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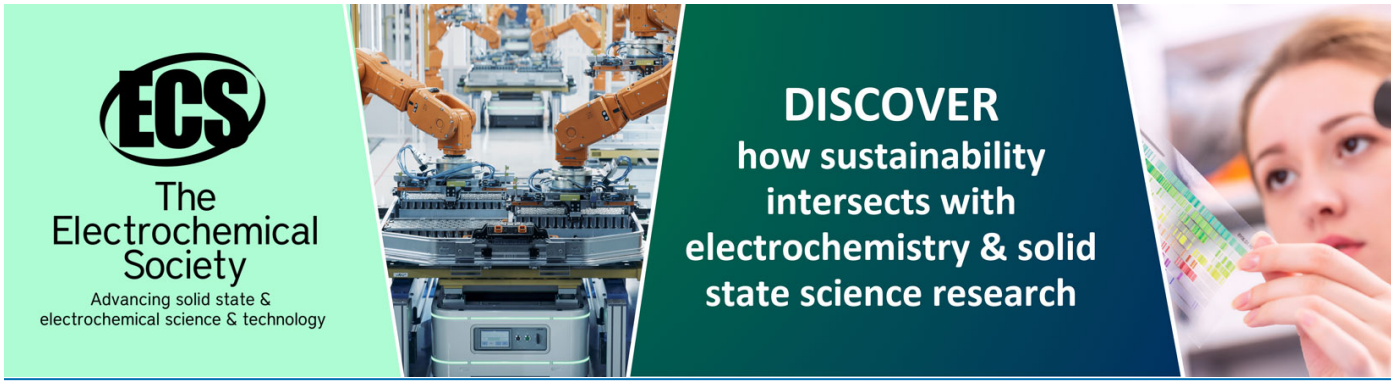

Genome sequencing of *Acinetobacter radioresistens* LY strain and XF strain, isolated from peanut bacterial wilt nursery

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Abstract. *Acinetobacter radioresistens* was widely found in nature and it has been used to biodegrade methyl parathion and phenol for reducing pesticide pollution. Here, we report two draft genome sequences of *A.radioresistens* LY strain and XF strain which was isolated from bacterial wilt (BW) infected peanut (*Arachis hypogaea*) samples in Lin Yi city and Xiang Fan city of China, respectively. *A.radioresistens* may have relationship with *Ralstonia solanacearum* which causing BW. The studies may help to control peanut BW.

1. Introduction

Acinetobacter are widely found in soil and water [1-2]. It is reported that *Acinetobacter radioresistens* can biodegrade methyl parathion (MP) [3] and phenol [4] for reducing pesticide pollution. Here, two strains of *A. radioresistens* were identified from peanut plant which is infected by bacterial wilt at Lin Yi city and Xiang Fan city of China, respectively. In the present study two draft genome of *A. radioresistens* (LY strain and XF strain) were reported. *A. radioresistens* may have relationship with *Ralstonia solanacearum* which causing BW. The studies may help to control peanut BW.

A single colony of two strains were cultured by TZC plate (nutrient agar supplemented with 0.05% tetrazolium chloride) and incubated at 28 ºC for 48 h. Then one single clone was inoculated into liquid YGPA (1L including: 5 g yeast extract, 5 g peptone, 10 g glucose, pH = 7.2) and shook at 28 ºC for 48 h. And the DNAs were got by Genomic DNA Kit (Tiangen, Beijing, China). The *A. radioresistens* genomes of two strains have sequenced using Illumina MiSeq. The average size of insert fragment was 400 base pair (bp). 449.8 M and 420.8 M clean data have been got for LY strain and XF strain with 138-fold coverage, respectively. For LY strain, 147 contigs (0.221 Mbp mean length) and 137 scaffolds (0.238 Mbp mean length) were gained from 951,691 trimmed reads (236 bp mean length). Finally, 3.2 Mbp draft genome sequence was assembled de novo by using Newbler v2.8 (20110517_1502). For XF strain, 906,087 trimmed

reads (232 bp mean length) were used to assemble 3.0 Mbp draft genome sequence. 263 contigs (0.116 Mbp mean length) and 256 scaffolds (0.119 Mbp mean length) were obtained.

Glimmer v3.0 software was used to predict protein coding sequence [5]. Rfam, RNAmmer v1.2 and tRNAscan-SE were employed for prediction of non-coding RNA genes [6-8]. Genes encoding protein were found and analyzed using blastall software and Swiss-Prot (https://www.uniprot.org/). KEGG annotation were analyzed by KEGG databases.

The genome GC% content of LY strain and XF strain were 41.8% for and 42.1%, respectively. For LY strain, it consists of 3,022 genes encoding protein accounting for 85.8% of whole genome. Mean length was 926 bp and average GC% content was 43.3%. In total, 89 RNA genes (5 rRNAs, 71 tRNAs and 13 ncRNA) were identified which covered 0.54% of the genome sequence. The average length was 168 bp. For XF strain, 2,845 genes encoding protein were identified which covers 86.3% of whole genome with 927.7 bp average length. Mean GC% content of ORF sequence was 43.5%. Total 78 RNA genes (4 rRNAs, 61 tRNAs and 13 ncRNA) were got covering 0.38% of the genome sequence. The average length was 151 bp. This is the first report of *A. radioresistens* found in the bacterial wilt nursery. The studies may help to exploit a new method to control bacterial wilt.

2. Nucleotide sequence accession number

The GenBank accession numbers of *A. radioresistens* LY strain was QIBR00000000 and XF strain was QIBT00000000. The SRA accession numbers were SRR8442722 and SRR8453715, respectively and were associated with BioProject number PRJNA471387 and PRJNA471390.

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