LBNL-62928
Preprint

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Title

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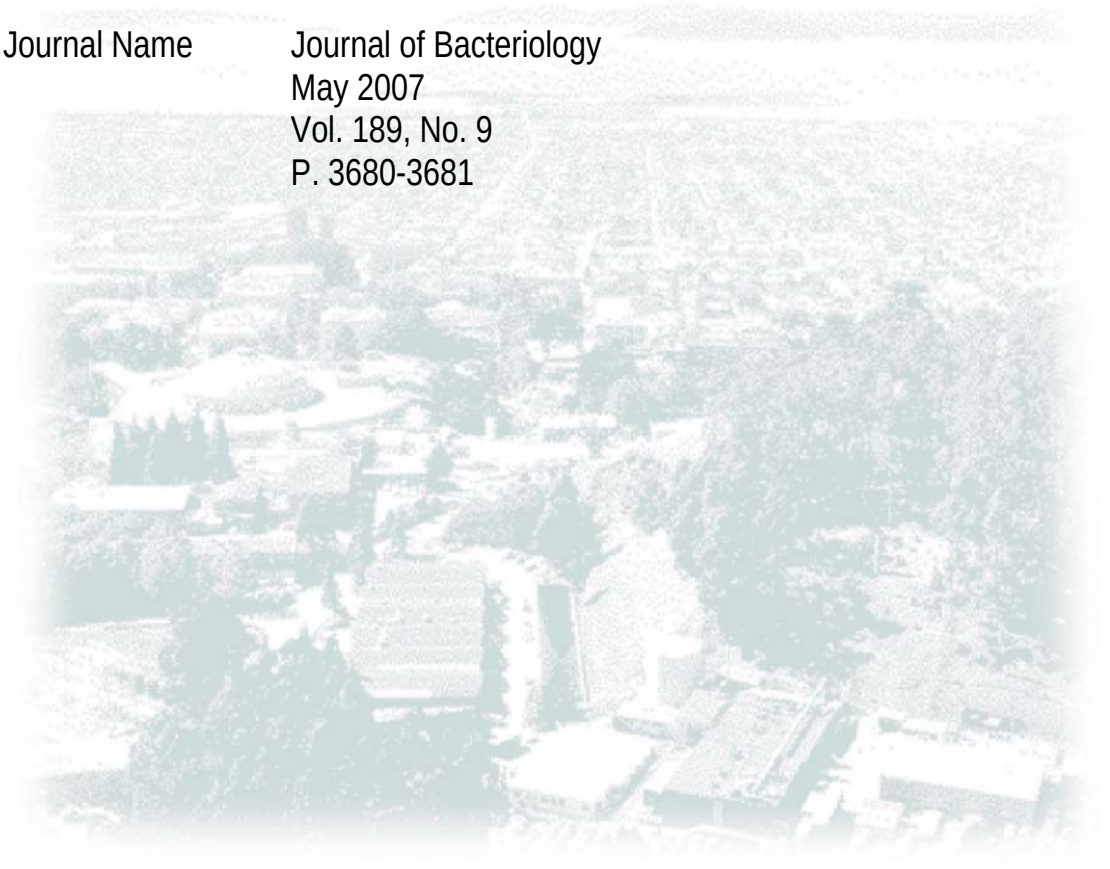
Division Genomics

Journal Name Journal of Bacteriology
May 2007
Vol. 189, No. 9
P. 3680-3681



The Complete Genome Sequence of *Bacillus thuringiensis* Al Hakam

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Abstract

Bacillus thuringiensis is an insect pathogen that is widely used as a biopesticide (3). Here we report the finished, annotated genome sequence of *B. thuringiensis* Al Hakam, which was collected in Iraq by the United Nations Special Commission (2).

Methods, Results and Discussion

The *Bacillus thuringiensis* Al Hakam genome was sequenced at the Joint Genome Institute (JGI) using plasmid and fosmid DNA libraries. Draft assemblies were based on 246217 total reads. All libraries provided 23x coverage of the genome. The Phred/Phrap/Consed software package (http://www.phrap.com) was used for sequence assembly and quality assessment. After shotgun sequencing, reads were assembled with parallel phrap (High Performance Software, LLC). Possible mis-assemblies were corrected by transposon bombing (Epicentre Biotechnologies) of bridging clones. Gaps between contigs were closed by editing in Consed, by custom primer walks, or by PCR amplification. The complete genome of *B. thuringiensis* Al Hakam achieves an average of 24-fold sequence coverage per base with an error rate of less than 1 in 100,000. The sequences comprising the *B. thuringiensis* Al Hakam genome can be accessed using the GenBank accession numbers CP000485 and CP000486.

Gene predictions were obtained and annotation was performed as described previously (1). The 5.31 Mb genome of *B. thuringiensis* Al Hakam contains two replicons: a circular chromosome (5.26 Mb) encoding a predicted 4969 ORFs, and the pALH1 circular phage, which contains 62 predicted ORFs. The G+C content of the chromosome is 35%, while that of the phage is 36%. The *B. thuringiensis* Al Hakam genome encodes 105 tRNAs, 13 rRNA operons, and contains at least 21 pseudogenes. There were no additional plasmids identified in the assembly. Blast searches against the *B. thuringiensis* Al Hakam genome using known insecticidal genes (*cry*, *cyt* and *vip*) as queries revealed no chromosomally (or phage) encoded ORFs with significant similarity. Therefore, we conclude that this genome contains no homologues of the known *cry*, *cyt* or *vip* genes. However, if they were present originally, it is possible that the plasmid(s) encoding these genes was lost during culture.

Previous AFLP analyses have shown that *B. thuringiensis* Al Hakam is a member of the *B. cereus* group that is of intermediate relatedness (in terms of sequence identity) to *B. anthracis* (2). The *B. thuringiensis* Al Hakam genome provides new sequence data that can be used to further study the evolutionary relationships among *B. cereus* group organisms.

This program is supported by the U.S. Department of Energy under contract no. W-7405-ENG-36.

This work was performed under the auspices of the US Department of Energy's Office of Science, Biological and Environmental Research Program, and by the University of California, Lawrence Livermore National Laboratory under Contract No. W-7405-Eng-48, Lawrence Berkeley National Laboratory under contract No. DE-AC02-05CH11231 and Los Alamos National Laboratory under contract No. DE-AC52-06NA25396.

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