

(1993), Klier, et al., EMBO J. 1: 791-799 (1982), Kronstad, et al., J. Bacteriol. 154: 419-428 (1983)).

[0008] *Bacillus thuringiensis* strains often contain multiple epigenetic elements which are known to harbor genes expressing vegetative insecticidal proteins (VIP's) and Bt crystalline insecticidal and nematocidal proteins. It is believed that many other Bt insecticidal/nematocidal genes are present within these sequences, some of which may only be expressed under conditions which cannot be artificially simulated, some of which may be cryptic, and some of which may be actively expressed but which have not been previously identified due to their limited availability as a result of very low levels of expression. Identification of whole or substantial portions of DNA sequences of individual plasmids would greatly facilitate identification of genes encoding novel insect inhibitory proteins. However, when one tries to isolate and purify plasmid DNA of a *B. thuringiensis* species for constructing genomic DNA libraries used in sequencing it would be difficult to eliminate the contamination of chromosomal DNA. Such contamination would complicate greatly the sequencing effort of individual plasmids and subsequently hinder construction of genetic maps of individual plasmids of the *B. thuringiensis* species. Thus, it would be desirable to generate the complete DNA sequence of the chromosomal genome exclusive of epigenetic sequences of a *B. thuringiensis* species, because the complete DNA sequence of the chromosome could be used as a background to significantly minimize the interference of chromosomal DNA sequences in identification of whole or a substantial portion of individual plasmids and of novel genes encoding insect inhibitory proteins.

[0009] Furthermore, although it is unexpected that the complete DNA sequence of the *Bacillus thuringiensis* chromosomal genome exclusive of epigenetic sequences would provide a substantial number of Bt crystalline insecticidal/nematocidal and VIP genes for second generation insect/pest control in crop species, comparison of the open reading frames present within the *Bacillus thuringiensis* chromosomal genome with other bacterial genome sequences, in particular other *Bacillus* species genomic sequences would allow the subtraction of common sequences and thus the identification of sequences novel and unique to *Bacillus thuringiensis*, and which may play a role in the regulation of expression or activity of genes encoding insecticidal proteins, and may also provide a plethora of useful genes for future insect resistance management technologies and applications. Therefore, it is advantageous to generate the complete DNA sequence of the chromosomal genome exclusive of epigenetic sequences of a *B. thuringiensis* species.

[0010] Chromosomal genome sequence information from *B. thuringiensis* allows comparisons of those sequences with sequences from other *B. thuringiensis* strains as well as comparisons with DNA sequences from other organisms, including plants, mammals such as humans, bacteria, and fungi such as yeasts. In addition, genome sequencing and mapping provides increased opportunities for identification and isolation of agents of commercial interest, as well as insight into mechanisms of genome interactions.

SUMMARY OF THE INVENTION

[0011] The present invention provides an isolated and purified nucleic acid molecule having a first nucleotide sequence, wherein: (1) the first nucleotide sequence hybridizes under stringent conditions to a second nucleotide sequence selected

from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 8283 or complement thereof, wherein the hybridizing portion of the second nucleotide sequence is at least 50 nucleotides in length; (2) the first nucleotide sequence is a portion of third nucleotide sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 8283; or (3) the first nucleotide sequence is the complement of (1) or (2).

[0012] In a preferred embodiment, the hybridizing portion of the second nucleotide sequence is at least 100 nucleotides in length. In a more preferred embodiment, the hybridizing portion of the second nucleotide sequence is at least 200 nucleotides in length. In a further more preferred embodiment, the hybridizing portion of the second nucleotide sequence encodes any polypeptide or protein or set forth in Table 1.

[0013] The present invention also provides an isolated and purified nucleic acid molecule comprising a nucleotide sequence, wherein: (1) the nucleotide sequence encodes any polypeptide or protein set forth in Table 1; or (2) the nucleotide sequence is the complement of (1).

[0014] The present invention, in another aspect, provides a substantially purified polypeptide or protein comprising an amino acid sequence, wherein the amino acid sequence is defined as follows: (1) the amino acid sequence is encoded by a first nucleotide sequence which specifically hybridizes to the complement of a second nucleotide sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 8283; or (2) the amino acid sequence is encoded by a third nucleotide sequence that is at least 50% identical to a portion of the complement of a sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 8283. In alternative embodiments, the above described third nucleotide sequence is at least 55% identical, at least 60% identical, at least 65% identical, at least 70% identical, at least 75% identical, at least 80% identical, at least 85% identical, at least 90% identical, or at least 95% identical to a portion of a sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 8283; and, the above described third nucleotide sequence is identical to a portion of a sequence selected from SEQ ID NO: 1 through SEQ NO: 8283.

[0015] The present invention also provides a recombinant construct comprising: (A) a promoter region which functions in a host cell to cause the production of an mRNA molecule; which is operably linked to (B) a structural nucleotide sequence, wherein the structural nucleotide sequence encodes a polypeptide or protein set forth in Table 1; which is operably linked to (C) a 3' non-translated sequence that functions in said cell to cause termination of transcription.

[0016] The present invention also provides a recombinant construct comprising: (A) a promoter region which functions in a host cell to cause the production of an mRNA molecule wherein the promoter region is selected from the group consisting of promoter sequences located within SEQ ID NO: 1 through SEQ ID NO: 8283 or complements thereof; which is linked to (B) a structural nucleotide sequence encoding a polypeptide; which is linked to (C) a 3' non-translated sequence that functions in said cell to cause termination of transcription.

[0017] The present invention also provides a transformed cell having an exogenous nucleic acid molecule which comprises: (A) a promoter region which functions in said cell to cause the production of an mRNA molecule; which is operably linked to (B) a structural nucleic acid molecule, wherein the structural nucleotide encodes any polypeptide or protein