GENOME ANNOUNCEMENT

The Complete Genome Sequence of *Bacillus thuringiensis* Al Hakam[▽]

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***Bacillus thuringiensis* is an insect pathogen that is widely used as a biopesticide (E. Schnepf, N. Crickmore,
J. Van Rie, D. Lereclus, J. Baum, J. Feitelson, D. R. Zeigler, and D. H. Dean, Microbiol. Mol. Biol. Rev.
62:775–806, 1998). Here we report the finished, annotated genome sequence of *B. thuringiensis* Al Hakam, which
was collected in Iraq by the United Nations Special Commission (L. Radnedge, P. Agron, K. Hill, P. Jackson,
L. Ticknor, P. Keim, and G. Andersen, Appl. Environ. Microbiol. 69:2755–2764, 2003).**

The *Bacillus thuringiensis* Al Hakam genome was sequenced at the Joint Genome Institute using plasmid and fosmid DNA libraries. Draft assemblies were based on 246,217 total reads. All libraries provided 23-fold coverage of the genome. The Phred/Phrap/Consed software package was used for sequence assembly and quality assessment. After shotgun sequencing, reads were assembled with parallel phrap (High Performance Software, LLC). Possible misassemblies were corrected by transposon bombing (Epicenter 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 4,969 open reading frames (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 and 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 chromosome-encoded (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 phylogenetically more closely related to *B. anthracis*

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and other "Branch F" *Bacillus* isolates than to many of the commercially important *B. thuringiensis* isolates (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.

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