Draft Genome Sequence of *Bacillus thuringiensis* Strain S2160-1 with High Mosquitocidal Activity

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**Abstract** *Bacillus thuringiensis* strain S2160-1 had been identified with high mosquitocidal activity, it was proposed as an alternative to Bti. Here we reported the genome sequence of Bt Strain S2160-1. A total of 703M (96.3% of the all 730 M reads) high-quality bases (112-fold genome coverage) were assembled into a 6.32-MbBt genome with a scaffold N50 length of 266,799 bp and contig N50 length of 104,502 bp. The 6.32 Mb genome of S2160-1 contains three replicons, including a 5.46 Mb chromosome sequence and a 853 kb plasmid sequence that consist of two plasmids with the size of 544 kb and 309Kb respectively. The average GC content of the chromosome sequence is 35.03%, while that of the plasmid sequences are 32.66%, and 33.04%. The four toxins of the insecticide genes *cry30Ea*, *cry30Ga*, *cry50Ba* and *cry54Ba* previously cloned in *Bt* S2160-1 were confirmed by genomic sequencing. Additional Two *cry* genes that might encode two known140kDa and 130kDa toxins were identified in Scaffold 55, 46 and 73.

**Keywords** *Bacillus thuringiensis*; Strain S2160-1; Genome sequence; Mosquitocidal activity

*Bacillus thuringiensis* subspecies *israelensis*, commonly referred to as Bti, is a bacterium found naturally in soils and first discovered in 1976 in Israel. Bti produces toxins which are effective in killing various species of mosquitoes, fungus gnats, and blackflies (Sanahuja et al. 2011; Schnepf et al. 1998). However, a new *Bacillus thuringiensis* strain, Bt S2160-1 was proposed as an alternative to Bti (Zhang et al. 2012), which produces high mosquitocidal toxins with proteomic profile of 140kDa, 130kDa, 75kDa and 30kDa (Fang and Zhang, 2012). In the previous study, the *Cry30Ea*, *Cry30Ga*, *Cry50Ba* and *Cry54Ba* in BtS2160-1 were identified by PCR approach but three distinguishing bands of parasporal proteins with 140 kDa, 130 kDa and 30 kDa in size still remains unknown (Zhang et al. 2012). The dominant toxin of this strain has not yet been identified as well. To further understand the genetic basis and toxic mode of this *Bacillus thuringiensis* strain, we sequenced its whole genome.

The sequencing of Bt S2160-1 genome was performed in the Beijing Genomics Institute (BGI, Shenzhen, China) by using an IlluminaHiseq2000 Sequencing platform. A total of 703M (96.3% of the all 730 M reads) high-quality bases (112-fold genome coverage) were assembled into a 6.32-MbBt genome with a
scaffold N50 length of 266,799 bp and contig N50 length of 104,502 bp. The scaffolding was performed by the SOAPdenovo v1.05 (BGI) with the parameter 63 K-mer. And there were 207 contigs in the final assembly. Over 89.85% of the assembly was represented by 82 scaffolds and the largest scaffold was 670,660 bp. The 34.81% GC content of the Bt S2160-1 genome is similar to that of other Bti.

The 6.32 Mb genome of S2160-1 contains three replicons, including a 5.46 Mb chromosome sequence and a 853 kb plasmid sequence that consist of two plasmids with the size of 544 kb and 309 kb respectively. The average GC content of the chromosome sequence is 35.03%, while that of the plasmid sequences are 32.66% and 33.04%. The whole genome contains 6,404 protein-encoding genes, 59 tRNA, and 2 rRNA-encoding operons. Approximately 20.06% of all coding sequences (a total of 6,404) were assigned to COGs, and 1268 CDSs can be annotated into the KEGG orthology system by using KAAS.

Bt Toxin genes were predicted via BTToxinDB™. The four toxins of the insecticide genes cry30Ea, cry30Ga, cry50Ba and cry54Bap previously cloned in Bt S2160-1 were confirmed by sequencing. Additional two cry genes that might encode two known 140 kDa and 130 kDa toxins were identified in Scaffold 55, 46 and 73.

![Figure 1 The draft map of Bt2160-1](image)

**Nucleotide sequence accession**

The draft genome sequence of Strain S2160-1 has not yet included in the GenBank but deposited in the database maintained by The HITAR Institute Canada Inc. The annotated chromosome and plasmids would be available upon request.

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