The genome annotation was performed using the (BASys) server (https://www.basys.ca/) and the output was downloaded in GenBank format resulting in 3742 (CDSs).[13] The genome was further annotated with Rapid Annotation using Subsystems Technology (RAST) server (http://rast.nmpdr.org/).[14] Among the predicted 3742 protein-coding genes by BASys, 79.4% (2971genes) have been assigned putative functions according to the subsystem categorization. A total of 71 tRNA genes encompassing all 20 amino acids were identified using the tRNAscan-SE program,[15] 14 rRNA genes were identified using RNAmmer[16] and the insertion sequence (IS) elements were annotated by ISsaga.[17] All the contigs were submitted to the Gene bank and NCBI has published sequence data in April 2015. The further analysis is going on.

Nucleotide sequence accession numbers: This WGS project has been deposited at DDBJ/EMBL/GenBank under the accession JZFB00000000. The version described in this paper is version JZFB01000000. Bioproject registered under accession: PRJNA275383 ID: 275383. The *Acinetobacter* sp. V2 isolate was deposited at the Leibniz Institute DSMZ-German Collection of Microorganisms and Cell Cultures and is available under the Accession No. DSM 101893.

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