Genome Sequence of *Acinetobacter* sp. Strain HA, Isolated from the Gut of the Polyphagous Insect Pest *Helicoverpa armigera*

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In this study, *Acinetobacter* sp. strain HA was isolated from the midgut of a fifth-instar larva of *Helicoverpa armigera*. Here, we report the draft genome sequence (3,125,085 bp) of this strain that consists of 102 contigs, 2,911 predicted coding sequences, and a G+C content of 41%.

Acinetobacter sp. strain HA was isolated from the midgut of a fifth-instar larva of *Helicoverpa armigera* collected from an agricultural field in Maharashtra, India (7). The strain exhibited enhanced esterase activity and facilitated the metabolism of the insecticide cypermethrin, which can thus contribute to insect resistance (1). Here, we report the draft genome sequence of strain HA using the Roche 454 GS (FLX Titanium) system (3-kb paired-end library; 511,555 reads) that led to ~45-fold coverage of the entire genome. The reads generated were assembled into 102 contigs by using Ray *de novo* assembler version 0.0.3 set at a k-mer length of 25 (3). The final assembly was validated using paired-end constraints (N_{50} contigs, 68.4 kb). The draft genome was annotated using RAST version 4.0 (2), NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP; <http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html>), and the KEGG database (4).

The draft genome of *Acinetobacter* sp. HA represents a genome size of 3,125,085 bp with an average G+C content of 41%. A total of 2,911 protein-coding sequences and 932 hypothetical proteins were predicted on annotation. The genome contains 66 tandem repeats, and the coding density was calculated to be 84.83%. Sixty-four predicted tRNA genes, representing all amino acids, were identified by using tRNAscan-SE (6). Four copies of 5S rRNA, 2 copies of 23S rRNA, and 2 copies of 16S rRNA were found in the sequence by using RNAmmer (5). In addition, 123 predicted transposase genes but no gene coding for pyruvate kinase, a key component in carbohydrate metabolism, were found. However, 3 polyglutamic acid (PGA) synthesis-related protein-coding genes responsible for biofilm formation were present. Also, the presence of genes coding for esterase enzyme have been observed. Annotations by RAST revealed 383 subsystems and 45 genes relevant to resistance to antibiotics, and toxic compounds were found. Among these, 9 genes coding for cobalt-zinc-cadmium resistance and 14 coding for multidrug resistance efflux pumps were found. RAST results also indicated *Acinetobacter lwoffii* SH145 (score, 520), *Acinetobacter baumannii* AB0057 (score, 518), and *Acinetobacter baumannii* ACICU (score, 518) as the closest neighbors of strain HA. Detailed analysis of the genome sequence of *Acinetobacter* sp. HA will further

provide a comprehensive understanding toward predicting its role in metabolizing insecticides and hence conferring resistance to *Helicoverpa armigera*.

Nucleotide sequence accession number. The genome sequence of *Acinetobacter* sp. strain HA is available in GenBank under accession number [AJXD000000000](https://www.ncbi.nlm.nih.gov/nuclseq/AJXD000000000).

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