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(54) **CONSTRUCTION OF A QUADRUPLE
ENTEROTOXIN-DEFICIENT MUTANT OF
BACILLUS THURINGIENSIS**

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10, 2010.

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(52) **U.S. Cl.**

CPC **C12N 15/75** (2013.01); **A01N 63/00**
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(2013.01); **C12N 1/20** (2013.01)

(58) **Field of Classification Search**

None

See application file for complete search history.

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(57) **ABSTRACT**

Some HBL and NHE enterotoxins are known to cause
food-borne diseases in humans. Enterotoxin-deficient
mutants of member strains of the *Bacillus cereus* group that
do not produce HBL, HBL_{a1}, HBL_{a2}, or NHE enterotoxins
are disclosed. Enterotoxin-deficient mutants are suitable for
use as biocontrol agents. Methods for making the mutants
and for using the mutants are described.

10 Claims, 4 Drawing Sheets

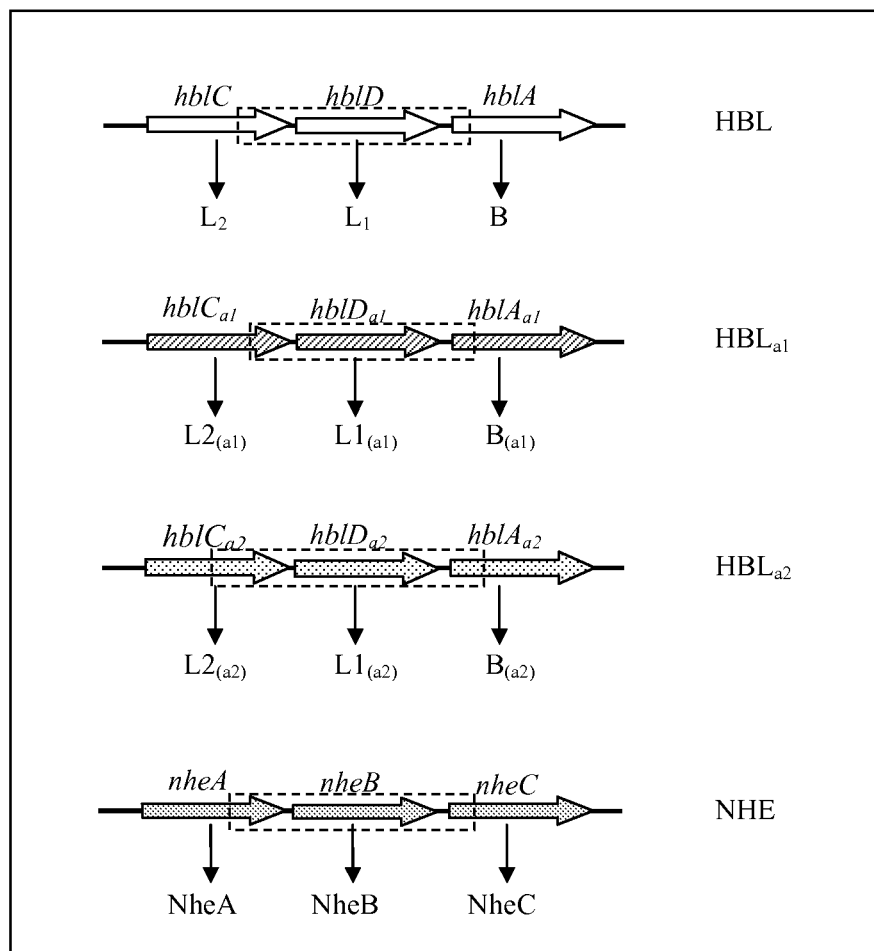


Fig. 1

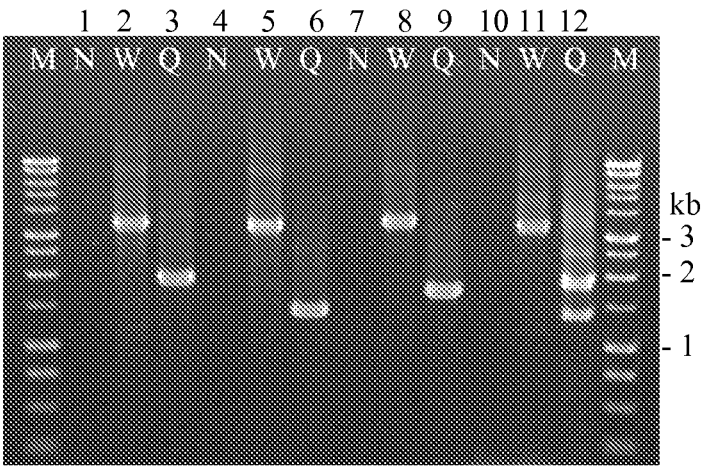


Fig. 2

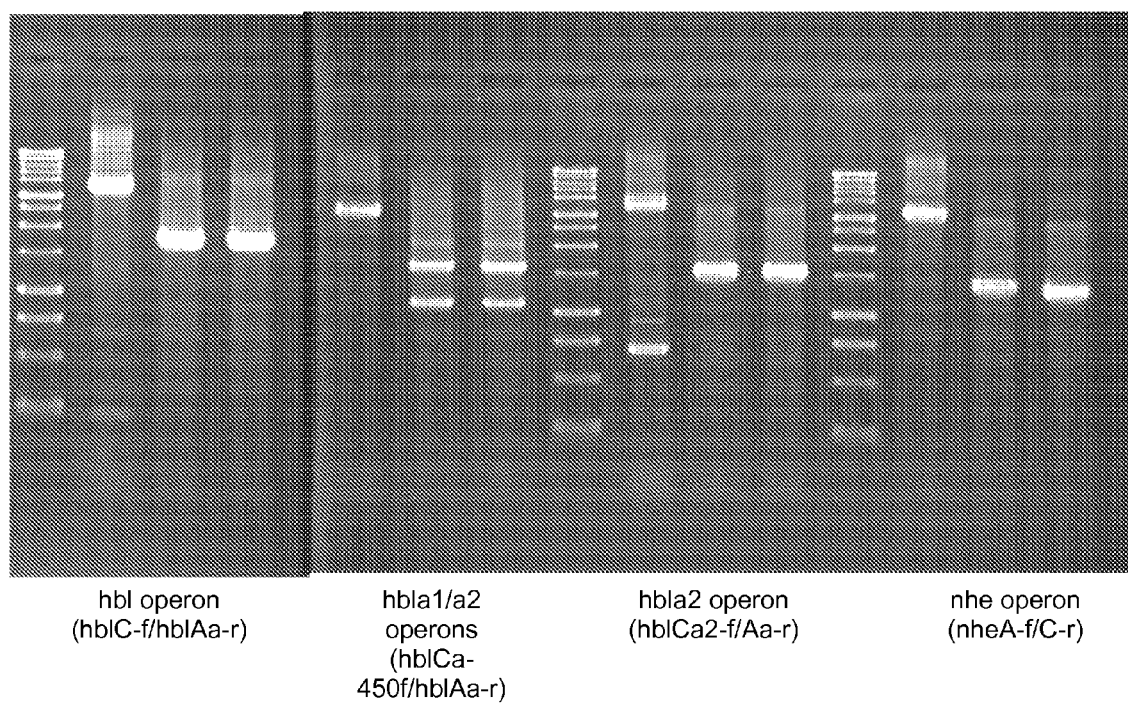


Fig. 3

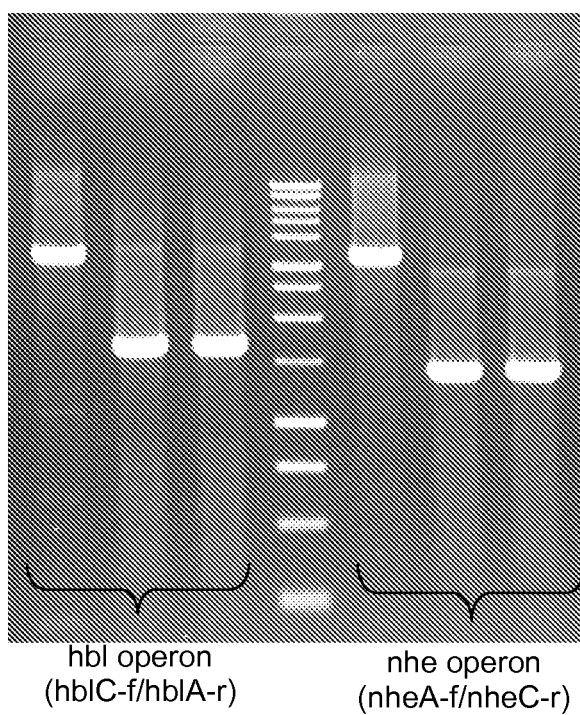


Fig. 4

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CONSTRUCTION OF A QUADRUPLE ENTEROTOXIN-DEFICIENT MUTANT OF BACILLUS THURINGIENSIS

CROSS-REFERENCE TO RELATED APPLICATIONS

This application is a continuation application of U.S. patent application Ser. No. 13/154,857, filed Jun. 7, 2011, which claims the benefit of U.S. Provisional Patent Application Ser. No. 61/353,314, filed Jun. 10, 2010, each of which is incorporated herein by reference as if set forth in its entirety.

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH OR DEVELOPMENT

This invention was made with government support under 05-CRHF-0-6055 awarded by USDA/CSREES. The government has certain rights in the invention.

BACKGROUND OF INVENTION

“Biological control” or “biocontrol” is defined as pathogen suppression by the use of a second organism. Mechanisms of biological control are diverse. Biocontrol has long been thought to be safer for the environment and human health than synthetic pesticides (Cook et al. 1996; Benbrook et al., 1996). As bacterial biocontrol agents have reached the federal regulatory agencies for review, the agencies and the public have voiced concerns over the relatedness of some agents to human pathogens.

Bacillus species are widely used in agriculture as biocontrol agents of pathogens (e.g., oomycetes such as *Pythium* sp. and *Phytophthora* sp.) and insects (Handelsman et al. 1990; Silo-Suh et al. 1998; Shang et al. 1999). *Bacillus thuringiensis* is a biocontrol agent that produces insecticidal crystal toxin proteins, encoded by cry genes, that specifically kill insects including Lepidopterans, Dipterans, Coleopterans, Hymenopterans, and also kill nematodes. Methods for stabilizing and applying such toxins, or strains harboring the toxins, are known for a wide variety of field crop situations. Although distinct *B. thuringiensis* strains vary in target range and efficacy, the toxins required for biological control, and methods for preparing inocula for use in the field, are generally similar among strains.

Because *B. thuringiensis* is closely related genetically to food contaminant bacterium *Bacillus cereus*, concerns have been raised in the U.S. and Europe about its widespread use on food crops. Phylogenetic chromosomal marker studies show no taxonomic basis for separate species status for the two. While *B. thuringiensis* carries plasmids bearing the cry genes that encode insecticidal crystal toxins, *B. cereus* does not. On the other hand, *B. cereus* expresses chromosomally-encoded enterotoxin genes, the products of which are responsible for food-borne disease in humans, haemolysin BL (HBL), non-haemolytic enterotoxin (NHE) and cytotoxin K (CytK) (Beecher & MacMillan, 1991; Lund & Granum, 1996; Lund et al., 2000). Depending upon the strain, different toxins can be responsible for disease.

HBL and NHE are both three-component toxin complexes, which are restricted to the *B. cereus* group (From et al., 2005). HBL includes three component proteins, L2, L1 and B (Beecher & MacMillan, 1991), encoded by the genes hblC, hblD, and hblA, respectively, that are co-transcribed from the hblCDA operon (Heinrichs et al., 1993; Ryan et al.,

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1997; Lindback et al., 1999). NHE includes the proteins NheA, NheB and NheC, encoded by the nheABC operon (Granum et al., 1999).

Single component CytK belongs to the family of β -barrel pore-forming toxins (Fagerlund et al., 2008). Two cytK gene variants, cytK-1 and cytK-2, are known (Lund et al., 2000; Fagerlund et al., 2004). The original CytK-1 protein was isolated from a strain of *B. cereus* that caused three fatalities in a food poisoning outbreak (Lund et al., 2000). The CytK-2 version of the protein was subsequently identified from other strains of *B. cereus* (Fagerlund et al., 2004). This form is 89% identical to CytK-1 at the amino acid level and exhibits about 20% toxicity relative to CytK-1 toward human intestinal cells (Fagerlund et al., 2004).

A homolog of HBL has been discovered in the *B. cereus* group. Beecher and Wong (2000) showed that HBL_a, isolated from a strain of *B. cereus* that also produced HBL, had similar toxicity as HBL and the homologous proteins could be interchanged. The 36 to 45 amino acids of the N-terminal sequence of the individual HBL_a component proteins were reported in the Beecher and Wong study, but the gene sequences for HBL_a were not known. However, an HBL_a operon has been identified in the *B. cereus* UW85 partial genome sequence (D. Rasko, J. Ravel, J. Handelsman, unpublished). *B. weihenstephanensis* strain KBAB4 (Genbank accession CP000903) and *B. cereus* strain 03BB 108 (Genbank accession ABDM00000000) also contain HBL_a sequences. The sequences disclosed in all cited Genbank accession numbers are incorporated herein by reference in their entirety as if set forth herein. The N-terminal sequences of the predicted HBL_a proteins from UW85 are 100%, 69%, and 94% identical to the respective B_a, L_{1a}, and L_{2a} N-terminal sequences reported by Beecher and Wong (2000).

Some efforts to reduce or eliminate enterotoxin activity disrupted the components of the enterotoxin. U.S. Pat. No. 6,602,712 (Handelsman and Klimowicz; incorporated herein by reference as if set forth in its entirety) describes a *Bacillus* strain that exhibits reduced HBL enterotoxin activity. An alteration in the hblA gene of the hbl locus renders inactive the B component of the HBL protein. The other HBL components and other enterotoxin gene sequences were not disrupted. A corresponding component in the HBL_a homolog may compensate for the lack of B component encoded by hblA.

When components NheB and NheC were eliminated from a *B. cereus* strain that lacked HBL and CytK, the strain lost haemolytic activity against erythrocytes from a variety of species (Fagerlund et al., 2008).

Prior attempts to eliminate the complete nhe operon in *B. cereus* and *B. thuringiensis* have failed (Ramaraio & Lereclus, 2006; Fagerlund et al., 2008).

Many commercial *B. thuringiensis* strains, including subsp. *kurstaki* strain VBTS 2477, express such enterotoxin genes (Arnesen et al., 2008). The safety and public acceptance of *B. thuringiensis* on food crops would be enhanced by an enterotoxin-deficient *B. thuringiensis* strain that retains insecticidal activity but which does not produce an enterotoxin or its corresponding components. No *B. thuringiensis* strain is available that has reduced or zero levels of the enterotoxins or the functional components of the enterotoxins, including those components for NHE and HBL. Without the complete removal of these enterotoxins, the risk of toxicity remains.

BRIEF SUMMARY OF THE INVENTION

The present invention relates to enterotoxin-deficient bacterial strains in the *B. cereus* group, which contains *B.*

cereus, *B. thuringiensis*, *B. anthracis*, *B. mycoides*, *B. pseudomycoides*, and *B. weihenstephanensis*. The strains advantageously lack the components that encode the enterotoxin products associated with human toxicity. In some strains, the operons of four enterotoxins identified in a *B. thuringiensis* strain were altered to make the components, including the NHE enterotoxin, non-functional and thus the enterotoxins themselves non-functional. All of the components for NHE are altered in the inventive strains; no functional component for the enterotoxin products associated with human toxicity remains. Also, a new HBL homolog is described and made non-functional in the *B. thuringiensis* strains VBTS 2477 and VBTS 2478.

In a first aspect, the invention is summarized as a method for obtaining a mutant *Bacillus*, the method including the steps of mutating a *Bacillus* to produce a mutant *Bacillus* that does not form active HBL, NHE, HBL_{a1}, and HBL_{a2} enterotoxins, and selecting the mutant *Bacillus*. In some embodiments of the first aspect, the mutating step introduces a mutation in an operon that encodes all components of the NHE enterotoxin and all components of at least one of the HBL, HBL_{a1}, and HBL_{a2} enterotoxins. In other embodiments of the first aspect the mutating step deletes a portion of the operon. Mutation in the operon can yield a polynucleotide that encodes a portion of a first enterotoxin component spliced to a portion of a last enterotoxin component. Certain starting strains may already lack one or more of the genes that would encode an enterotoxin. As such, an enterotoxin deficient strain can be produced by altering the enterotoxin-encoding genes that are present.

In some embodiments of the first aspect, the *Bacillus* to be mutated is *Bacillus thuringiensis* subspecies *kurstaki* strain VBTS 2477.

In some embodiments of the first aspect, the *Bacillus* to be mutated and the mutant *Bacillus* comprise at least one gene that encodes a protein having insecticidal properties.

In a second aspect, the invention relates to an isolated *Bacillus thuringiensis* strain that does not produce does not produce NHE enterotoxin and does not produce at least one of HBL, HBL_{a1}, and HBL_{a2} enterotoxins. In one embodiment of the second aspect, the *B. thuringiensis* strain is insecticidal. In other embodiments of the second aspect, the *B. thuringiensis* strain produces δ -endotoxin. In other embodiments of the second aspect, the *B. thuringiensis* strain is subspecies *kurstaki* strain VBTS 2477.

In a preferred embodiment of the second aspect, the insecticidal *B. thuringiensis* strain carries disabling mutations in the nhe, hbl, hbl_{a1}, and hbl_{a2} operons. In this strain, at least one of the mutated hbl, nhe operons can have the sequence of at least one of SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, and SEQ ID NO: 113 respectively.

In a third aspect, the invention relates to a method for obtaining a mutant *B. thuringiensis* subspecies *kurstaki* strain VBTS 2477 by mutating strain VBTS 2477 to prevent formation of active HBL, NHE, HBL_{a1}, and HBL_{a2} enterotoxins, and selecting a mutant of strain VBTS 2477 including at least one mutation. In one embodiment of the third aspect, the mutating step includes making deletions in hbl, nhe, hbl_{a1}, and hbl_{a2} relative to strain VBTS 2477.

In a fourth aspect, the invention relates to an insect control method including the step of applying to at least one surface of a plant a formulation comprising a mutant *Bacillus* that does not form active HBL, NHE, HBL_{a1}, and HBL_{a2} enterotoxins. In one embodiment of the fourth aspect, application of the formulation is achieved by spraying, dusting, or drenching the plant with the formulation.

In some embodiments of the fourth aspect, the plant is susceptible to infestation by Lepidopterans, Dipterans, Coleopterans, Hymenopterans. In other embodiments of the fourth aspect, the plant is susceptible to infestation by nematodes.

Quadruple and double enterotoxin-deficient *B. thuringiensis* strains, such as those exemplified herein, that do not include any added DNA are not considered genetically engineered under the EPA definition of genetic engineering (Federal Register 1997, 17910-17958) and are not subject to any regulations that do not otherwise apply to a wild type strain.

These and other features, aspects and advantages of the present invention will be more fully understood from the description that follows. The description of preferred embodiments is not intended to limit the invention but rather to cover all modifications, equivalents and alternatives. Reference should therefore be made to the claims herein for interpreting the scope of the invention.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 depicts the HBL and NHE operons in *B. thuringiensis* VBTS 2477. The dotted rectangles indicate the deletion that was introduced in each operon. Vertical arrows point to the protein product of the gene.

FIG. 2 depicts a PCR analysis of *B. thuringiensis* VBTS 2477 and quadruple enterotoxin deletion mutant. PCR primers (see Table 2) were used to amplify: hbl_{a1}, lanes 1-3 (hblCa-F/hblAa-R) (SEQ ID NO:73/SEQ ID NO:78); nhe, lanes 4-6 (nheA-F/nheC-R) (SEQ ID NO:79/SEQ ID NO:84); hbl lanes 7-9 (hblC-F/hblA-R) (SEQ ID NO:67/SEQ ID NO:72); hbl_{a2}, lanes 10-12 (hblCa-Bam-F/hblAa-Bam-R) (SEQ ID NO:100/SEQ ID NO:103). Abbreviations: M: molecular weight standards (1 kb ladder; Promega Corporation, Madison, Wis.), N: negative control, W: wild-type strain, Q: quadruple mutant.

FIG. 3 depicts PCR confirmation of quadruple enterotoxin-deficient mutant of VBTS 2478. WT, VBTS 2478 wild type; 1B and 3B, two quadruple mutants of strain 2478; M, DNA 1 kb ladder from Promega Corporation (from bottom to top (size in kb): 0.25, 0.5, 0.75, 1, 1.5, 2, 2.5, 3, 4, 5, 6, 8, 10, respectively).

FIG. 4 depicts PCR confirmation of the double enterotoxin-deficient mutant of VBTS 2481. WT, VBTS 2481 wild type; d1 and d2, two double mutants of VBTS 2481; M, DNA 1 kb ladder from Promega Corporation.

DETAILED DESCRIPTION OF THE INVENTION

The present invention is exemplified by a quadruple enterotoxin-deficient *B. thuringiensis* mutant strain lacking enterotoxin protein components implicated in human food poisoning. In a preferred embodiment of the present invention, the quadruple enterotoxin-deficient *B. thuringiensis* mutant strain has endogenous insecticidal properties. In four operons that each encode three protein components in wild-type *B. thuringiensis*, the mutant strain lacks functional coding sequences for each component. Based on insect bioassays, the LC50 of the quadruple enterotoxin-deficient strain was the same as the wild-type strain (See Table 8, infra).

In a first aspect, the applicants exemplify a defined *B. thuringiensis* strain that differs from wild-type strain VBTS 2477 at four operons (HBL, NHE, HBL_{a1}, and HBL_{a2}) and is deficient for cytotoxic enterotoxins. The quadruple entero-

toxin-deficient mutant of the present invention does not produce an active HBL, NHE, HBL_{a1} and HBL_{a2} enterotoxin, nor does it produce any component of the respective wild-type enterotoxin. Whereas the wild-type polynucleotides of each operon encode three genes, the enterotoxin-deficient mutant differs from the wild-type strain in that it lacks sequences that span the three-gene portion. (FIG. 1). A DNA sequence that encodes a portion of the first enterotoxin component is adjacent to a DNA sequence that encodes a portion of the last enterotoxin component of each operon, creating a version of each operon where DNA sequences from the end of the first gene, the entire middle gene, and the beginning of the final gene in the operon are removed. The skilled artisan will appreciate that the invention can readily be achieved in a strain having a different deletion or using another type of mutation (insertion, missense) in the coding sequence of each operon component. In addition to any change that inactivates a component, the polynucleotide encoding the component can also include additional changes that may not otherwise alter the function of the component. Such mutants would fall within the scope of the invention as long as they are unable to produce all three components of the subject enterotoxin by virtue of a change in all three polynucleotides that encode the three components of the enterotoxin. Isolated preparations of naturally occurring mutants can also fall within the scope of the present invention.

The enterotoxin-deficient mutant of the present invention is exemplified using *B. thuringiensis*, and particularly in terms of changes relative to *B. thuringiensis* strain VBTS 2477, but can be mutants of any member of the *B. cereus* group of bacteria. Preferably, the mutant is also characterized by having a biological control activity when used as an active agent in an inoculum, as described infra.

In a second aspect, the invention is a method for producing an enterotoxin-deficient mutant of the present invention, wherein the method includes the step of modifying in a *Bacillus* strain the operon that encodes the NHE enterotoxin and at least one of the HBL, HBL_{a1} and HBL_{a2} enterotoxins. In a preferred embodiment, method includes the step of modifying in a *Bacillus* strain the operon that encodes the NHE, HBL, HBL_{a1} and HBL_{a2} enterotoxins. Modification can be achieved by altering the polynucleotides that encode NHE and at least one of the HBL, HBL_{a1}, and HBL_{a2} components, for example, by gene replacement. A suitable method for gene replacement, described in the accompanying Examples, employs a vector, or vectors, carrying a desired mutation that alters the operon such that it no longer encodes a functional enterotoxin. Comparable replacement of genes in the other operons that encode HBL, HBL_{a1}, and HBL_{a2} enterotoxins ensures absence of these other enterotoxins from the strain. The order of the gene replacement is not vital. The vector, or vectors, can be cured from cells at a non-permissive temperature, and further permits screening of mutants on the basis of resistance or sensitivity to an antibiotic.

The invention has particular utility when applied in strains of *B. thuringiensis* that produce biocontrol insecticidal δ -endotoxins. Such strains include, but are not limited to, *B. thuringiensis* subsp. *kurstaki* strain VBTS 2477 (ATCC Reference Number SD-5811; having cry toxin genes Cry1Aa, 1Ab, 1Ac, 1Ia, 2Aa, 2Ab, Vip3Aa1). One or more mutations that inactivate at least the hbl, nhe, hbl_{a1} and hbl_{a2} operons of the respective enterotoxin can be introduced into a *B. thuringiensis* strain, thereby eliminating the enterotoxin from the strain. Since *B. thuringiensis* is closely related genetically to *B. cereus*, it is further specifically envisioned that other enterotoxin-deficient *Bacillus* strains can be produced in accord with this disclosure, and that some enterotoxin deficient *Bacillus* strains will also have insecticidal activity.

In a further aspect, the invention is a method for biological control of insect pests, where the method comprises applying an inoculum that includes as an active agent a novel quadruple enterotoxin-deficient mutant of a strain in the *Bacillus* group. The active agent is preferably an enterotoxin-deficient *B. thuringiensis* strain. The mutants of the present invention can be used in a method for biological control in the same ways as *B. thuringiensis* subsp. *kurstaki* strain VBTS 2477 and other such insecticidal strains are used, such methods for preparing and inoculating the biological control agent on a target or targets being known to the skilled artisan. A suitable assay for monitoring the biocontrol activity of an enterotoxin-deficient strain of the present invention is an insect bioassay such as that described herein (Example 1).

The invention will be more fully understood upon consideration of the following non-limiting Examples.

EXAMPLES

Example 1

Materials and Methods

Bacterial strains, plasmids, and growth conditions. The strains and plasmids used in the present study are listed in Table 1. *Escherichia coli* was grown in Luria-Bertani (LB) medium at 37° C. *B. thuringiensis* was grown in either LB or 0.5×Tryptic Soy Broth (TSB) or on 0.5×Tryptic Soy Agar (TSA) at 28° C., 37° C., or 40.5° C. For conjugation, *B. thuringiensis* was grown in Brain Heart Infusion (BHI) medium. Antibiotics were used at the following concentrations: for *E. coli*, ampicillin (Amp) at 200 µg/ml, chloramphenicol (Cm) at 10 µg/ml; for *B. thuringiensis*, erythromycin (Ery) at 3 µg/ml for selection of pMAD or 5 µg/ml for selection of pBKJ236, polymyxin B at 60 µg/ml for conjugations with pBKJ236, and tetracycline (Tet) at 10 µg/ml for selection of pBKJ223.

TABLE 1

Bacterial strains and plasmids used in this study.		
Strain or plasmid	Description	Source or Reference
Strains		
<i>Bacillus thuringiensis</i> <i>kurstaki</i> strain VBTS 2477	Wild-type	Valent Biosciences Inc. (ATCC Accession Number SD-5811)

TABLE 1-continued

Bacterial strains and plasmids used in this study.		
Strain or plasmid	Description	Source or Reference
2477 single mutant	2477 Δhbl_{a1}	This study
2477 double mutant	2477 Δhbl_{a1} Δnhe	This study
2477 triple mutant	2477 Δhbl_{a1} Δnhe Δhbl	This study
2477 quadruple mutant	2477 Δhbl_{a1} Δnhe Δhbl Δhbl_{a2}	This study
<i>E. coli</i> DH5 α	General purpose strain	Hanahan, 1983
<i>E. coli</i> GM2929	dcm-6 dam-13::Tn9, Cm ^r	<i>E. coli</i> Genetic Stock Center
<i>E. coli</i> SS1827	Helper strain for conjugation into <i>B. thuringiensis</i> , Amp ^r	Janes and Stibitz, 2006
Plasmids		
pMAD	Temperature-sensitive gene replacement vector, Ery ^r , expresses β -galactosidase gene	Arnaud et al., 2004
pBKJ236	Temperature-sensitive gene replacement vector, Ery ^r , contains 18-bp recognition site for I-SceI restriction enzyme	Janes and Stibitz, 2006
pBKJ223	Facilitator plasmid, encodes I-SceI enzyme, Tet ^r	Janes and Stibitz, 2006

DNA isolation and manipulation. Genomic DNA was isolated from cultures of *B. thuringiensis* that were grown overnight with shaking DNA was isolated either by the boiling cell-lysis method (Raffel et al., 1996), or by Protocol #3 in the Easy-DNA Kit (Invitrogen, Carlsbad, Calif.), except that prior to the addition of Solution A the cells were pelleted, resuspended in sterile water and vortexed for 2-3 min. with 50 μ l of 0.1-mm diameter silica beads to enhance cell lysis. Plasmid DNA was isolated from *E. coli* using the Qiagen Spin Miniprep Kit (Qiagen Inc., Valencia, Calif.).

Transformations and Conjugations. Competent cells of *E. coli* were electroporated in 0.2-cm cuvettes with a Gene Pulser apparatus (Bio-Rad Laboratories, Hercules, Calif.) set at 2.5 kV, 200 Ω , and 25 μ F. Cells were transferred to 1 ml LB, allowed to recover for 1 hr at 37° C. with shaking, and then plated on selective media. Competent cells of *B. thuringiensis* were prepared as described previously (Silo-Suh, 1994) or by the method described in Janes and Stibitz (2006). Because *B. thuringiensis* restricts methylated DNA, recombinant plasmids isolated from *E. coli* DH5 α were passed through *E. coli* GM2929 (methylation-deficient strain) before being introduced into *B. thuringiensis*. pBKJ236:: Δhbl_{a2} was introduced into the *B. thuringiensis* triple mutant by conjugation as described in Janes and Stibitz (2006).

Screening for presence of enterotoxin genes. Gene sequences for HBL (hblC, hblD, hblA), NHE (nheA, nheB, nheC) and cytK were obtained from strains of *B. cereus* and *B. thuringiensis*, and from the unpublished *B. cereus* UW85 partial genome sequence (D. Rasko, J. Ravel, J. Handelsman) (Table 2, SEQ ID NOS: 1-66). Sequences were aligned using the DNASTAR (Madison, Wis.) program MegAlign and regions of high conservation were selected for PCR primer sequences (see Table 3 for SEQ ID NOS: 67-86). Primers for cytK (SEQ ID NOS: 85 and 86) were designed that would amplify either variant of the gene (cytK-1 or cytK-2). The HBL_a primers (SEQ ID NOS: 73-78) were based on the UW85 hbl_a sequence only and were chosen so that they differed from the corresponding hbl region by 2-6 nucleotides to ensure amplification from the homologous set of genes. Primers were synthesized at Integrated DNA Technologies (Coralville, Iowa). Typical PCR reactions contained 1 μ l of genomic DNA, 2 μ l of 10x Taq buffer, 0.5 μ M of each primer, 0.2 mM of each dNTP, 0.2 μ l Taq DNA

polymerase (Promega, Madison, Wis.) in a final volume of 20 μ l. PCR cycle conditions consisted of an initial 1 min. denaturation at 94° C., followed by 35 cycles of 30 sec at 94° C., 1.5 min. at 55° C., 2 min. at 72° C., and a final extension of 5 min. at 72° C. PCR products were analyzed on 0.8% agarose gels.

TABLE 2

Gene sequences for HBL, NHE, and cytK used to design PCR primers.		
Gene	Organism	SEQ ID NO.
hblC	<i>B. thuringiensis</i> subsp. <i>kurstaki</i> 2477 (partial)	1
	<i>B. cereus</i> UW85	2
	<i>B. cereus</i> ATCC 14579	3
	<i>B. cereus</i> F837-76	4
	<i>B. cereus</i> G9421	5
	<i>B. thuringiensis</i> 97-27 serovar <i>konkukian</i>	6
hblD	<i>B. thuringiensis</i> subsp. <i>kurstaki</i> 2477	7
	<i>B. cereus</i> UW85	8
	<i>B. cereus</i> ATCC 14579	9
	<i>B. cereus</i> F837-76	10
	<i>B. cereus</i> G9421	11
	<i>B. thuringiensis</i> serovar <i>konkukian</i> 97-27	12
hblA	<i>B. thuringiensis</i> 2477 subsp. <i>kurstaki</i> (partial)	13
	<i>B. cereus</i> UW85	14
	<i>B. cereus</i> ATCC 14579	15
	<i>B. cereus</i> F837-76	16
	<i>B. cereus</i> G9421	17
	<i>B. thuringiensis</i> serovar <i>konkukian</i> 97-27	18
hblCa	<i>B. thuringiensis</i> subsp. <i>kurstaki</i> 2477 hblCa1 (partial)	19
	<i>B. thuringiensis</i> subsp. <i>kurstaki</i> 2477 hblCa2 (partial)	20
	<i>B. cereus</i> UW85	21
	<i>B. cereus</i> AS4-12 (tentative; only have 1-2x coverage)	22
	<i>B. cereus</i> 03BB108	23
	<i>B. weihenstephanensis</i> KBAB4	24
hblDa	<i>B. thuringiensis</i> subsp. <i>kurstaki</i> 2477 hblDa1	25
	<i>B. thuringiensis</i> subsp. <i>kurstaki</i> 2477 hblDa2	26
	<i>B. cereus</i> UW85	27
	<i>B. cereus</i> AS4-12 (tentative; only have 1-2x coverage)	28
	<i>B. cereus</i> 03BB108	29
	<i>B. weihenstephanensis</i> KBAB4	30
hblAa	<i>B. thuringiensis</i> subsp. <i>kurstaki</i> 2477 hblAa1 (partial)	31
	<i>B. thuringiensis</i> subsp. <i>kurstaki</i> 2477 hblAa2 (partial)	32
	<i>B. cereus</i> UW85	33
	<i>B. cereus</i> AS4-12 (tentative; only have 1-2x coverage)	34
	<i>B. cereus</i> 03BB108	35
	<i>B. weihenstephanensis</i> KBAB4	36

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TABLE 2-continued

Gene sequences for HBL, NHE, and cytK used to design PCR primers.		
Gene	Organism	SEQ ID NO.
nheA	<i>B. thuringiensis</i> subsp. <i>kurstaki</i> 2477 (partial)	37
	<i>B. cereus</i> UW85	38
	<i>B. cereus</i> 1230-88	39
	<i>B. cereus</i> 10987	40
	<i>B. cereus</i> ATCC 14579	41
	<i>B. cereus</i> E3LL	42
	<i>B. thuringiensis</i> serovar <i>konkukian</i> 97-27	43
	<i>B. thuringiensis</i> HD12	44
	<i>B. thuringiensis</i> subsp. <i>kurstaki</i> 2477	45
	<i>B. cereus</i> UW85	46
nheB	<i>B. cereus</i> 1230-88	47
	<i>B. cereus</i> 10987	48
	<i>B. cereus</i> ATCC 14579	49
	<i>B. cereus</i> E3LL	50
	<i>B. thuringiensis</i> serovar <i>konkukian</i> 97-27	51
	<i>B. thuringiensis</i> HD12	52

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TABLE 2-continued

Gene sequences for HBL, NHE, and cytK used to design PCR primers.		
Gene	Organism	SEQ ID NO.
nheC	<i>B. thuringiensis</i> subsp. <i>kurstaki</i> 2477 (partial)	53
	<i>B. cereus</i> UW85	54
	<i>B. cereus</i> 1230-88	55
	<i>B. cereus</i> 10987	56
	<i>B. cereus</i> ATCC 14579	57
	<i>B. cereus</i> E3LL	58
	<i>B. thuringiensis</i> serovar <i>konkukian</i> 97-27	59
	<i>B. thuringiensis</i> HD12	60
	<i>B. cereus</i> 391-98 (cytK-1)	61
	<i>B. cereus</i> 1230-88 (cytK-2)	62
cytK	<i>B. cereus</i> FM-1 (cytK-2)	63
	<i>B. cereus</i> ATCC 10987 (cytK-2)	64
	<i>B. cereus</i> ATCC 14579 (cytK-2)	65
	<i>B. thuringiensis</i> 97-27 (cytK-2)	66

TABLE 3

Primers used for detection of enterotoxin genes in <i>Bacillus thuringiensis</i> <i>kurstaki</i> strain VBTS 2477.			
Primer	Sequence (5'-3') ^a	Melt Temp. (° C.)	Product size (nt)
hblC-F (SEQ ID NO: 67)	CAA GAG CTG TCA CGA ATC	50.2	875
hblC-R (SEQ ID NO: 68)	CTG CTT GAT TAG CAC GAT C	50.2	
hblD-F (SEQ ID NO: 69)	CCT ATC AAT ACT CTC GCA AC	50.6	664
hblD-R (SEQ ID NO: 70)	CAT CAG GTC ATA CTC TTG TG	51.0	
hblA-F (SEQ ID NO: 71)	CCT GGT AGA ATC GTA CAA G	49.5	708
hblA-R (SEQ ID NO: 72)	GAG CTG CAT TCT CAA TAT GC	51.7	
hblCa-F (SEQ ID NO: 73)	GCA AGT CCG AAT GTA CAA C	51.5	1110
hblCa-R (SEQ ID NO: 74)	CTT CGA GTT GAG TTG TTA CAC	51.3	
hblDa-F (SEQ ID NO: 75)	CTG CTA CGA ATG GTA GTA C	49.6	947
hblDa-R (SEQ ID NO: 76)	CTT GAT CCA CTG TCT GAT AC	49.9	
hblAa-F (SEQ ID NO: 77)	CCT GAC AAC AAC TAC TGT AG	50.0	996
hblAa-R (SEQ ID NO: 78)	GTC TTT CGC TGC ATT CAG	51.5	
nheA-F (SEQ ID NO: 79)	GTT AGG ATC ACA RTC ACC	47.3-49.4	655
nheA-R (SEQ ID NO: 80)	TCG TTT GRC TAT CTG CAG	49.1-52.3	
nheB-F (SEQ ID NO: 81)	GAT ACA GCT AGA GGA AAT GC	50.3	721
nheB-R (SEQ ID NO: 82)	GAT CCC ATT GTG TAC CAT TG	51.1	
nheC-F (SEQ ID NO: 83)	CAG CWG GAT TCC AAG ATG T	52.3	883
nheC-R (SEQ ID NO: 84)	CCA RCT ATC TTT CGC TGT	49.4-52.0	
cytKdeg-F (SEQ ID NO: 85)	GCW GTR GAA GAA ACG ACT G	50.6-53.8	486
cytKdeg-R (SEQ ID NO: 86)	CCA ACC CAG TTW SCA GTT CC	55.6-56.9	

^aDegenerate bases: W = T or A; R = A or G; S = C or G.

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Sequence analysis of enterotoxin operons in *Bacillus thuringiensis* subsp. *kurstaki* strain VBTS 2477. To obtain near full-length sequence of the hbl, hbl_{a1}, and nhe enterotoxin operons present in *B. thuringiensis* subsp. *kurstaki* strain VBTS 2477, primers near the ends of each operon were used to amplify the operon (i.e., hblC-F/hblA-R (SEQ ID NO: 67/SEQ ID NO: 72); hblCa-F, hblAa-R (SEQ ID NO: 73/SEQ ID NO: 78), nheA-F/nheC-R (SEQ ID NO: 79/SEQ ID NO: 84)), the products were purified using AMPure magnetic beads (Agencourt Bioscience, Beverly, Mass.), and the full sequence was obtained by primer walking. For hbl_{a2}, sequence was obtained from the PCR products generated with the following primer pairs using genomic DNA from the Δhbl_{a1} mutant: hblCa-F/hblDa-R (SEQ ID NO: 73/SEQ ID NO: 76), and hblDa-F/hblAa-R (SEQ ID NO: 75/SEQ ID NO: 78). Typical sequencing reactions contained 1 μA of BigDye Terminator v. 3.1 mix (Applied Biosystems, Foster City, Calif.), 1.5 μl of sequencing buffer v. 3.1 (Applied Biosystems), 0.5 μM of each primer, and 5 μl of template DNA in a final reaction volume of 20 μl. Cycle conditions were an initial 3 min. denaturation at 95° C., followed by 35 cycles of 10 sec. at 96° C., 3 min. 30 sec. at 58° C., and a final extension of 7 min. at 72° C. Excess dye terminators were removed using the CleanSeq magnetic bead sequencing reaction clean up kit (Agencourt Bioscience, Beverly, Mass.). Sequencing gels were run on an Applied Biosystems 3730x1 automated DNA sequencing instrument at the University of Wisconsin Biotechnology Center. Data were analyzed using PE-Biosystems version 3.7 of Sequencing Analysis. Contigs were assembled using the DNASTAR software SeqMan. The nucleotide sequences of the near full-length enterotoxin operons, 2477_hbl,

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2477_hbla1, 2477_hbla2, 2477_nhe, and 2477cytK-2 were deposited in Genbank under Accession numbers EU925141 (SEQ ID NO: 87), EU925142 (SEQ ID NO: 88), EU925143 (SEQ ID NO: 89), EU925144 (SEQ ID NO: 90), and EU925145 (SEQ ID NO: 91), respectively.

Generation of deletion constructs. The deletion constructs were created by a method of PCR referred to as gene splicing by overlap extension, or SOEing PCR, as described in Horton et al. (1989). The primers used to create the deletion constructs are presented in Table 4 (SEQ ID NOS: 92-105). In the first round of PCR, two primer pairs were used to amplify in separate reactions a portion of the first and last gene in the enterotoxin operon. The 5' ends of the reverse primer of the first gene and the forward primer of the last gene were designed with complementary sequences of 16-18 nucleotides which enable the two fragments to be spliced together in the second round of PCR. In the second round of PCR, the fragments from the first round were mixed, along with the forward primer of the first gene and the reverse primer of the last gene (each containing a Bam HI site for cloning). Initially, the complementary ends of the two PCR fragments anneal and act as primers for extension of the spliced product, which is further amplified by the outer-most primers. For generation of the Δhbl_{a1} and Δhbl_{a2} constructs, the same set of outer primers were used (hblCa_Bam-F (SEQ ID NO:100), hblAa₁₃ Bam-R (SEQ ID NO:103)), but different overlapping primers were selected so that the constructs contained different sized deletions. This made for easy discrimination between the two mutations by PCR. The nucleotide sequences of the mutant operons are set forth herein: 2477Δhbl (SEQ ID NO: 110), 2477Δhbl_{a1} (SEQ ID NO: 111), 2477 Δhbl_{a2} (SEQ ID NO: 112), and 2477Δnhe (SEQ ID NO: 113).

TABLE 4

Primers used for generation of deletion constructs by SOEing PCR.

SOEing Primer	Sequence(5'-3') ^a	Melt Temp. (° C.)	Product size (nt)
hblC_Bam-F (SEQ ID NO: 92)	GATAGGATCCGTACAGCTAGAGGAAGTC	58.9	735
hblCtail-R (SEQ ID NO: 93)	CTTCATTTGCATGGCTTTCATCAGGTCATACTCTTG TG	62.8	
hblAtail-F (SEQ ID NO: 94)	AAAGCCATGCAAAATGAAGCGAGAATGAAGAGACCTTGC	65.3	712
hblA_Bam-R (SEQ ID NO: 95)	CAATGGATCCCTGTAGCAACTCCAACCTAC	60.4	
nheA_Bam-F (SEQ ID NO: 96)	CTGTGGATCCCAGGGTTATTGGTTACAGC	62.2	815
nheA_tail-R (SEQ ID NO: 97)	ATACTCCGCTGCTTCTCTCGTTTGACTATCTGCAG	64.3	
nheC_tail-F (SEQ ID NO: 98)	AGAAGCAGCGGAGTATGATTGAGCATCAAAGAGATGC	64.6	744
nheC_Bam-R (SEQ ID NO: 99)	CAATGGATCCCAGCTATCTTTTCGCTGT	62.1	
hblCa_Bam-F (SEQ ID NO: 100)	CATTGGATCCGAAAGAGTGGTCATCCGAAC	62.1	901
hblCa1_tail-R (SEQ ID NO: 101)	TGAAACTACGCTCAATTT CTCCATCTACTTGTTAGC	61.9	
hblAa1_tail-F (SEQ ID NO: 102)	AAATTGAGCGTAGTTTCAACCAGTAGCTGCTTTTGCAAG	64.1	934
hblAa_Bam-R (SEQ ID NO: 103)	CTTAGGATCCGATCTGCTTTTGGGATGC	60.9	

TABLE 4-continued

Primers used for generation of deletion constructs by SOEing PCR.			
SOEing Primer	Sequence(5'-3') ^a	Melt Temp. (° C.)	Product size (nt)
hblCa_Bam-F (SEQ ID NO: 100)	CATT GGATCC GAAAGAGTGGTCATCCGAAC	62.1	630
hblCa2_tail-R (SEQ ID NO: 104)	<u>TTCTTTT</u> GATCCTTTTCTCTATCGTTTCACGTGCTTC	61.2	
hblAa2_tail-F (SEQ ID NO: 105)	<u>AGAAAAGGATCAAAAGA</u> ATGCAAGAGAGCATGCTAC	61.5	691
hblAa_Bam-R (SEQ ID NO: 103)	CTTAG GGATCC GATCTGCTTTTGGGATGC	60.9	

^aBam HI site residues are in bold; complementary tails are underlined.

Typical conditions for the first round of PCR reactions were 1 µl genomic DNA, 5 µl 10X Pfu buffer, 0.5 µl of each primer, 0.4 mM dNTPs, and 0.5 µl Pfu DNA polymerase (Stratagene, La Jolla, Calif.) in a total volume of 50 µl. For the Δhbl_{a2} construct, the template included the PCR fragments obtained with the hblCa-F/hblDa-R (SEQ ID NO:73/SEQ ID NO:76) and hblDa-F/hblAa-R (SEQ ID NO:75/SEQ ID NO:78) primer sets used with genomic DNA from the Δhbl_{a1} mutant. PCR cycle conditions were 30 cycles of 30 sec. at 94° C., 30 sec. at 55° C., and 1 min. at 72° C. The PCR fragments were purified using AMPure magnetic beads. Reaction conditions for the second round of PCR were the same as the first round except the template was 0.5 µl of the PCR fragments of the 5' and 3' regions of the operon, and Taq DNA Polymerase (Promega) was used instead of Pfu DNA Polymerase. The same PCR program was used for the second round of amplification. The spliced PCR product was gel-purified using the QIAEX II gel purification kit (Qiagen).

The resulting deletion constructs were digested with Bam HI (Promega) and ligated to either pMAD (Δhbl_{a1}, Δnhe, Δhbl) or pBKJ236 (Δhbl_{a2}) that had been Bam HI-digested and treated with shrimp alkaline phosphatase (Promega). The recombinant vectors were confirmed by restriction digest analysis and the inserts were sequenced.

Gene replacement using pMAD or pBKJ236/pBKJ223. Gene replacement with the pMAD constructs was carried out in a manner similar to the method described in Arnaud et al., 2004. For construction of the first mutant (Δhbl_{a1}; SEQ ID NO: 111) of the series, pMAD::Δhbl_{a1} was electroporated into *B. thuringiensis* VBTS 2477 and transformants were selected on 0.5×TSA with Ery (3 µg/ml) and X-Gal (50 µg/ml) after two days of incubation at 28° C., the permissive temperature for plasmid replication. The gene replacement was carried out in two steps by first selecting for a single recombination event resulting in integration of the plasmid at the enterotoxin locus, and then screening for excision of the plasmid by a second recombination event and subsequent loss of the plasmid. Transformants were grown on plates containing Ery at 40.5° C., the nonpermissive temperature for replication of pMAD, to select for clones in which the plasmid had integrated into the chromosome via a single crossover event. Integrants were then grown at the permissive temperature in nonselective media to allow for a second crossover event, and then diluted into fresh media and grown at the nonpermissive temperature to cure any freely replicating plasmid. Cultures were plated for single colonies on 0.5×TSA with X-Gal at 40.5° C. and screened for white colonies, putative double recombinants. PCR analysis was performed on genomic DNA to determine

whether the double recombinants had reverted to wild-type hbl_{a1} or had undergone a successful gene replacement. The nhe and hbl operons were replaced with the Δnhe (SEQ ID NO: 113) and Δhbl (SEQ ID NO: 110) deletion constructs in an iterative manner to obtain the triple mutant.

A quadruple mutant using the pMAD::Δhbl_{a2} construct was not obtained due to an unexpected low frequency of recombination in the integrant containing this construct. Therefore, the pBKJ236/pBKJ223 gene replacement system was used, as described previously (Janes and Stibitz, 2006) which enhances the frequency of the second crossover event. In this system, the construct containing Δhbl_{a2} (SEQ ID NO: 112), was introduced on a temperature-sensitive plasmid vector, pBKJ236, which carries an 18-bp recognition site for I-SceI. pBKJ236::Δhbl_{a2} was introduced into the triple mutant by conjugation, and integrants were selected on BHI with Ery at 37° C., the non-permissive temperature for replication. Integration at the hbl_{a2} locus was verified by PCR analysis using one primer specific to the chromosome and one specific to the vector (hblDa2-F (SEQ ID NO: 106), 5'-GCT GCT AAA CAA AGT TGG AAT G-3', pBKJ236-R (SEQ ID NO: 107), 5'-CGT AAT ACG ACT CAC TAT AGG G-3'). Following the integration of Δhbl_{a2} at the enterotoxin locus, a facilitator plasmid, pBKJ223, was introduced. pBKJ223 encodes the I-SceI restriction enzyme which cleaves the DNA at the site of integration, creating a substrate for recombination. pBKJ223 was electroporated into the integrant and selected on media containing Tet. A resulting transformant was grown in 0.5×TSB with Tet overnight at 28° C. and plated for single colonies on 0.5×TSA with Tet and incubated at 37° C. Colonies were screened for sensitivity to Ery to identify putative double recombinants that had lost pBKJ236 via a second crossover event. The double recombinants were screened by PCR with hblCa_Bam-F/hblAa_Bam-R (SEQ ID NO:100/SEQ ID NO:103) primers to identify clones that had retained the Δhbl_{a2} locus. The quadruple mutant was grown in 0.5×TSB at 37° C. and single colonies were patched onto plates with and without Tet to identify isolates that had been cured of pBKJ223.

Commercial assays for detection of enterotoxin proteins. Two commercial immunoassay kits were used to detect the L₂ component of HBL and the NheA protein of NHE. Cultures of *B. thuringiensis* VBTS 2477, the single, double, triple, and quadruple mutants were grown for 18 hr. in 125 ml flasks containing 12 ml of BHI with 0.1% glucose. The cultures were spun down and the supernatant was filter-sterilized through a 0.22 µm pore-sized filter (Millipore Corp, Billerica, Mass.). The cell-free culture supernatants

were then assayed with the Oxoid *Bacillus cereus* enterotoxin reverse passive latex agglutination (BCET-RPLA) kit (Fisher Scientific, Pittsburgh, Pa.) and the Tecra *Bacillus* Diarrhoeal Enterotoxin (BDE) Visual Immunoassay (VIA)

(3M, St. Paul, Minn.) according to the manufacturer's instructions, with the exception that in the Oxoid assay four additional dilutions were included for each sample. The assays were performed on two independent sets of cultures.

Insect bioassays. Bioassays were carried out using 4-day old *Trichoplusia ni* larvae (cabbage looper), 4-day old *Plutella xylostella* larvae (diamondback moth), or 2-day old *Spodoptera exigua* larvae (beet armyworm). Bacterial cultures used for treatments were grown in flasks and fermentors using media containing organic nitrogen sources (such as flours, yeast extract, fish meal, etc.) and dextrose with typical salts used in fermentation processes. Cultures were grown under aerobic conditions at 28° C. with agitation until sporulation was complete. All bacterial treatments were incorporated into warmed liquid diet which was then allowed to solidify in plates. Two or three replications were conducted for each study. Each replication tested seven dose levels of Bt whole culture (i.e., spores, vegetative materials, and constituents produced during the vegetative and sporulation phases) and an untreated control. Doses were set in a wide range to target the estimated LC₅₀. For *T. ni* and *S. exigua*, 30 larvae were tested per dose. For *P. xylostella* 40 larvae were tested per dose. Insects were incubated at 28°±2° C. for *T. ni* and *S. exigua*, and at 25°±2° C. for *P. xylostella* with a 12-h light/12-h dark cycle for three days. Larval mortality values from all of the replications were pooled and using log-probit analysis, a single regression line was used to estimate the 50% lethal concentration (LC₅₀).

Results

Detection and sequence analysis of enterotoxin genes in *Bacillus thuringiensis* Kurstaki strain VBTS 2477. *B. thuringiensis* strain VBTS 2477 was screened for the presence of genes that encode three enterotoxins implicated in food poisoning outbreaks: HBL, NHE, and CytK. PCR primers were therefore designed to discriminate between the HBL and HBL_a genes. Results from the PCR screen of VBTS 2477 indicated that all 10 enterotoxin genes (hblC, hblD, hblA, hblC_{a1}, hblD_{a1}, hblA_{a1}, nheA, nheB, nheC, and cytK) were present (data not shown). Sequencing of the cytK gene in VBTS 2477 revealed that it is the less toxic cytK-2 version. The HBL_a genes are 77-84% identical to the HBL set in UW85.

A third HBL homolog was discovered following construction of the single deletion mutant Δhbl_{a1}. A PCR product was obtained from the single mutant with the hblDa-F/hblDa-R primer set, indicating the presence of another hblD_a homolog in VBTS 2477. Further analysis revealed this gene was part of a third hbl operon in VBTS 2477 (FIG. 1) which exhibits higher sequence similarity to hbl_a than to hbl. Therefore, this third set of HBL genes was denoted as hbl_{a2}, and the hbl_a detected originally was designated hbl_{a1}. Sequence analysis of the three near full-length hbl operons in VBTS 2477 shows that the hbl_{a1} and hbl_{a2} gene sequences

are 96-97% identical (Table 5) and the deduced protein sequences are 97-98% identical. The hbl genes are 76-84% identical to hbl_{a1} and hbl_{a2} genes, while the deduced proteins are 68-85% identical (Table 5).

TABLE 5

Nucleotide sequence identity (%) of the hbl homologues in VBTS 2477.								
Gene	hblC	hblC _{a1}	Gene	hblD	hblD _{a1}	Gene	hblA	hblA _{a1}
hblC	100	82	hblD	100	83	hblA	100	78-83
hblC _{a2}	81	96	hblD _{a2}	84	97	hblA _{a2}	76-78	96

Sequence analysis of the cytK gene in strain VBTS 2477 revealed that it is the less toxic variant, cytK-2 (Fagerlund et al., 2004). The CytK-2 protein is 89% identical to CytK-1 at the amino acid level and exhibits only about 20% of the toxicity of CytK-1 toward human intestinal cells (Fagerlund et al., 2004), making its role in virulence uncertain. cytK-2 was not deleted from strain VBTS 2477.

Generation of deletion constructs and gene replacement. SOEing PCR was used to generate deletion constructs of HBL, HBL_{a1}, HBL_{a2}, and NHE that contained a portion of the first enterotoxin gene spliced to a portion of the last enterotoxin gene of the operon, essentially creating a version of the operon missing a large internal portion of the operon encompassing the end of the first gene, the entire middle gene, and the beginning of the final gene. The deletion constructs contained about 600-900 nucleotides on either side of the deletion for homologous recombination. The deletion constructs were cloned into a temperature-sensitive gene replacement vector (pMAD for Δhbl_{a1}, Δnhe, and Δhbl; pBKJ236 for Δhbl_{a2}) and successive gene replacements were carried out to introduce the deletions in the order Δhbl_{a1}, Δnhe, Δhbl, and Δhbl_{a2} (FIG. 2). Attempts were made to obtain a Δhbl_{a2} mutant using the pMAD::Δhbl_{a2} construct; however, an unexpected low frequency of recombination was observed in the integrant, and the double recombinants identified had reverted to wild-type hbl_{a2}. Therefore, the pBKJ236/pBKJ223 gene replacement system used previously in *B. anthracis* was used to generate the final deletion. This two-plasmid system utilizes a temperature-sensitive gene replacement plasmid (pBKJ236) and a second plasmid that promotes recombination at the site of the integrated gene replacement vector (Janes and Stibitz, 2006).

Detection of enterotoxin proteins with commercial kits. *B. thuringiensis* strain VBTS 2477, the single mutant (Δhbl_{a1}) and the double (Δhbl_{a1} Δnhe) mutant each exhibited a strong agglutination response (Table 6) when tested with the Oxoid BCET-RPLA kit, which detects the L₂ component of HBL (Beecher & Wong, 1994). The triple deletion mutant, in which hbl is deleted, exhibited a negative phenotype, indicating that expression of the L₂ protein was abolished in this mutant. Since the hbl_{a2} operon remained intact in the triple mutant, either L_{2(a2)} is not expressed in strain VBTS 2477 or it does not react with the anti-L₂ antibody in the RPLA kit. Hemolysis on sheep blood agar suggests that L_{2(a2)} is expressed in VBTS 2477 since the hemolytic activity of the quadruple mutant is diminished compared to the triple mutant (data not shown). Therefore, it is likely that L_{2a} is antigenically distinct from L₂. In the Tecra BDE assay, which detects NheA, both the wild type and the single mutant (Δhbl_{a1}) exhibited positive reactions (Table 6). The double mutant, in which nhe had been deleted, exhibited a negative reaction, as did the triple and quadruple mutants.

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TABLE 6

Detection of HBL and NHE proteins in <i>B. thuringiensis</i> subsp. <i>kurstaki</i> strain VBTS 2477 and deletion mutants by commercial immunoassays.			
Strain	Genotype	Oxoid RPLA ^a	Tecra BDE ^b
VBTS 2477	Wildtype	1024	4
Single mutant	Δhbl_{a1}	1024	4
Double mutant	$\Delta hbl_{a1} \Delta nhe$	1024	1
Triple mutant	$\Delta hbl_{a1} \Delta nhe \Delta hbl$	Neg	1
Quadruple mutant	$\Delta hbl_{a1} \Delta nhe \Delta hbl \Delta hbl_{a2}$	Neg	1

^aRPLA assay results are reported as the highest dilution (in a series of two-fold dilutions) that gives a positive agglutination.

^bBDE assay results are reported according to the manufacturer's instructions where scores of 3, 4, or 5 are positive, and 1 or 2 are negative.

Toxin production and efficacy. SDS-PAGE analysis indicated that VBTS 2477 and the quadruple mutant produce similar quantities of the insecticidal crystal protoxins (Table 7). The wild type and quadruple mutant had similar insecticidal activity against three lepidopteran species: cabbage looper, diamondback moth, and beet armyworm (Table 8).

TABLE 7

Crystal toxin accumulation in cultures from 7.5 L fermentors.*			
Strain	Protoxin in culture broth (mg ml ⁻¹)	Proportion of crystal toxin as 135-kDa protoxin (%)	Proportion of crystal toxin as 60-kDa protoxin (%)
VBTS 2477	8.4	63	37
VBTS 2477, quadruple mutant	11.6	69	31

*Protein quantified by gel analysis software (BioRad Quantity One @ 4.1.1) of SDS-PAGE gels stained with Colloidal Blue (Invitrogen). Values represent the result of a single experiment.

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TABLE 8

Insecticidal activity against lepidopteran larvae. <i>B. thuringiensis</i> cultures from 7.5 L fermentors were fed to 4-day old <i>T. ni</i> , 2-day old <i>S. exigua</i> , and 4-day old <i>P. xylostella</i> larvae. Larval mortality was assessed after 3 days.			
Insecticidal activity LC ₅₀ * (µg ml ⁻¹ diet against each lepidopteran species)			
Strain	<i>T. ni</i> (95% CI)	<i>S. exigua</i> (95% CI)	<i>P. xylostella</i> (95% CI)
VBTS 2477	168 (158-178)	653 (538-773)	11.5 (7.48-18.1)
VBTS 2477, quadruple mutant	145 (131-160)	632 (545-730)	11.1 (9.91-12.8)

*Values represent the mean of three replicates for *T. ni*, two replicates for *S. exigua* and *P. xylostella*. For each replicate 30 larvae of *T. ni* and *S. exigua*, and 40 larvae of *P. xylostella* were tested. CI indicates confidence interval.

Example 2

Materials and Methods

A quadruple mutant ($\Delta hbl_{a1} \Delta nhe \Delta hbl \Delta hbl_{a2}$) was created in *B. thuringiensis* subsp. *aizawai* strain VBTS 2478.

Preparation of competent cells of strain *B. thuringiensis* subsp. *aizawai* (Bta) strain VBTS 2478. Competent cells of Bta strain VBTS 2478 were prepared using the protocol described for strain VBTS 2477.

Gene replacement in *B. thuringiensis* subsp. *Aizawai* (Bta) strain 2478. We determined by PCR analysis that Bta strain VBTS 2478 has the genes that encode HBL, HBL_{a1}, HBL_{a2}, and NHE (data not shown). Bta strain VBTS 2478 was transformed using the protocol described for VBTS 2477. The following constructs were used in construction of the quadruple enterotoxin-deficient mutant of VBTS 2478: pMAD:: $\Delta 2477hbl$, pMAD:: $\Delta 2477hbl_{a1}$, pMAD:: $\Delta 2477hbl_{a2}$, and pMAD:: $\Delta 2477nhe$. These constructs were transformed into VBTS 2478 sequentially, and gene replacements were performed iteratively. Transformants were selected on LB agar plates containing 1 µg/ml of Ery and 50 µg/ml of X-Gal (details as in Example 1). Integrants were obtained by growing transformants at the nonpermissive temperature (the replication origin on pMAD is temperature sensitive). Following second cross-over events, target gene deletion was confirmed by PCR analysis of genomic DNA using appropriate primer pairs (Tables 1, 3, and 9).

TABLE 9

Primers used in gene replacement in <i>B. thuringiensis</i> strains 2478 and 2481.			
Name	Sequence (5' to 3')	Note	SEQ ID NO.
hblCa2-f	CTTCTACAGGGAAGGATTAGAA	specific for hbl _{a2} in strain VBTS 2478*	108
hblCa-450f	CTTAATTCAGAGGAACAGGA	Specific for both hbl _{a1} and hbl _{a2} *	109

*After mutagenesis of hbl_{a1} in strain 2478, PCR analysis confirmed the existence of a second hbl_a homolog, hbl_{a2}.

The sequencing data of hbl_{a2} showed that this operon was truncated at the 5' end.

Commercial assays for detection of enterotoxin proteins. Cultures of VBTS 2478 and the VBTS 2478 quadruple enterotoxin-deficient mutant were grown in Brain Heart Infusion broth for 16 hours at 32° C. with shaking at 200 rpm. Optical densities for the cultures ranged from 1.50 to 1.73. Cultures were centrifuged at 13000×g at 4° C. The supernatant was sterilized by passing through 0.2μ low protein binding filters. Samples were aliquoted and stored at -20 C. until use. VBTS 2478 wild type and mutant samples were assayed according to directions specified in the Oxoid BCET-RPLA detection kit to test for production of Hbl enterotoxin, and according to directions specified in the Tecra BDEVIA detection kit for production of Nhe enterotoxin.

Results

Construction of quadruple enterotoxin-deficient mutant of *B. thuringiensis* subsp. *aizawai* (Bta) strain VBTS 2478. PCR confirmed successful construction of a quadruple enterotoxin-deficient mutant of Bta strain VBTS 2478 (FIG. 3). Partial sequences for hblA_{a2} and hblD_{a2} in strain 2478 are depicted by SEQ ID NOs.: 114 and 115 respectively.

Detection of enterotoxin proteins with commercial kits. *B. thuringiensis* strain VBTS 2478 exhibited a strong agglutination response when tested with the Oxoid BCET-RPLA kit, which detects the L₂ component of HBL (Beecher & Wong, 1994). The quadruple deletion mutant (Δhbl_{a1} Δnhe Δhbl Δhbl_{a2}), in which hbl and hbl homologs are deleted, exhibited a negative phenotype, indicating that expression of the Hbl proteins was abolished in this mutant (data not shown). In the Tecra BDE assay, which detects NheA, wild type VBTS 2478 exhibited a positive reaction, whereas the quadruple mutant, in which nhe had been deleted, exhibited a negative reaction, indicating that Nhe enterotoxin was not produced (data not shown).

Example 3

Materials and Methods

A double mutant (Δhbl Δnhe) was created in *B. thuringiensis* strain VBTS 2481.

Preparation of competent cells of *B. thuringiensis* subsp. *israelensis* (Bti) strain VBTS 2481. Competent cells of Bti strain VBTS 2481 were prepared using a protocol similar to that described for strain VBTS 2477.

Gene replacement in *B. thuringiensis* subsp. *israelensis* (Bti) strain VBTS 2481. PCR analysis of genomic DNA using degenerate primers specific for hbl_{a1} and hbl_{a2} did not yield any products indicating that VBTS 2481 does not contain hbl_{a1} or hbl_{a2}; PCR analysis did confirm that VBTS 2481 contains hbl and nhe (data not shown). Bti strain VBTS 2481 was transformed using a protocol similar to that described for VBTS 2477. The following constructs were used in construction of the double enterotoxin-deficient mutant of VBTS 2481: pMAD::Δ2477hbl, and pMAD::Δ2477nhe. These constructs were transformed into VBTS 2481 sequentially, and gene replacements were performed iteratively. Transformants were selected on LB agar plates containing 1 μg/ml of Ery and 50 μg/ml of X-Gal (details as in Example 1). Integrants were obtained by growing transformants at the nonpermissive temperature (the replication origin on pMAD is temperature sensitive). Additional steps can be taken, if needed, to stabilize genetic material found in *Bacillus* strains, for example, the plasmid carrying cry genes. Methods for stabilizing plasmids during gene replacement are known in the art.

Results

Construction of double enterotoxin-deficient mutant of *B. thuringiensis* subsp. *israelensis* (Bti) strain VBTS 2481. PCR confirmed successful construction of double enterotoxin-deficient mutant of VBTS 2481 (FIG. 4). Partial sequences for strain 2481 hblC (single coverage), hblA (single coverage), nheA (single coverage), and nheC (single coverage) are depicted by SEQ ID NOs.: 116, 117, 118, and 119 respectively.

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 <213> ORGANISM: Bacillus thuringiensis

<400> SEQUENCE: 7

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ggcaattatg cattaggccc cgaaggactg aagaaagcat tagctgaaac agggctcat	180
attctagtaa tggatttata cgcaaaaaca atgattaagc aaccaaagt aaatttatct	240
aatatcgatt taggctcaga ggggggagag ttgctcaaaa atattcacct taatcaagag	300
ctgtcacgaa tcaatgcgaa ttactggta gatacagcga agccacagat tcaaaaaact	360
gctcgttaata ttgtaaatta cgatgaacaa ttcaaaatt attacgacac attagtagaa	420
actgtacaaa agaagataa ggcaggtcta aaagagggt taaatgattt aattactaca	480
atcaatacaa attcaaaaga agttacagat gtgattaaga tgctacaaga cttcaaagg	540
aaattatatc aaaattctac agatttttaa aataatgttg gtggtccaga tgggaaagg	600
ggattaactg caatattagc aggtcaacag gcaacgattc cacaacttca agctgaaatt	660
gagcaacttc gttctactca gaaaaacat ttgatgatg tattagcatg gtcaattggt	720
gggtgattgg gagcagctat tttagtatt gcagctattg gaggagcgg agttattgtt	780
gtaactggcg gtacagcaac accggctgtt gttggtggac tctcggtct tggcgagct	840
ggtatcggtc taggaactgc ggctggtgtc acagcatcta agcatatgga ttcctataat	900
gaaatttcta acaaaatcgg agaattaagt atgaaagcag atcgtgctaa tcaagcagtt	960
ctttcgctta ctaacgcgaa agaaacattg gcatatttat accagactgt agatcaagcg	1020
atattgtctc taacaaatat tcaaaagcaa tggaatacaa tgggcgcaaa ttatacagat	1080
ttattggata atatcgattc tatgcaagac cacaattct ctttaatacc agatgattta	1140
aaagcggcta aagaaagttg gaatgatatt cataaagatg cagaattcat ttcaaaagat	1200
attgctttta aacaggagta g	1221

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<210> SEQ ID NO 8
 <211> LENGTH: 1221
 <212> TYPE: DNA
 <213> ORGANISM: *Bacillus cereus*

<400> SEQUENCE: 8

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ggcaattatg cattaggacc cgaaggactg aagaaagcat tggctgaaac aggggtctcat      180
attctagtaa tggatttata tgcaaaaaca atgattaagc aaccaaagt aaatttatct      240
aatatcgatt tagggtcaga ggggggagag ttgctcaaaa atattcacct taatcaagag      300
ctgtcacgaa tcaatgcgaa ttactgggta gatacagcga agccacagat tcaaaaaact      360
gctcgtaata ttgtaaatta cgatgaacaa tttcaaaatt attacgacac attagtagaa      420
actgtacaaa agaagataa ggcagggtcta aaagagggta taaatgattt aattactaca      480
atcaatacaa attcaaaaga agttacagat gtgattaaga tgctacaaga cttcaaagga      540
aaactatatc aaaattctac agattttaa aataatgttg gtggtccaga tgggaaaggt      600
ggattaactg caatattagc aggtcaacag gcaacgattc cacaacttca agctgaaatt      660
gagcaacttc gttctactca gaaaaaacat tttgatgatg tattagcatg gtcaattggg      720
ggtggttggt gagcagctat tttagttatt gcagctattg gaggagcggg agttattggt      780
gtaactggcg gtacagcaac accggctggt gttggtggac tctcggtctt tgggtgcagct      840
ggatcgggtc taggaactgc ggtggtgtgc acagcatcta agcatatgga ctctataat      900
gaaatttcta acaaaatcgg agaattaagt atgaaagcag atcgtgctaa tcaagcagtt      960
ctttcactta ctaacgcgaa agaaacattg gcatatttat atcagactgt agatcaagcg     1020
atattgtctc taacaaatat tcaaaagcaa tggaatacaa tgggcgcaaa ttatacagat     1080
ttattggata atatcgattc tatgaagac cacaattctt ctttaatacc agatgattta     1140
aaagccgcta aagaaagttg gaatgatatt cataaagatg cagaattcat ttcaaaagat     1200
attgctttta aacaggagta g                                     1221
  
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<210> SEQ ID NO 9
 <211> LENGTH: 1221
 <212> TYPE: DNA
 <213> ORGANISM: *Bacillus cereus*

<400> SEQUENCE: 9

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ggcaattatg cattaggccc cgaaggactg aagaaagcat tagctgaaac aggggtctcat      180
attctagtaa tggatttata cgcaaaaaca atgattaagc aaccaaagt aaatttatct      240
aatatcgatt taggctcaga ggggggagag ttgctcaaaa atattcacct taatcaagag      300
ctgtcacgaa tcaatgcgaa ttactgggta gatacagcga agccacagat tcaaaaaact      360
gctcgtaata ttgtaaatta cgatgaacaa tttcaaaatt attacgacac attagtagaa      420
actgtacaaa agaagataa ggcagggtcta aaagagggta taaatgattt aattactaca      480
atcaatacaa attcaaaaga agttacagat gtgattaaga tgctacaaga cttcaaaggg      540
aaactatatc aaaattctac agattttaa aataatgttg gtggtccaga tgggaaaggt      600
  
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ggattaactg caatattagc aggtcaacag gcaacgattc cacaacttca agctgaaatt	660
gagcaacttc gttctactca gaaaaaacat tttgatgatg tattagcatg gtcaattggt	720
ggtggattgg gagcagctat tttagttatt gcagctattg gaggagcggg cgttattggt	780
gtaactggcg gtacagcaac accggctggt gttggtggac tctcggtctt tgggtgcagct	840
ggtattgggt taggaacagc ggctggtgtc acagcatcta agcatatgga ctctataat	900
gaaatttcta acaaaatcgg agaattaagt atgaaagcag atcgtgctaa tcaagcagtt	960
ctttcgctta ctaacgcgaa agaaacattg gcataattat atcagactgt agatcaagcg	1020
atattgtctc taacaaatat tcaaaagcaa tggaatacaa tgggcgcaaa ttatacagat	1080
ttactggata atatcgattc tatggaagac cacaaattct ctttaatacc agatgattta	1140
aaagccgcta aagaaagttg gaatgatatt cataaagatg cagaattcat ttcaaaagat	1200
attgctttta aacaggagta g	1221

<210> SEQ ID NO 10

<211> LENGTH: 1155

<212> TYPE: DNA

<213> ORGANISM: Bacillus cereus

<400> SEQUENCE: 10

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ggcaattatg cattaggccc cgaaggacta aagaaagcat tggctgaaac aggggtctcat	180
attctagtaa tggatttata cgcaaaaaca atgattaagc aaccaaagt aaatttatct	240
aatatcaatt taggctcaga ggggggagag ttgctcaaaa atattcacct taatcaagag	300
ctgtcacgaa tcaatgcgaa ttactgggta gatacagcga agccacagat tcaaaaaact	360
gctcgttaata ttgtaaatta cgatgaacaa tttcaaaatt attacgacac attagtagaa	420
actgtacaaa agaagataa ggcagggtcta aaagagggca taaatgattt aattactaca	480
atcaatacaa attcaaaaga agttacagat gtgattaaga tgctacaaga cttcaaaggg	540
aaactatata aaaattctac agattttaa aataatgttg gtggtccaga tgggaaaggt	600
ggtttaactg caatattagc aggtcaacag gcaacgattc cacaacttca agctgaaatt	660
gagcaacttc gtgtactca gaaaaaacat tttgatgatg tattagcatg gtcaattggt	720
ggtggattgg gagcagctat tttagttatt gcagctattg gaggagcggg agttattggt	780
gtaactggcg gtacagcaac accggctggt gttggtggac tctcggtctt tgggtgcagct	840
ggtattgggt taggaacagc ggctggtgtc acagcatcta agcatatgga ctctataat	900
gaaatatcta acaaaatcgg agaattaagt atgaaagcag atcgtgctaa tcaagcagtt	960
tcttttcgct ttactaacgc gaaagaaaca ttggcatatc tatatcagac tgtagatcaa	1020
gcgatattgt ctctaacaaa tattcaaaag caatggaata caatgggcgc aaattataca	1080
gatttactgg ataatatcga ttctatgcaa gaccacaaat tctctttaat accagatgaa	1140
tttaaaagcc gctaa	1155

<210> SEQ ID NO 11

<211> LENGTH: 1062

<212> TYPE: DNA

<213> ORGANISM: Bacillus cereus

<400> SEQUENCE: 11

ttggctgaaa cagggtctca tattctagta atggatttat acgcaaaaac aatgattaag	60
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caacccaaatg taaattttatc taatatcgat ttaggtcag aggggggaga gttgtcaaa	120
aatattcacc ttaatcaaga gctgtcacga atcaatgcga attactgggt agatacagcg	180
aagccacaga ttcaaaaaac tgctcgtaat attgtaaatt acgatgaaca atttcaaaat	240
tattacgaca cattagtaga aactgtacaa aagaaagata aggcagggtct aaaagagggc	300
ataaatgatt taattactac aatcaataca aattcaaaag aagttacaga tgtgattaag	360
atgctacaag acttcaaagg gaaactatat caaaattcta cagattttta aaataatgtt	420
gggtgtccag atgggaaagg tggattaact gcaatattag caggtcaaca ggcaaccatt	480
ccacaacttc aagctgaaat tgagcaactt cgttctactc agaaaaaca tttgatgat	540
gtattagcat ggtcaattgg tgggtgattg ggagcagcta ttttagttat tgcagctatt	600
ggagagcggt tagttattgt tgtaactggc ggtacagcaa caccagctgt tgttggtgga	660
ctttcagctc ttggagcagc tggatcgggt ctaggaactg cggctgggtg tacagcatct	720
aagcatatgg actcctataa cgaattttct aacaaaatcg gagaattaag tatgaaagca	780
gatcgtgcta atcaagcagt tctttcgctt actaacgcga aagaaacatt ggcatattta	840
tatcagactg tagatcaagc gatattgtct ctaacaaata ttcaaaagca atggaataca	900
atgggcgcaa attatacgga tttactggat aatatcgatt ctatgcaaga ccacaaattc	960
tctttaatac cagatgattt aaaagctgct aaacaaagtt ggaatgatat tcataaagat	1020
gcagaattca tttcaaaaga tattgctttt aaacaggagt ag	1062

<210> SEQ ID NO 12

<211> LENGTH: 1221

<212> TYPE: DNA

<213> ORGANISM: Bacillus thuringiensis

<400> SEQUENCE: 12

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ggcaattatg cattaggccc cgaaggactg aagaaagcat tggctgaaac aggggtctcat	180
attctagtaa tggatttata cgcaaaaaca atgattaagc aaccaaattg aaattttatct	240
aatatcgatt taggtcaga ggggggagag ttgctcaaaa atattcacct taatcaagag	300
ctgtcacgaa tcaatgcgaa ttactgggta gatacagcga agccacagat tcaaaaaact	360
gctcgtaata ttgtaaatca cgatgaacaa tttcaaaatt attacgacac attagtagaa	420
actgtacaaa agaaagataa ggcagggtcta aaagagggta taaatgattt aattactaca	480
atcaatacaa attcaaaaga agttacagat gtgattaaga tgctacaaga cttcaaaggg	540
aaactatatc aaaattctac agatttttaa aataatgttg gtggtccaga tgggaaagggt	600
ggattaactg caatattagc aggtcaacag gcaacgattc cacaacttca agctgaaatt	660
gagcaacttc gttctactca gaaaaaacat tttgatgatg tattagcatg gtcaattgggt	720
gggtgattgg gagcagctat tttagttatt gcagctattg gaggagcgggt agttattgtt	780
gtaactggcg gtacagcaac accggctggt gttggtggac tctcggtctt tgggtgcagct	840
ggatcgggtc taggaactgc ggtcgggtgc acagcatcta agcatatgga ctctataat	900
gaaattttcta acaaaatcgg agaattaagt atgaaagcag atcgtgctaa tcaagcagtt	960
ctttcgctta ctaacgcgaa agaaacattg gcatatttat atcagactgt agatcaagcg	1020
atattgtctc taacaaatat tcaaaagcaa tggaatacaa tgggcgcaaa ttatacagat	1080

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ttattggata atatcgattc tatgcaagac cacaaattct ctttaatacc agatgattta	1140
aaagcgcgcta aagaaagttg gaatgatatt cataaagatg cagaattcat ttcaaaagat	1200
attgctttta aacaggagta g	1221

<210> SEQ ID NO 13
 <211> LENGTH: 972
 <212> TYPE: DNA
 <213> ORGANISM: *Bacillus thuringiensis*

<400> SEQUENCE: 13

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gatacggctc tttctgcaaa tgaagcgaga atgaaagaga ccttgcaaaa ggctggatta	180
tttgcaaaat ctatgaatgc ctattcttat atgttaatta agaactcctga tgtgaatttt	240
gagggaaatta ccattaatgg atatgtagat ttacctggta gaactgtaca agatcaaaag	300
aatgcaaggg cacatgccgt tacttgggat acgaaagtaa aaaaacagct ttagatata	360
ttgaatggta ttgttgaata cgatacaaca ttgataatt attatgaaac aatgatagag	420
gcgattaata caggggatgg agaaacttta aaagaaggga ttacagattt acgaggtgaa	480
attcaacaaa atcaaaagta tgcacaacaa ctaatagaag aattaactaa attaagagac	540
tctattggac acgatgttag agcatttggga agtaataaag agctcttgca gtcaatttta	600
aaaaatcaag gtgcagatgt tgatgccgat caaaagcgtc tagaagaagt attaggatca	660
gtaaaactatt ataacaatt agaactgat gggtttaatg taatgaaggg tgctattttg	720
ggctctaccaa taattggcgg tatcatagtg ggagtagcaa gggataattt aggtaagtta	780
gagcctttat tagcagaatt acgtcagacc gtggattata aagtaacctt aaactgtgta	840
gttgaggttg cttacagtaa tattaatgaa atgcacaagg cgcttgatga tgctattaac	900
gctcttactt atatgtccac gcagtggcat gatttagatt ctcaatatc gggcgttcta	960
gggcatattg ag	972

<210> SEQ ID NO 14
 <211> LENGTH: 1128
 <212> TYPE: DNA
 <213> ORGANISM: *Bacillus cereus*

<400> SEQUENCE: 14

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gatacggctc tttctgcaaa tgaagcgaga atgaaagaga ccttgcaaaa ggctggatta	180
tttgcaaaat ctatgaatgc ctattcttat atgttaatta agaactcctga tgtgaatttt	240
gagggaaatta ccattaatgg atatgtagat ttacctggta gaactgtaca agatcaaaag	300
aatgcaaggg cacatgccgt tacttgggat acgaaagtaa aaaaacagct ttagatata	360
ttgaatggta ttgttgaata cgatacaaca ttgataatt attatgaaac aatgatagag	420
gcgattaata caggggatgg agaaacttta aaagaaggga ttacagattt acgaggtgaa	480
attcaacaaa atcaaaagta tgcacaacaa ctaatagaag aattaactaa attaagagac	540
tctattggac acgatgttag agcatttggga agtaataaag agctcttgca gtcaatttta	600
aaaaatcaag gtgcagatgt tgatgccgat caaaagcgtc tagaagaagt attaggatca	660
gtaaaactatt ataacaatt agaactgat gggtttaatg taatgaaggg cgctattttg	720

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ggtctaccaa taattggcgg tattatagtg ggagtagcaa gggataatth aggtaagtta	780
gagcctttat tagcagaatt acgtcagacc gtggattata aagtaacctt aaatcgtgtg	840
gttgaggttg cttacagtaa tattaatgaa atgcacaagg cccttgatga tgctattaac	900
gctcttactt atatgtccac gcagtggcat gatttagatt ctcaatatte gggcgttcta	960
gggcatattg agaatgcagc tcaaaaagcc gatcaaaata aatttaaatt cttaaaacct	1020
aatttaaattg cagcgaaaga cagttggaaa acattacgaa cagatgctgt tacattaata	1080
gaaggaataa aggaattaaa agtggaaact gttactccac aaaaatag	1128

<210> SEQ ID NO 15
 <211> LENGTH: 1128
 <212> TYPE: DNA
 <213> ORGANISM: Bacillus cereus

<400> SEQUENCE: 15

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gatacggctc tttctgcaaa tgaagcgaga atgaaagaga ccttgcaaaa ggctggatta	180
tttgcaaaat ctatgaatgc ctattcttat atgttaatta agaactctga tgtgaatttt	240
gagggaaatta ccattaatgg atatgtagat ttacctggta gaatcgtaca agatcaaaaag	300
aatgcaaggg cacatgctgt tacttgggat acgaaagtaa aaaaacagct ttagatata	360
ttgaatggta ttgttgaata cgatacaaca ttgacaatt attatgaaac aatggtagaa	420
gcgattaata caggggatgg agaaacttta aaagaaggga ttacagattt gcgaggtgaa	480
attcaacaaa atcaaaagta tgcacaacaa ctaatagaag aattaactaa attaagagac	540
tctattggac atgatgttag agcttttggga agtaataaag agctcttgca gtcaatttta	600
aaaaatcaag gtgcagatgt tgatgccgat caaaagcgtc tagaagaagt attaggatca	660
gtaactattt ataacaatt agaactctgat gggtttaatg taatgaaggg tgctattttg	720
ggtctaccaa taattggcgg tattatagtc ggagtagcaa gggataatth aggtaagtta	780
gagcctttat tagcagaatt acgtcagacc gtggattata aagtaacctt aaatcgtgta	840
gttgaggttg cttacagtaa tattaatgaa atgcacaagg cccttgatga tgctattaac	900
gctcttactt atatgtccac gcagtggcat gatttagatt ctcaatatte gggcgttcta	960
gggcatattg agaatgcagc tcaaaaagcc gatcaaaata aatttaaatt cttaaaacct	1020
aatttaaattg cagcgaaaga cagttggaaa acattacgaa cagatgctgt tacattaata	1080
gaaggaataa aggaattaaa agtggaaact gttactccac aaaaatag	1128

<210> SEQ ID NO 16
 <211> LENGTH: 1128
 <212> TYPE: DNA
 <213> ORGANISM: Bacillus cereus

<400> SEQUENCE: 16

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gatacggctc tttctgcaaa tgaagcgaag atgaaagaaa ctttgcaaaa ggctggatta	180
tttgcaaaat ctatgaatgc ctattcttat atgttaatta aaaaactctga tgtgaatttt	240
gagggaaatta ctattaatgg atatgtagat ttacctggta gaatcgtaca agatcaaaaag	300

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aatgcaagag cacatgctgt tacttgggat acgaaagtga aaaaacagct ttagatata	360
ttgactggta ttgttgaata tgatcgacg ttgacaatt attatgaaac aatggtagag	420
gcaattaata caggggatgg agaaacttta aaagaaggga ttacagattt gcgaggtgaa	480
attcaacaaa atcaaaagta tgcacaacaa ctaatagaag aattaactaa attaagagac	540
tctattggac acgatgttag agcatttggga agtaataaag agctcttgca gtcaatttta	600
aaaaatcaag gtgcagatgt tgatgccgat caaaagcgtc tagaagaagt attaggatca	660
gtaaactatt ataaacaatt agaactgat gggtttaattg taatgaaggg tgctattttg	720
ggctaccaa taattggcgg tattatagtg ggagtagcaa gggataattt aggtaagtta	780
gagcctttat tagcagaatt acgtcagacc gtggattata aagtaacctt aaatcgtgta	840
gttgagttg cttacagtaa tattaatgaa atcgacaagg cgcttgatga tgctattaac	900
gctcttactt atatgtccac gcagtggcat gatttagatt ctcaatatc gggcgttcta	960
gggcataattg agaatgcagc tcaaaaagcc gatcaaaata aatttaaatt cttaaaacct	1020
aatttaaattg cagcgaaaga tagttggaaa acattacgaa cagatgctgt tacattaaaa	1080
gaaggaataa aggagttaaa agtagaaact gttactccac aaaaatag	1128

<210> SEQ ID NO 17
 <211> LENGTH: 1128
 <212> TYPE: DNA
 <213> ORGANISM: *Bacillus cereus*

<400> SEQUENCE: 17

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gatacagctc ttctcgcaaa tgaagcgaga atgaaagaga ccttgcaaaa ggctggatta	180
tttgcaaaat ctatgaatgc ctattcttat atgttaatta agaactctga tgtgaatttt	240
gaggaatta cgattaatgg gtatgttagat ttacctgga gaatcgtaca agatcaaaa	300
aatgcaaggg cacatgctgt tacttgggat acgaaagtga aaaaacagct ttagatata	360
ttgaatggta ttgttgaata cgatacaaca ttgacaatt attatgaaac aatggtagag	420
gcgattaata caggggatgg agaaacttta aaagaaggga ttacagattt gcgaggtgaa	480
attcaacaaa atcaaaagta tgcacaacaa ctaatagaag aattaactaa attaagagac	540
tctattggac acgatgtgag agcatttggga agtaataaag agctcttgca gtcaatttta	600
aaaaatcaag gtgcagatgt tgatgccgat caaaagcgtc tagaagaagt attaggatca	660
gtaaactatt ataaacaatt agaactgat gggtttaattg taatgaaggg tgctattttg	720
ggctaccaa taattggcgg tatcatagtg ggagtagcaa gggataattt aggtaagtta	780
gagcctttat tagcagaatt acgtcagacc gtggattata aagtaacctt aaatcgtgta	840
gttgagttg cttacagtaa tattaatgaa atgcacaagg cgcttgatga tgctattaac	900
gctcttactt atatgtccac gcagtggcat gatttagatt ctcaatatc gggcgttcta	960
gggcataattg agaatgcagc tcaaaaagcc gatcaaaata aatttaaatt cttaaaacct	1020
aatttaaattg cagcgaaaga cagttggaaa acattacgaa cagatgctgt tacattaaaa	1080
gaaggaataa aggaattaaa agtggaact gttactccac aaaaatag	1128

<210> SEQ ID NO 18
 <211> LENGTH: 1128
 <212> TYPE: DNA
 <213> ORGANISM: *Bacillus thuringiensis*

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<400> SEQUENCE: 18

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gattcagctc tttctgcaaa tgaagcgaga atgaaagaga ccttgcaaaa ggctggatta	180
tttgcaaaat ctatgaatgc ctattcttat atgttaatta aaaatccgga tgtgaatttt	240
gagggaaatta ccattaatgg atatgttagat ttacctggta gaatcgtaca agatcaaaag	300
aatgcaagag cacatgctgt tacttgggat acgaaagtaa aaaaacagct tttagataga	360
ttgaatggta ttgttgaata cgatacaaca ttgacaatt attatgaaac aatggtagag	420
gcgattaata caggggatgg agaaacttta aaagaaggga ttacagattt gcgaggtgaa	480
attcaacaaa atcaaaagta tgcacaacaa ctaatagaag aattaactaa attaagagac	540
tctattggac acgatgttag agcatttgga agtaataaag agctcttgca gtcaatttta	600
aaaaatcaag gtgcagatgt tgatgccgat caaaagcgtc tagaagaagt attaggatca	660
gtaaactatt ataacaatt agaactgat gggtttaatg taatgaaggg tgctattttg	720
ggctaccaa taattggcgg tatcatagtg ggagtagcaa gagataattt aggtaagtta	780
gagcctttat tagcagaatt acgtcagacc gtggattata aagtaacctt aaatcgtgta	840
gttgagttg cttacagtaa tattaatgaa atgcacaagg cacttgatga tgctattaac	900
gctcttactt atatgtccac gcagtggcat gatttagatt ctcaatattc gggcgttcta	960
gggcataatt agaattgcgc tcaaaaagcc gatcaaaata aatttaaatt cttaaaaacct	1020
aatttaaattg cagcgaaaga cagttggaaa acattacgaa cagatgctgt tacattaaaa	1080
gaaggaataa aggagttaaa agtagaaact gttactccac aaaaatag	1128

<210> SEQ ID NO 19

<211> LENGTH: 1084

<212> TYPE: DNA

<213> ORGANISM: *Bacillus thuringiensis*

<400> SEQUENCE: 19

actcatttct attaaacaag atatgaaaga gtggtcaccc gaactttatc ctaaattaat	60
tctattaaat tcaaaaagta aaggatttgt aactaaattt aatagttatt atccaacatt	120
aaaaggattt gtatagataa aggaagataa agaagggttt acagatagac tggaagtcct	180
tcaagacatg accatcacaa accaagaaag tgtgcaacgt caaattaatg agttaacaga	240
tctaaaacta caggtagata agaagtgaa aaatcttgat actgatgtgg caaaaacaca	300
gagtgtcctt aattcagagg gaacaggaaa aatagataag ttaaaaaatg aaatgctaga	360
tacaaaaaaa tcaattcaaa atgatttaca gcaaatagcg ttattaccag gagctttaa	420
tgaacaagga ctaaaggat tccaagaaat ttatagtcta tcaaaagata tcattgaacc	480
ggctgctcaa acagcagtag tagcgtataa caaaggaaaa gaaataaaca atgctattgt	540
agacgcagag aataaagcag agcaagaagc aaaagaaaaa ggaaaatcag ctatagaaat	600
tgaggctgcc aaaaaagaag cacgtgaagc gatagagaaa agtaaaaaag gtgaaatcgc	660
tgcagctgca gttacaaaaa cgaagagta tgatcttatg aaagtaattg atcctgaaaa	720
aattaaaaaa acatataata cttttgctga aattaataaa ctaacagcag agcaacgtgc	780
atatttaaat gatttagaga aacaaaatca gaaattatat gacttaacga ctaaattaac	840
agtagcagat ttacaaaaat caatgattct tttcatgcaa aatgatttgc atacatttgc	900

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taaccaagta gatggagaaa ttgagcta	960
aatataatagt attacaaat tategactga agttgatacc aataacaccc agtctcaaaa	1020
agatacatta agacgattaa aaagtgtaac aactcaactc gaagaacaag ttataaaatt	1080
ttaa	1084

<210> SEQ ID NO 20
 <211> LENGTH: 1078
 <212> TYPE: DNA
 <213> ORGANISM: *Bacillus thuringiensis*

<400> SEQUENCE: 20

tctaattaaa caagatatga aagagtggc atccgaactt taccctaaat taattctatt	60
aaattcaaaa agtaaaggat ttataactaa atttaaatagt tattatccaa cattaaaagg	120
attttagat aataaggaag ataagaagg gtttacagat agactggaag ttcttcaaga	180
catgactata acaaatcaag aaagtgtgca acgtcaaatt aatgagttaa cagattttaa	240
attactggta gataagaagt tgaanaacct tgatactgat gtggtaaaag cacaagtgt	300
ccttaattca gaggaacag gaaaaataga taagttaaaa aatgaaatgc tagatacaaa	360
aaaatctatt caaatgatt tgcagcaaat agcattatta ccaggcgcgt taaatgaaca	420
agggctaaag gtattccaag aaatttatag tctatcgaaa gatattcattg aaccggctgc	480
tcaaacagca gtagtagcgt ataacaagg aaagaaata acaaatgcca ttgtagacgc	540
agagaagaaa gcagagcaag aagcaaaaga aaagggaaaa tcagctatag aaattgaagc	600
tgccaaaaaa gaagcagtg aaacgataga gaaaagtaaa aaaggtgaaa tcgctgcagc	660
tgagttaca aaacgaag agtatgatct tatgaagtgt attgatcctg aaaaaataaa	720
aaaaacatat aatacttttg ctgaaattaa taaactaaca gctgagcaaa gagcatattt	780
aatgattta gagaacaaa atcagaaatt atatgactta acaactaaat taacagtagc	840
agatttaca aaatcaatga ttcttttcat gcaaatgac ttgcatacat ttactaatca	900
agtagatgga gaaattgagt taatgaacg ttacaaagag gatttgatc taataataaa	960
tagtattaca aaattatcga ctgaagtga taccaataat actcaggctc aaaaagatat	1020
attaagacga ttaaaagtgt taacaattca acttgaagaa caagtttata aattttga	1078

<210> SEQ ID NO 21
 <211> LENGTH: 1320
 <212> TYPE: DNA
 <213> ORGANISM: *Bacillus cereus*

<400> SEQUENCE: 21

atgaagaata aaattatgac aggattttta ataacatcaa ttgctaccgg ggcgactatt	60
cctatcaata ctctcgcaac gccaatcgtc caagcagaaa caaacaaga gaatatagat	120
atttcctcag cgttacgaaa aataggtgca cactccaaat taacacaaac ctttatcgat	180
ggagccttag caagtccgaa tgtacaactt gaagaagttc catctttaa tacaactcaa	240
tttctaatta aacaagatat gaaagagtgg tcatccgaac tttatcctaa attaattcta	300
ttaaattcaa aaagtaaagg atttgtaact aaatttaata gttattatcc aatattaaaa	360
gggttttag ataatagga agataaagaa ggatttacag atagactgga agtccttcaa	420
gacatgacca tcacaaacca agaaagtgtg caacgtcaaa ttaatgagtt aacagatcta	480
aaactacagg tagataagaa gttgaaaaat cttgatactg atgtgacaaa agcacagagt	540
gtccttaatt cagaggaac aggaaaaata gataagttaa aaatgaaat gctagatata	600

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aaaaaatcaa ttcaaatga ttacagcaa attgcattat taccaggggc tttaaatgaa 660
caagggctaa aggtattcca agaaatttat agtctatcga aagatatcat tgaaccggct 720
gctcaaacag cagtagtagc gtatacaaaa ggaaagaaa taaacaatgc tattgtagac 780
gcagagaata aagcagagca agaagcaaaa gaaaaggaa aatcagctat agaaattgag 840
gctgcaaaaa aagaagcacg tgaagcgata gagaaaagta aaaaagggtga aatcgctgca 900
gctgcagtta caaaaacgaa agagtatgat cttatgaaag tgattgatcc tgaaaaaatt 960
aaaaaacat ataatacttt tctgtaaatt aataaactaa cagcagagca acgtgcatat 1020
ttaaatgatt tagaaaaaca aaatcagaaa ttatatgact taacaactaa attaacagta 1080
gcagatttac aaaaatcaat gattcttttc atgcaaatg atttgcatac atttgctaac 1140
caagtagatg gagaaattga gctaataaaa cgttacaaag aggatttggg tctaataaat 1200
aatagtatta caaaattatc gactgaagtt gataccaata aactcagtc tcaaaaagat 1260
acattaagac gattaaaaag tgtaacaact caactcgaag aacaagtta taaattctaa 1320

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<210> SEQ ID NO 22

<211> LENGTH: 1319

<212> TYPE: DNA

<213> ORGANISM: *Bacillus cereus*

<400> SEQUENCE: 22

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atgaagaata aaattatgac aggattttta ataacatcaa ttgctaccgg ggcgactatt 60
cctatcaata ctctcgcaac gccaatcgtc caagcagaaa caaacaaga gaatatagat 120
atttcctcag cgttacgaaa aataggtgca cactccaaat taacacaaac ctttatcgat 180
ggagccttag caagtccgaa tgtacaactt gaagaagttc catctttaa tacaactcaa 240
tttctattaa acaagatatg aaagagtggg catccgaact ttatcctaaa ttaattctat 300
taaattcaaa aagtaaagga tttgtaacta aatttaatat ttattatcca atattaaaag 360
ggtttataga taatagggaa gataaagaag gatttacaga tagactggaa gtccttcaag 420
acatgaccat cacaaccaa gaaagtgtgc aacgtcaaat taatgagtta acagatctaa 480
aactcaggt agataagaag ttgaaaaatc ttgatactga tgtgacaaaa gcacagagtg 540
tccttaattc agagggaaaca ggaaaaatag ataagttaaa aaatgaaatg ctagatacaa 600
aaaaatcaat tcaaatgat ttacagcaaa ttgcattatt accaggggct ttaaatgaac 660
aagggtctaa ggtattccaa gaaatttata gtctatcgaa agatatcatt gaaccggctg 720
ctcaaacagc agtagtagcg tataacaaag gaaaagaaat aaacaatgct attgtagacg 780
cagagaataa agcagagcaa gaagcaaaag aaaagggaaa atcagctata gaaattgagg 840
ctgcaaaaaa agaagcacgt gaagcgatag agaaaagtaa aaaagggtga atcgctgcag 900
ctgcagttac aaaaacgaaa gagtatgatc ttatgaaag gattgatcct gaaaaaatta 960
aaaaaacata taatactttt gctgaaatta ataaactaac agcagagcaa cgtgcatatt 1020
taaatgattt agaaaaacaa aatcagaaat tatatgactt aacaactaaa ttaacagtag 1080
cagatttaca aaaatcaatg attcttttca tgcaaatga tttgcataca tttgctaacc 1140
aagtagatgg agaaattgag ctaatgaaac gttacaaaga ggatttggat ctaataaata 1200
atagtattac aaaattatcg actgaagttg ataccaataa cactcagtc tcaaaaagata 1260
cattaagacg attaaaaagt gtaacaactc aactcgaaga acaagtttat aaattctaa 1319

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<210> SEQ ID NO 23

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<211> LENGTH: 1323

<212> TYPE: DNA

<213> ORGANISM: *Bacillus cereus*

<400> SEQUENCE: 23

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atgaaaaatg atctcactaa aaaatttgta ataacatcag ttgtttttgg attagcaatt    60
tctaactatg tattttcacc tgctatagtc atacaagctg agacacaaca agaacgaata    120
gatattttctt cctccttacg caagtttagt gcacaatcta aactaataca aacatatatc    180
gatcaaaatt taataacacc taatatacag ttgaaggaaa tgccatcttt aaatacgaat    240
caatttttaa ttaagcgaga tatgaaagag tggtcacatc aactacatcc aaatttaatc    300
ctactaaatt caaatagtaa aggatatgta actaaattta ataactatta tccaacatta    360
aagggatttg tagataataa ggaagataaa gaaggctttt tagatagact ggaagtactt    420
caagatatga ctataagaaa ccaagaaagt gtccagcatc aaattaatga attaacagat    480
tttaaattac aactagataa aaagcttaaa gatctcgaca ctgatgtggc aaaggcacia    540
gggttactag tttctgagaa aacagcaaaa atagatcttg ttaaaaatga attgctgatt    600
acaaaaaaag caattcaaag taatttacag gaaatagcat tattaccagg agctttaaat    660
gaacaagggc taaaggtatt ccaagaaatt tatagtctat cgaaagatat cattgaacca    720
tctgctcaaa cagcagtagt agcgtataac aaaggaaaag aaataacaa tgctattgtc    780
gaagcagaga agaaagcaga gcaagaggca agggagaaag gtaaatcaat tctagaaatt    840
gaagccgcaa aaaaagaagc acgtgaagaa atttcgaaaa gtaaaaaagg tgaaattgct    900
gcagctgcgg ttacaaaaac aaaagagtat gatcttatga aaatagttaa ttctgaaaaa    960
attaaaaaaa catatagtac ctctgccgaa attaataaac taacggcaga acagcgagcg    1020
catttatatg atttagagaa acaaaaccaa aaatttatatg atttaacaag aaaattaaca    1080
gtagcaggat tacaaaaatc aatgattatt cttatgcaaa atgatttgca tacatttgtt    1140
agccaagtag atagagaaat tgatcttcag aaacgttata aagaagattt aaacctatta    1200
aaaaagagta ttacaacatt attgacaaat gttgatagtg taaacaataa gtctcaaaaa    1260
gatactttaa gaatattgaa aacattaacc ggtcaacttg aggaacaggt taataaattt    1320
taa
1323

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<210> SEQ ID NO 24

<211> LENGTH: 1320

<212> TYPE: DNA

<213> ORGANISM: *Bacillus weihenstephanensis*

<400> SEQUENCE: 24

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atgaagaata aaattatgac aggattttta ataacatcaa tcgttactgg agcgactatt    60
cctatcaata ctctcgcaac gccaatcggt caggcagaaa tgaacaaga aaatatagat    120
atttcctcag cattacgaaa aataggtgca cactccaaat taacacaaac ctttatagat    180
ggagcccttag caagtccgaa tgtgcaactt gaagaagttc catctttaa tacaactcaa    240
tttctaatta aacaagatat gaaagagtgg tcatcagaac tatatccaaa attaattcta    300
ctaaattcaa aaagtaaagg atttgcaacc aaatttaata gctattatcc aacattaata    360
ggattttag atataagga agataaagaa gggtttatag atagactgga agttctccaa    420
gatatgacta taacaaacca agaaaacgtg caacgtcaga ttaatgagtt aacagatctt    480
aaactacagg tagataagaa actgaaaaat cttgatacag atgtggtaaa agcacagagt    540
gtacttagtt cagaggggaa aggaaaaata gacaagttaa aaatgaaat gctaaatata    600

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aaaaaatcaa ttcaaaatgc tttagagcaa atagcattat taccaggagc tttaaatgaa	660
caagggctaa aggtattcca agaaatttat agcctatcaa aagatatcat tgaaccggct	720
gctcaaacag cggtagtagc gtataacaaa ggaaagaaa taaataatac tattgtagaa	780
gcagagaaga aagcagagca ggaagcaaca gaaaaggaa aatcagctat agaaattgaa	840
gctgcaaaaa aagaagcacg tgaagcgata gagaaaagta aaaaagggtga gattgctgca	900
gctgcagtta caaaaacgaa agagtatgat cttatgaaag tgattgatcc tgaaaaaatt	960
aaaaaacat atagtacctt tgccgaaatt aataaactaa cagcagagca aagagtatat	1020
ttaaatgatt tagagaaaca aaatcagaaa ttatatgact taacaactaa attaacagta	1080
gcagatctac aaaaatcaat gattcttttc atgcaaaatg atttgcatac atttgcta	1140
caagtagatg gagaaattga gctaataaaa cggtataaag aggatttgaa tctaataaat	1200
aatagtatta aaaaattatt gactgaagtt gatactagta aactcagtc tcaaaaagat	1260
acattaagac gactaaaaaa tgtaacaaat caactcgaag aacaagtcca taaatttta	1320

<210> SEQ ID NO 25

<211> LENGTH: 1230

<212> TYPE: DNA

<213> ORGANISM: Bacillus thuringiensis

<400> SEQUENCE: 25

atgatgaaat ttccatttaa ggttataact ttagccactt tagcaacggt tataactgct	60
acgaatggta gtactattca tgcacttgca caagaacaga cagctcaaga acataaaata	120
gaaaattatg cgttaggacc tgaaggggta aagaaagcgt tggctgcaac tggctctcat	180
attcttgtaa tggatttgta cgcaaaaact atgattaagc aaccgaatgt aaatttatcc	240
aacattgatt taggttcagg aggaggagaa ttaatcaaaa atatccacct gaatcaggaa	300
ctgtcacgaa tcaatgcaaa ttactgggta gatacagcga agccaaacat tcaaaaaaca	360
gctcgttaata ttgtaaatga tgatgagcaa ttccaaaatt attacgacac attagtagat	420
actgtaaaaa agaagataa gatgagcctt aaagaaggaa taggggattt aatcgataca	480
attcatacaa attcaaatga agttactgac gtcattaaga tggtagaggc tttcaaaaca	540
aagttgtata caaatactgt agattttaaa aataatgttg gtggtccaga tggacaggga	600
ggattgacgg ctatattagc gggaaaacaa gcaactagtc cacaacttca ggccgaaatt	660
gagaatttac gttctacaca gaaatcacat tttgataatg tattagcctg gtcaattggc	720
ggtggactag gagcagctat tttagttatt ggaacgattg caggagcggg agtaattgtt	780
gtgactgggt gtacagctac accagctgtt gttggcggtc ttacagctct aggagcagct	840
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gaaatttcga ataaaatcgg agaattaagt atgaaagctg atctggctaa tcaagcgggt	960
atttcactta ctaatacga agacactcta acatatttgt atcagacagt ggatcaagca	1020
ataatgtctc taacaagtat tcagacaaca tggaataaaa tgggggctaa ttataaagat	1080
ttatatgata atatcgatca aatgcaagaa cataaacttt cgttaatacc tgacgattta	1140
aaagctgcta aacaaagttg gaatgacatt cataaggacg cagaattcat ttcaaaagac	1200
attgctttta aacaagaaaa aacaaactaa	1230

<210> SEQ ID NO 26

<211> LENGTH: 1230

<212> TYPE: DNA

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<213> ORGANISM: *Bacillus thuringiensis*

<400> SEQUENCE: 26

atgatgaaat ttccatttaa agttataacc ttagctactt tagcaacgat tataaccgct	60
acaaatggta gtactattca tgcacttgca caagaacaga cagctcaaga acagaaaata	120
gaaaattatg cgtaggacc tgaaggatta aagaaagcgt tggctgaaac aggctctcat	180
attcttgtaa tggatttcta cgcaaaaact atgattaagc aaccgaatgt aaatttatcc	240
aacattgatt taggttcggg tggagaagaa ttaatcaaaa atattcacct gaatcaagaa	300
ctgtcacgaa tcaatgcaaa ttactgggta gatacagcga agccaaacat tcaaaaaaca	360
gcacgtaata ttgtaatta tgaatgagca tttcaaaatt attacgacac attagtagat	420
actgtaaaaa agaaggataa ggtgagcctc aaagaaggaa taggggattt aatctataca	480
attcatacaa attcaaatga agttacggaa gtcattaaga tggtagaggc tttcaaaaca	540
aagttgtata caaatactgt agatttttaa aataatgttg gtggtccaga tggacaggga	600
ggattgacgg ctatattagc gggaaaacaa gcgctagtcc cacaacttca ggccgaaatt	660
gagaatttac gttctacaca gaaaacacat ttgataatg tattagcctg gtcaattggt	720
ggtggattag gacgagctat tttagttatt ggaacgattg caggagcggg agtaattggt	780
gtgactgggt gtacagctac gccagctgtt gttggtggtc ttacagctct aggagccgct	840
ggtatcgggt taggaacagc agctggcgtc gaggcattca atcatatgaa ttcttataat	900
gaaatttcga ataaaatcgg agaattaagt atgaaagctg atttggttaa tcaagcgggt	960
atttcactta ctaatacga agacactcta acatatttgt atcagacagt ggatcaagca	1020
ataatgtctc taacaagtat tcagcaacaa tggaataaaa tgggggctaa ttataaagat	1080
ttatatgata atatcgatca aatgcaagaa cataaaactt cggttaatacc tgacgattta	1140
aaagctgcta aacaaagttg gaatgatatt cataaggatg cagaattcat ttcaaaagac	1200
attgctttta aacaagaaaa acaaaactag	1230

<210> SEQ ID NO 27

<211> LENGTH: 1215

<212> TYPE: DNA

<213> ORGANISM: *Bacillus cereus*

<400> SEQUENCE: 27

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acgaatggta gtactattca tgcacttgca caagaacaga aaatagaaaa ttatgcgtta	120
ggacctgaag gattaaagaa agcgttggct gcaactggct ctcatattct tgtaatggat	180
ttgtacgcaa aaactatgat taagcaaccg aatgtaaatt tatccaacat tgatttaggt	240
tcaggaggag gagaattaat caaaaatata cacctgaatc aggaactgtc acgaatcaat	300
gcaaattact ggttagatac agcgaagcca aacattcaaa aaacagctcg taatattgta	360
aattatgatg agcaatttca aaattattac gacacattag tagatactgt aaaaaagaaa	420
gataagatga gccttaaaga aggaataggg gatttaatcg atacaattca tacaaattca	480
aatgaagtta ctgacgtcat taagatgtta gaggccttca aaacaaagtt gtatacaaat	540
actgtagatt ttaaaaaata tgttgggtgt ccagatggac agggaggatt gacagctata	600
ttagcgggaa aacaagcact agtccacaaa cttcaggcgg aaattgagaa tttacgttct	660
acacagaaat cacattttga taatgtatta gcctgggttaa ttggcgggtg actaggagca	720
gctattttag ttattggaac gattgcagga gcggtagtaa ttgttggtac tgggtgtaca	780

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gctacaccag ctgttgttgg cggctcttaca gctctaggag cagctggtat cggtttagga	840
acagcagctg gtgtcgaggc atctaatacat atgaattctt ataataaaat ttcgaataaa	900
atcggagaat taagtatgaa agctgatctg gctaatacaag cggttatttc acttactaat	960
acgaaagaca ctctaacata tttgtatcag acagtggatc aagcaataat gtctctaaca	1020
agtattcagc aacaatggaa taaaatgggg gctaattata aagatttata tgataatatc	1080
gatcaaatgc aagaacataa actttcgtta atacctgacg atttaaaagc tgctaaacaa	1140
agttggaatg atattcataa ggacgcagaa ttcatttcga aagacattgc ttttaacaa	1200
gaaaaacaa actaa	1215

<210> SEQ ID NO 28

<211> LENGTH: 1215

<212> TYPE: DNA

<213> ORGANISM: Bacillus cereus

<400> SEQUENCE: 28

atgatgaaat ttccatttaa ggtcataact ttagccactt tagcaacggt tataactgct	60
acgaatggta gtactattca tgcacttgca caagaacaga aaatagaaaa ttatgcgtta	120
ggacctgaag gattaaagaa agcgttggct gcaactggct ctcatattct tgtaatggat	180
ttgtacgcaa aaactatgat taagcaaccg aatgtaaatt tatccaacat tgatttaggt	240
tcaggaggag gagaattaat caaaaatata cacctgaatc aggaactgtc acgaatcaat	300
gcaaattact ggtagatac agcgaagcca aacattcaaa aaacagctcg taatattgta	360
aattatgatg agcaatttca aaattattac gacacattag tagatactgt aaaaaagaaa	420
gataagatga gccttaaaga aggaataggg gatttaatcg atacaattca tacaattca	480
aatgaagtta ctgacgtcat taagatgtta gaggccttca aaacaaagtt gtatacaaat	540
actgtagatt ttaaaaaataa tgttgggtgt ccagatggac agggaggatt gacagctata	600
ttagcgggaa aacaagcact agtcccacaa cttcaggccg aaattgagaa tttacgttct	660
acacagaaat cacattttga taatgtatta gcctgggttaa ttggcgggtg actaggagca	720
gctatttttag ttattggaac gattgcagga gcggtagtaa ttgttgtgac tgggtgtaca	780
gctacaccag ctgttgttgg cggctcttaca gctctaggag cagctggtat cggtttagga	840
acagcagctg gtgtcgaggc atctaatacat atgaattctt ataataaaat ttcgaataaa	900
atcggagaat taagtatgaa agctgatctg gctaatacaag cggttatttc acttactaat	960
acgaaagaca ctctaacata tttgtatcag acagtggatc aagcaataat gtctctaaca	1020
agtattcagc aacaatggaa taaaatgggg gctaattata aagatttata tgataatatc	1080
gatcaaatgc aagaacataa actttcgtta atacctgacg atttaaaagc tgctaaacaa	1140
agttggaatg atattcataa ggacgcagaa ttcatttcga aagacattgc ttttaacaa	1200
gaaaaacaa actaa	1215

<210> SEQ ID NO 29

<211> LENGTH: 1230

<212> TYPE: DNA

<213> ORGANISM: Bacillus cereus

<400> SEQUENCE: 29

atgaaaaaaa ctccatttaa ggtgttaact tttatcactt tggcatcaat tataactact	60
actaacggta gtgctattca tgtatttgca caagatcgga ctttacaaga aaaaaaata	120

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gaaatttata cattaggacc tgaagggtc aagaaagaat tggctaaaac cggatcta	180
attctcgtaa tggacttgta cgcaaaaaca atgattaaac agccaaacgt aaacttatcc	240
agtattgatt taggttcagg aggagaagaa ttaatcaaaa acattcaatt gaatcaggaa	300
ttatcacgaa tcaatgcaag ttactggta gatacagcga agccaaagat tcaaaaaaca	360
gtacgtaaca ttgtaaatta tgatgagcaa tttcaaaatt attacgacac attagtagat	420
actgtaaaaa agaatgataa gatgaacctc aaagaaggaa taggggattt aatccataca	480
attcatacaa attcaaatga agttacggaa gtcattaaga tgtagaggc tttcaaaaca	540
aagttgtata caaatactgt agactttaa aataatgttg ggggccctga tggtaagggt	600
ggattaacgg ctatactagc cggaaaacag gcattgggtc cacaacttca ggctgaaatt	660
gagaatttac gttctacgca gaaattacat ttgataatg tattagcctg gtcaattggt	720
ggtggattag gagcagctat tttagttatt ggagcgattg caggagcggg agtaattggt	780
gtgactgggt gtacagctac accagctggt gttggcgggt ttacagctct aggagcagct	840
ggtatcggt taggaacagc agctggtgtt gaggcacta atcatatgaa ttcctataat	900
gaaatttcaa ataaatcgg agaattaagt atgaaagctg atttagctaa ccaagcgggt	960
atatcactta ctaatacaaa agacacttta acatatttgt atcagacagt ggatcaagcg	1020
ataatgtctc taacaagtat tcagcaacaa tggaataaaa tgggagctaa ttataaagat	1080
ttatatgata atatcgatca aatgcaagaa cataaactat ctttaatacc tgatgattta	1140
aaggctgcta aacaaagttg ggatgaaatt cataaggacg cagaattcat ttcaaaagac	1200
attgctttta aacaagaaaa acaaaactga	1230

<210> SEQ ID NO 30

<211> LENGTH: 1227

<212> TYPE: DNA

<213> ORGANISM: Bacillus weihenstephanensis

<400> SEQUENCE: 30

atgaaatttc catttaaggt cataactttg gccactttag caacgggttat aactgctacg	60
aatggtagta ctattcacgc acttgcacaa gaacagacag cacaagaaca gaaaatagaa	120
aattatgctg taggacctga aggggttaaag aaagtgttgg ctaaaacagg ctctcatatt	180
cttgtaatgg atttgtacgc aaaaacaatg attagcaac cgaatgtaaa tttatccaac	240
attgathtag gttcaggagg gggagaatta atcaaaaaca ttcacctgaa tcaagaactg	300
tcacgaatca atgcaaatga ctggctagat acagcgaagc caaacattca aaagacagca	360
cgtaatatgg taaattatga tgaacaattt caaaattatt acgacacact agtagatact	420
gtaaaaaaga aagataaggc gggcctcaaa gaaggaatag gggatttaat cggtaacaatt	480
catacaaat caaatgaagt tacggaaatt attaagatgt tagaagcttt caaaacaaag	540
ttgtatacaa atactgtaga ttttaaaaat aatgttgagg gtccagatgg acaaggggga	600
ttaacggcta tatttagcggg aaaacaagca ctagtccac aacttcaggc cgaaattgag	660
aatttacgtt ctacgcagaa agcacatttt gataatgtat tagcctgggtc aattggtggt	720
ggattaggag cagctatttt agttattgga acgattgcag gagcggtagt aattgttgtg	780
accggtggca cagcgacacc agctgttgtt ggtggtctaa cggctctagg ggcagctggt	840
atcggtttag gaacagcagc tgggtttgag gcactaate atatgaactc ctataatgaa	900
atttcgaata aaattggaga attaatgatg aaagctgatt tagctaacca agcagttatt	960
tcacttacta atacaaaaga cactttaaca tatttgtatc aaacagttga tcaagcaatt	1020

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atgtctctaa caagtattca gcaacaatgg aatacgtatg gagcgaatta taaagatcta 1080
tatgataata tcgaccaaata gcaagaacat aaactttctt taatacctga tgatttaaag 1140
gctgcaaaac aaagttggaa tgatattcat aaggatgcag aattcatttc aaaagacatt 1200
gcttttaaac aagaaaaaac aaattaa                                     1227

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<210> SEQ ID NO 31
<211> LENGTH: 1002
<212> TYPE: DNA
<213> ORGANISM: Bacillus thuringiensis

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<400> SEQUENCE: 31

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gtgaataata attttcctta taaactactt gctgtatcga cgtttttaac cctgacaaca      60
actactgtag ttccaccagt agctgctttt gcaagtgaag gtaaaataga acaaaccagt      120
acggaagata tatctctttc tgtaaacagt gaaaagatga aaaaagcttt gcaagatgct      180
gggggtatttg caaaatccat gaattgattac tcttatttgt taattaataa tccagatggt      240
aactttgaag gaattgatat taaaggatat acaaatctac ctagtcaaat tgcacaagat      300
caaaagaatg caagagagca tgctacaaa tgggatgctc acataaaaaa acaactttta      360
gataccctta caggaattgt agagtatgat accacatttg acaattatta cgatacatta      420
gtagaagcaa ttaatgaagg agatgcagat acattaaaag aaggcattac agatttacia      480
ggtgagatta aaaaaacca agcatatata cagaatttaa ttcaagaact agctaagtta      540
agagatagta ttggagaaga tgcctgagca ttggaggtgc ataaagatat cttgcaatcg      600
attttaaaaa atcaagcatc tggaaatgat gaagatgaag aacgcctaaa tgatgtttta      660
gagcaataaa gacattttta acaagtagaa tcggatggaa taataactgt atcatatcct      720
tcaatcccta catggattgc tggaggtgtg atgatagggg tagcaagaaa taatttaggt      780
acgttagagc cgttattagt gcaattacgc caaacctgag actataaaat aacattaaat      840
cgtgtagttg gagttgcgta taataatatt actgaaatgc aaaaatgcaat tggatcagct      900
attaatgctc ttacctatat gtcagacaaa tggcatgatt tagattctca atattcagga      960
gtgcttaatc atattgataa agcatcccaa aaagcagatc aa                               1002

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<210> SEQ ID NO 32
<211> LENGTH: 1009
<212> TYPE: DNA
<213> ORGANISM: Bacillus thuringiensis

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<400> SEQUENCE: 32

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gtgaataata attttcctta taaactactt gctgtatcga cgtttttaac cctgacaaca      60
actactgtag ttccaccagt agctgctttt gcaagtgaag gtaaaataga acaaaccagt      120
acggaagata tatctctttc tgtaaacagt gaaaagatga aaaaagcttt gcaagatgct      180
gggggtatttg caaaatccat gaattgattac tcttatttgt taattaataa tccagatggt      240
aactttgaag gaattgatat taaaggatat acaaatctac ctagtcaaat tgcacaagat      300
caaaagaatg caagagagca tgctacaaa tgggatgcgc acataaaaaa acaactttta      360
gatactctta caggaattgt agagtatgat actacatttg acaattatta cgatacatta      420
gtagaagcaa ttaatgaagg agatgcagat acattaaaag aaggcattac agatttacia      480
ggtgagatta aaaaaacca agcatatata aagaatttaa tacaagaact agctaagtta      540
agagatagta ttggagaaga tgcctgagca ttggaggtgc ataaagatat cttgcaatcg      600

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attttaaaaa atcaagcatc tggaatagat gaagatgaaa aacgtctaaa tgatgtttta	660
gagcaagtaa gacatttttaa acaagtagaa tcggatggaa taataactgt atcagttccc	720
tcaatcccta catggattgc tggaggtgta atgatagggg tagcaagaaa taatttaagt	780
acgctggaac cgctattagc gcaattgcgc caaacggtag actataaaat tacattgaat	840
cgtgtagttg gagttgcgta taataatatt gctgaaatgc aaaatgcaat tggatcagct	900
attaatgctc tcacctatat gtcagcaciaa tggcatgatt tagattctca atattcagga	960
gtacttaatc atattgataa agcatcccaa aaagcagatc aaaataatt	1009

<210> SEQ ID NO 33
 <211> LENGTH: 1134
 <212> TYPE: DNA
 <213> ORGANISM: *Bacillus cereus*

<400> SEQUENCE: 33

gtgaataata attttcctta taaactactt gctgtatcga cgtttttaac cctgacaaca	60
actactgtag tttctccagt agctgctttt gcaagtgaaa gtaaaataga acaaacgagt	120
actgaagata tatctctttc tgtaaacagc gaaaagatga aaaaagcttt gcaagatgct	180
ggggtatttg caaaatccat gaatgattac tcttatttgt taattaataa tccagatggt	240
aactttgaag gaattgatat taaaggatat acaaatctac ctagtcaaat tgtacaagat	300
caaaagaatg caagagagca tgcatacaaaa tgggatgcgc acataaaaaa acaactttta	360
gataccctga caggaattgt agagtatgat accacatttg acaattatta cgatacatta	420
gtagaagcaa ttaatgaagg agatgcagat acattaaaag agggcattac agatttacia	480
ggtgagatta aacaaaacca agcatatata cagaatttaa tacaagaact agctaagtta	540
agagatagta ttggagaaga tgtccgagca tttggaggtc ataaagatat cttgcaatcg	600
attttaaaaa atcaagcatc tggaatagat gaagatgaaa aacgcctaaa tgatgtttta	660
gagcaataaa gacatttttaa acaagtagaa tcggatggaa taataactgt atcatatcct	720
tcaatcccta catggattgc tggaggtgtg atgataggag tagcaagaaa taatttaggt	780
acgcttagagc cgctattagc acaattacgc caaacggtag actataaaat aacattaaat	840
cgtgtagttg gagttgcgta taataatatt gctgaaatgc aaaatgcaat tggatcagct	900
attaatgctc ttacctatat gtcagcaciaa tggcatgatt tagattctca atattcagga	960
gtgcttaatc atattgataa agcatcccaa aaagcagatc aaaataaatt taaattctta	1020
aaacctaacc tgaatgcagc gaaagacagc tggaaaacat taagagcaga tgcgtttaca	1080
ttgaaagaag gaataaaaac attaaaaatg gatcctgttt cttcaaaaaa atag	1134

<210> SEQ ID NO 34
 <211> LENGTH: 1133
 <212> TYPE: DNA
 <213> ORGANISM: *Bacillus cereus*

<400> SEQUENCE: 34

gtgaataata attttcctta taaactactt gctgtatcga cgtttttaac cctgacaaca	60
actactgtag tttctccagt agctgctttt gcaagtgaaa gtaaaataga acaaacgagt	120
actgaagata tatctctttc tgtaaacagc gaaaagatga aaaaagcttt gcaagatgct	180
ggggtatttg caaaatccat gaatgattac tcttatttgt taattaataa tccagatggt	240
aactttgaag gaattgatat taaaggatat acaaatctac ctagtcaaat tgtacaagat	300
caaaagaatg caagagagca tgcatacaaaa tgggatgcgc acataaaaaa acaactttta	360

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gataccctga caggaattgt agagtatgat accacatttg acaattatta cgatacatta	420
gtagaagcaa ttaatgaagg agatgcagat acattaaaag agggcattac agatttacia	480
ggtgagatta aacaaaacca agcatatata cagaatttaa tacaagaact agctaagtta	540
agagatagta ttggagaaga tgtccgagca ttggagggtc ataaagatat cttgcaatcg	600
attttaaaa atcaagcatc tggaatagat gaagatgaaa aacgcctaaa tgatgtttta	660
gagcaataa gacattttta acaagtagaa tcggatggaa taataactgt atcatatcct	720
tcaatcccta catggattgc tggaggtgtg atgataggag tagcaagaaa taatttaggt	780
acgttagagc cggtattagc acaattacgc caaacggtag actataaaat aacattaaat	840
cgtgtagttg gagttgcgta taataatatt gctgaaatgc aaaatgcaat tggatcagct	900
attaatgctc ttacctatat gtcagcacia tggcatgatt tagattctca atattcagga	960
gtgcttaatc atattgataa agcatcccaa aaagcagatc aaaataaatt taaattctta	1020
aaacctaacc tgaatgcagc gaaagacagc tggaaaacat taagagcaga tgcgtttaca	1080
ttgaaagaag gaataaaaac attaaaaatg gatcctgttt cttcaaaaaa ata	1133

<210> SEQ ID NO 35
 <211> LENGTH: 1125
 <212> TYPE: DNA
 <213> ORGANISM: *Bacillus cereus*

<400> SEQUENCE: 35

gtgaataata attttcctta taaattactt gctgtatcgg cgtttttaac tctgacaaca	60
gctactgtag tttctccagt agctgcattt gcaagtgaat gtaaaattga acaaacgagt	120
acggaaaata tatctctttc tgtaaacagc gaaaagatga aaaaagcttt gcaagatgct	180
gggggatttg caaaatccat gaattgattac tcttatttgt taattaataa tccaggtggt	240
aactttgaag gaattgatat taaaggatat acaaatctac ctagtcaaat tatacaagat	300
caaaagaagg caagagagca tgctacaaaa tgggatacgc acataaaaaa acaactttta	360
gataccctta caggaattgt agagtatgat accacatttg acaattatta cgatacatta	420
gtaaaagcaa ttaatgaagg agatgcagat acattaaaag aaggcattac agatttacia	480
ggtgatatta aacaaaacca agcatatata cagaatttaa tacaagaact agctaagtta	540
agagatagta ttggagaaga tgtccgagca ttggagggtc ataaagatat cttgcaatcg	600
attttaaaa atcaagcatc tggaatagat gaagatgaaa aacgcctaaa tgatgtttta	660
gagcaataa gacattttta acaagtagaa tcggatggaa taataactac atatgtaccc	720
tcgattccta catggattgc tgggtgtata atgatagggt tagcaagaaa taatttaagt	780
acgttagaac cgctattagc gcagttgcgc caaacggtag actataaaat tacattgaat	840
cgtgtagttg gagttgcgta taataatatt gctgaaatgc agaatgcaat tggatcagct	900
attaatgctc ttacctatat gtcagcacia tggcaggatt tagattctca atattcaggg	960
gtacttaatc atattgataa agcatcccaa aaagcagatc aagataaatt taaattctta	1020
aaacctaacc tgaatgcagc gaaagacagt tggaaaacat taagagaaga tgcgtctaca	1080
ttaaaggaag ggataagaat attaaaagct tcttcaaaat cataa	1125

<210> SEQ ID NO 36
 <211> LENGTH: 1134
 <212> TYPE: DNA
 <213> ORGANISM: *Bacillus weihenstephanensis*

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<400> SEQUENCE: 36

atgaataaaa actttcctta taaactactt gctgtatcga cgtttttaac tctgacaaca	60
actactgtag tttctccagt ggcagccttc gcaagtgaat gtaaaatgga acaaactagt	120
accgaagata tatctctttc tgtaaacagc gaaaagatga aaaaagcttt gcaagatgct	180
gggggtatttg caaaatccat gaatgattac tcttatttgt taattaaaaa cccagatggt	240
aactttgaag gcattgacat taaaggatat acaaatctac ctagtcaaat tctacaagat	300
caaaagaatg caagagagca tgctacgaaa tgggattcac acataaaaaa acaactttta	360
gatacactga cggggattgt agagtatgat actaaattcg acaattatta tgacacatta	420
gtagaagcga ttaatgaagg ggatgcagac acattaaaag aaggcatgac agatttaca	480
ggtgagatta aacaaaatca agcatatata cagaatttaa tacaagaact agctaagtta	540
agagatagta ttggagaaga tgtccgggca tttggaggtc ataaagatat tttgcattcg	600
attctgaaaa accaagcatc tgggaattgat gaagatgaaa agcgccctaaa tgaagtttta	660
gagcaagtaa gacattttta acaagtagaa tcagatggaa taataactgt atcaattccc	720
tcaattccta cgtggattgc tgggtgtgta atgatagggg tagcaagaaa taatttaggt	780
acggttagagc cgttggttagc acaattacgt cagactatag attataaagt aacattaaat	840
cgtgtagttg gtgttgcgta taataatatt aatgaaatgc acaatgcgat tggatcggct	900
attaatgcac ttacctatat gtctgcacaa tggcatgatt tagattctca atattcggga	960
gtgcttagtc atattgataa agcatcccaa aaagcggatc aaaataaatt caaatccta	1020
aaacctaatt tgaatgcagc gaaagatagt tggaaaacat tgagagcggg tgcgtttaca	1080
ttaaaagaag ggataaaaac attaaaaatg gatcctgttt cttcaaaaaa atag	1134

<210> SEQ ID NO 37

<211> LENGTH: 964

<212> TYPE: DNA

<213> ORGANISM: Bacillus thuringiensis

<400> SEQUENCE: 37

atattatttt gcacagccag acattaaggt aaatgcgatg agtagcttag cgaatcatca	60
aaagtttgca aaggcgaatg tacgagagtg gattgatgaa tataatccga agctaattga	120
cttaaatcaa gagatgatga gatacagcac tagattcaat agttattata gtaagctcta	180
tgaactagca ggaaatgtaa atgaagatca gcaagcaaaa acagatttta tgagtgcata	240
tggaaaaatta caattgcaag tacagagcat ccaagagagt atggagcaag atttattaga	300
gttaaatcga tttaaaacag tattagacaa agatagtaac aacttatcaa ttaaagccga	360
tgaagcaata aaaacactgc aaggatcaag tggagatatt gtgaaattaa gagaagatat	420
taaaagaatt caaggggaaa ttcaagctga actaactact attttgaata gacctcaaga	480
aataattaaa ggttctatta atatcggtaa acaagtatct acaatcaca atcaaatgc	540
acaaacgaaa acaatcgatt ttgtttctat cggtaactta agtaatgaaa ttgtaaatgc	600
tgcagatagt caaacgagag aagcagcttt tcgcattcag caaaagcaaa aagagttatt	660
gccacttatt caaaagttat caaaaactga agcagaggcg actcaaatca cattcgttga	720
agatcaagta aatagcttta cagaattaat tgatcgtcaa attacaactt tagaaacggt	780
attaacggat tggaaagttt taaataataa tatgattcaa attcaaacaa atgttgaaga	840
aggcacgtat acagacagta gtttacttca aaaacatctt aatcaaatca aaaaagtaag	900
tgatgaaatg aataagcaaa caaatcaatt tgaagattac gttacaaacg ttgaagtaca	960

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ttaa	964
 <210> SEQ ID NO 38	
<211> LENGTH: 1161	
<212> TYPE: DNA	
<213> ORGANISM: Bacillus cereus	
 <400> SEQUENCE: 38	
gtgaaaaaga ctttaattac agggttattg gttacagcag tatctacgag ttgcttcatt	60
cctgtaagcg cttacgctaa ggaggggcaa acagaagtga aaacagtata tgcgcaaaat	120
gtaattgctc caaatacatt atccaattca attagaatgt taggatcaca atcaccgctt	180
attcaagcat acggattaat tatcttgcaa cagccagaca ttaaggtaaa tgcgatgagt	240
agcttaacga atcatcaaaa gtttgcaaag gcgaatgtaa gagaatggat tgatgaatat	300
aatccgaagc taattgactt aaatcaagaa atgatgagat acagcactag atttaatagc	360
tattatagta agctctatga actagcagga aacgtaaatg aagatcagca agcaaaagca	420
gattttatga gtgcatatgg aaaattacaa ttgcaagtac aaagcatcca agagagtatg	480
gagcaagatt tattagagtt aaatagattt aaaacagtat tagacaaaga tagtaacaac	540
ttatcaatta aagccgatga agcaataaaa aactgcaag gatcaagtgg agatattgtg	600
aaattaagag aagatattaa aagaattcaa ggggaaattc aagctgaact aactactatt	660
ttgaatagac ctcaagaaat cattaaaggt tctattaata tcggtaaaca agtatttaca	720
atcacaaatc aaactgcaca aacgaaaaca atcgattttg tttctatcgg tactttaagt	780
aatgaaattg taaatgctgc agatagtcaa acgagagaag cagctcttcg cattcaacaa	840
aagcaaaaag agttattacc acttattcaa aagttatcac aaactgaagc agaggcgact	900
caaattacat tcgttgaaga tcaagtaaat agctttacag aattaattga tcgtcaaatt	960
acaactttag aaacgttatt aacggattgg aaagttttaa ataataatat gattcaaatt	1020
caaacaaatg ttgaagaagg cacgtataca gacagtagtt tacttcaaaa acatttcaat	1080
caaattaaaa aagtaagtga tgaatgaat aagcaaacaa atcaatttga agattacgtt	1140
acaaacgttg aagtacatta a	1161

<210> SEQ ID NO 39
 <211> LENGTH: 1161
 <212> TYPE: DNA
 <213> ORGANISM: Bacillus cereus

<400> SEQUENCE: 39

gtgaaaaaga ctttaattac agggttattg gttacagcag tatctacgag tcgcttcatt	60
cctgtaagcg cttacgctaa ggaggggcaa acagaagtga aaacagtata tgcgcaaaat	120
gtaattgctc caaatacatt atccaattca attagaatgt taggatcaca atcaccgctt	180
attcaagcat acggattaat tattttgcaa cagccagaca ttaaggtaaa tgcgatgagt	240
agcttaacga atcatcaaaa gttcgcaaag gcgaatgtgc gagagtggat tgatgaatat	300
aatccgaagc taattgactt aaatcaagaa atgatgagat acagcactag atttaatagc	360
tattatagta agctctatga actagcagga aacgtaaatg aagatcagca agcaaaagca	420
gattttatga gtgcatatgg aaaattacaa ttgcaagtac agagcatcca agagagtatg	480
gagcaagatt tattagagtt aaatcgattt aaaacagtat tagacaaaga tagtaacaac	540
ttatcaatta aagccgatga agcaataaaa aactgcaag gatccagtgg agatattgtg	600

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aaattaagag aagatattaa aagaattcaa ggggaaattc aagctgaact aactactatt	660
ttgaatagac ctcaagaat tattaaggt tctattaata tcggtaaaca agtatttaca	720
atcacaaatc aaactgcaca aacgaaaaca atcgattttg tttctatcgg tactttaagt	780
aatgaaattg taaatgctgc agatagtcaa acgagagaag cagctcttcg cattcaacaa	840
aagcaaaaag agttattgcc acttattcaa aagttatcac aaactgaagc agaggcgact	900
caaattacat tcgttgaaga tcaagtaaat agctttacag aattaattga tcgtcaaatt	960
acaactttag aaacgttatt aacgatttgg aaagttttaa ataataatat gattcaaatt	1020
caaaagaatg ttgaagaagg cacgtatata gacagtagtt tacttcaaaa acatttcaat	1080
caaattaaaa aagtaagtga tgaatgaat aagcaacaa atcaatttga agattacgtt	1140
acaaacgttg aagtacatta a	1161

<210> SEQ ID NO 40
 <211> LENGTH: 1161
 <212> TYPE: DNA
 <213> ORGANISM: Bacillus cereus

<400> SEQUENCE: 40

gtgaaaaaga ctttaattac agggttattg gttacagcag tatctacgag ttgcttcatt	60
cctgtaagcg cttacgctaa ggagggggcaa ccagaagtga aaacagtata tgcacaaaat	120
gtaattgttc caaatacatt atccaattca attagaatgt taggatcaca gtcaccactt	180
atacaagcat atggactagt gattttacaa cagccagaca twaagggtgaa cgcgatgagt	240
agtttgacga atcatcaaaa gtttgcaaag gcaaatgtaa gagagtggat tgatgaatat	300
aatccgaagt taatcgactt aaatcaagag atgatgaggt atagtactag atttaatagc	360
tattatagta agctctatga actagcaggg aacgtaaatg aagatggaca agcaaaagca	420
gattttacag gtgcatatgg aaaattacaa ttgcaagtac aaagcatcca agagagtatg	480
gagcaagatt tattagagct aaatcgattt aaaacgggat tagataagga tagtaacaac	540
ttatcagtta aagctgatga agcaataaaa aactacaag gatcaagtgg agatattgtg	600
aaattaagag aagatattaa aagaattcaa ggggaaattc aagctgaatt aacgactatt	660
ttgaatagac ctcaagaat tattaaggt tctattaata tcggtaaaca agtatttaca	720
attacaaatc aaactgcaca aacgaaaaca attgatttcg tttctatcgg tactttaagt	780
aatgaaattg taaatgctgc agatagccaa acgagagaag cagctcttcg cattcagcaa	840
aagcaaaaag agctattgcc acttattcaa aagttatcac aaactgaagc agaggcaaca	900
caaattacat tcgttgaaga tcaagtaagt agtttcacag aactaatcga tcgtcaaatt	960
acaactttag aaacgttatt agcagattgg aaagttttaa acagtaatat gatccaaatt	1020
caaaagaatg ttgaagaagg cacatataca gacagtagtt tactacaaaa acatttcaac	1080
caaattaaaa aagtaagtga tgaatgaat aaacaaacga atcaatttga agattacgtt	1140
acaaacgttg aagtacatta a	1161

<210> SEQ ID NO 41
 <211> LENGTH: 1161
 <212> TYPE: DNA
 <213> ORGANISM: Bacillus cereus

<400> SEQUENCE: 41

gtgaaaaaga ctttaattac agggttattg gttacagcag tatctacgag ttgcttcatt	60
cctgtaagcg cttacgctaa ggagggggcaa acagaagtga aaacagtata tgcgcaaat	120

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gtaattgctc caaatacatt atccaattca attagaatgt taggatcaca atcaccgctt	180
attcaagcat acggattaat tatcttgcaa cagccagaca ttaaggtaaa tgcgatgagt	240
agcttaacga atcatcaaaa gtttgcaaag gcgaatgtac gagaatggat tgatgaatat	300
aatccgaagc taattgaactt aaatcaagaa atgatgagat acagcactag atttaatagc	360
tattatagta agctctatga actagcagga aacgtaaatg aagatcagca agcaaaagca	420
gattttatga gtgcatatgg aaaattacaa ttgcaagtac aaagcatcca agagagtatg	480
gagcaagatt tattagagtt aaatcgattt aaaacagtat tagacaaaga tagtaacaac	540
ttatcaatta aagccgatga agcaataaaa aactgcaag gatcaagtgg agatattgtg	600
aaattaagag aagatattaa aagaattcaa ggggaaattc aagctgaact aactactatt	660
ttgaatagac ctcaagaaat cattaaaggt tctattaata tcggtaaaaca agtatttaca	720
atcacaaatc aaactgcaca aacgaaaaca atcgattttg tttctatcgg tactttaagt	780
aatgaaattg taaatgctgc agatagtcac acgagagaag cagctcttcg cattcaacaa	840
aagcaaaaag agttattacc acttattcaa aagttatcac aaactgaagc agaggcgact	900
caaattacat tcgttgaaga tcaagtaaat agctttacag aattaattga tcgtcaaatt	960
acaactttag aaacgttatt aacggattgg aaagttttaa ataataatat gattcaaatt	1020
caaacaaatg ttgaagaagg tacgtataca gacagtagtt tacttcaaaa acatttcaat	1080
caaattaaaa aagtaagtga tgaaatgaat aagcaacaa atcaatttga agattacgtt	1140
acaaacgttg aagtacatta a	1161

<210> SEQ ID NO 42

<211> LENGTH: 1161

<212> TYPE: DNA

<213> ORGANISM: Bacillus cereus

<400> SEQUENCE: 42

gtgaaaaaga ctttaattac aggggttattg gttacagcag tatctacgag ttgttttatt	60
cctgtaagcg cttacgctaa ggagggggcaa acagaagtga aaacagtata tgcacaaaat	120
gtaattgctc caaatacatt atcgaattca attagaatgt taggatcaca atcaccactt	180
atacaagcat atggattagt tatttttcaa cagccagaca ttaaggtaaa cgcgatgagt	240
agtttgacga atcaccaaaa atttgcaaag gcaaagttaa gagagtggat tgatgaatat	300
aatccgaagt taatcgactt aaatcaagag atgatgaggt atagtactag atttaatagc	360
tattatagta agctctatga actagcagga aaagtcaatg aagatgaaca agcaaaagca	420
gatttttcaa atgcatatgg aaaattacaa ttgcaagtac aaagcatcca agagagtatg	480
gagcaagatt tattagagtt aaatcgattt aaatcggtat tagataaaga tagtaataac	540
ttatcaatta aagctgatga agcaataaaa aactgcaag gatcaagtgg agatattgtg	600
aaattaagag aagatattaa aagaattcaa ggggaaattc aagctgaatt aactactata	660
ttgaatagac ctcaagaaat tattaaaggt tctattaata tcggtaaaaca agtatttaca	720
attacaaatc aaactgcaca aacgaaaacg attgatttcg tttctatcgg tactttaagt	780
aatgaaattg taaatgctgc agatagccaa acgagagaag cagctcttcg cattcagcaa	840
aagcaaaaag agctattacc acttattcaa aaattatcac aaactgaagc agaagcgact	900
caaattacat tcgttgaaga tcaggtaaat agttttacag aactaattga tcgtcaaatt	960
acaacattag aaacgttatt aacggattgg aaagttttaa acaataatat gatocaaatt	1020

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caaaagaatg ttgaagaagg cacgtataca gatagtagtt tacttcaaaa acatttcaat	1080
caaattaaaa aagtaagtga tgaatgaat aaacaaacaa atcaatttga agattatgtt	1140
acaaacgttg aagtacatta a	1161

<210> SEQ ID NO 43
 <211> LENGTH: 1161
 <212> TYPE: DNA
 <213> ORGANISM: *Bacillus thuringiensis*

<400> SEQUENCE: 43

gtgaaaaaga ctttaattac agggttattg gttacagcgg tatctacgag ttgttttatt	60
cctgtaagcg cttacgctaa ggaggggcaa acagaagtga aaacagtata tgcacaaaat	120
gtaattgctc caaatacatt atcgaattca attagaatgt taggatcaca atcaccactt	180
atacaagcat atggattagt tattttacaa cagccagaca ttaaggtaaa cgcgatgagt	240
agtttgacga atcatcaaaa atttgcaaag gcaaatgtaa gagagtggat tgatgaatat	300
aatccgaagt taatcgactt aaatcaagag atgatgaggt atagtactag atttaatagc	360
tattatagta agctctatga actagcaggg aacgtaaatg aggatgaaca agcaaaagca	420
gattttacaa atgcatatgg aaagttacaa ttgcaagtac aaagcatcca agaaagtatg	480
gagcaagatt tattagagtt aaatcgattt aaatcggtat tagataaaga tagtaataac	540
ttatcaatta aagctgatga agcaataaaa acactgcaag gatcaagtgg agatattgtg	600
aaattaagag aagatattaa aagaattcaa ggagaaattc aagcagaatt aacgactatt	660
ttgaatagac ctcaagaaat tattaaaggt tctattaata tcggtaaaca agtgtttaca	720
attacaaatc aaactgcgca gacgaaaaca attgattttg tttctatcgg tactttaagt	780
aatgaaattg taaatgctgc agatagtcaa acgagagaag cagctcttcg cattcagcaa	840
aagcaaaaag agttattacc acttattcaa aaattatcac aaactgaagc agaagcgact	900
caaattacat tcgttgaaga tcaagtaagt agctttacag aactaattga tcgtcaaatt	960
acaacattag aaacgttatt aacggattgg aaagttttaa acaataatat gctccaaatt	1020
caaaagaatg ttgaagaagg cacgtataca gatagtagtt tacttcaaaa acatttcaat	1080
caaattaaaa aagtaagtga tgaatgaat aaacaaacaa atcaatttga agattatgtt	1140
acaaacgttg aagtacatta a	1161

<210> SEQ ID NO 44
 <211> LENGTH: 1161
 <212> TYPE: DNA
 <213> ORGANISM: *Bacillus thuringiensis*

<400> SEQUENCE: 44

gtgaaaaaga ctttaattac agggttattg gttacagcag tatctacgag ttgcttcatt	60
cctgtaagcg cttacgctaa ggaggggcaa acggaagtga aaacagtata tgcacaaaat	120
gtaattgctc caaatacatt atccaattca attagaatgt taggatcaca atcaccgctt	180
attcaagcat acggattaat tattttacaa cagccagata ttaaggtaaa tgcgatgagt	240
agcttaacga atcatcaaaa gtttgcaaag gcgaatgtac gagaatggat tgatgaatat	300
aatccgaagc taattgactt aaatcaagag atgatgagat acagcactag atttaatagc	360
tattatagta agctctatga attagcagga aacgtaaatg aagatcagca agcaaaagca	420
gattttatga gtgcatatgg aaaattacaa ttgcaagtac aaagcataca agagagtatg	480
gagcaagatt tattagagtt aaatcgattt aaaacagtat tagacaaaga tagtaacaac	540

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ttatcaatta aagccgatga agcaataaaa acaactgcaag gatcaagtgg agatattgtg	600
aaatcaagag aagatattaa aagaattcaa ggtgaaattc aagctgaatt aactactatt	660
ttgaatagac ctcaagaaat cattaaggt tctattaata ttggtaaaca agtatttaca	720
atcacaaaac aaactgcaca aacgaaaaca atcgattttg tttctatcgg tactttaagt	780
aatgaaattg taaatgctgc agatagtcaa acgaggggaag cagctcttcg cattcaacaa	840
aagcaaaaagg agttattgcc acttattcaa aagttatcac aaactgaagc agaggcgact	900
caaattacat tcgttgaaga tcaagtaagt agctttacag aattaattga tcgtcaaatt	960
acaactttag aaacgttatt aacggattgg aaagttttaa ataataatat gattcaaatt	1020
caaacaaatg tcgaagaagg cacgtatata gacagtagtt tacttcaaaa acatttcaat	1080
caaattaaaa aagtaagtga tgaatgaat aagcaacaa atcaattga agattacgtt	1140
acaaacgttg aagtacatta a	1161

<210> SEQ ID NO 45

<211> LENGTH: 1209

<212> TYPE: DNA

<213> ORGANISM: *Bacillus thuringiensis*

<400> SEQUENCE: 45

atgacaaaaa aaccatataa agtaatggct ctatcagcac ttatggcagt atttgagca	60
ggaaatatta tgccggctca tacgtatgca gctgaaagta cagtgaaca agctccagtt	120
catgcggtag caaaagctta taataactat gaagaatatt cattaggacc agaaggtttg	180
aaagatgcaa tggaaagaac aggttcaaat gctttagtaa tggatctgta tgctttaaca	240
attattaaac aaggtaatgt taactttgga aatgtatcga ctgttgatgc agctttaaaa	300
ggaaaagtga ttcagcacca agatacagct agaggaaatg cgaagcaatg gttagatgta	360
ttaaagccac agcttatttc aacgaatcaa aacatcatta actacaatac aaaattccaa	420
aactattatg atactttagt tgctgcggtg gatgcaaaag ataaagcgac tcttacgaaa	480
ggcctaacta gattatcaag tagtattaat gaaaataaag cgcaagtgga tcagttagta	540
gaagacttga aaaaattccg aaataaaatg acgtcggata cgcaaaactt caagggtgat	600
gcaaatcaaa ttacatctat attagctagt caagatgcag ggattccact tctgcaaaat	660
caaattacaa cgtacaatga agcaattagt aaatataatg caattattat cggttcatct	720
gttgcgacag ctctaggacc aattgcaatt attggtgggtg cagtagttat tgctacgggc	780
gcaggaacac cgctaggagt cgcattaatt gcaggtgggtg cagcagctgt aggcgggtgt	840
acagctggta tcgtattagc gaagaagaa cttgacaatg cacaagctga aattcaaaaa	900
ataactggac aaattacaac tgotcaatta gaagtagctg gggttaacgaa cattaaaaca	960
caaactgagt atttaacaaa tacgattgat actgcaatta cagcgttgca aaacatttca	1020
aaccaatggt atacaatggg atcaaaaatac aattctttac ttcaaaatgt ggattcaatt	1080
agtccaaacg atcttgtttt cattaaagaa gatttaaaaa ttgcgaaaga tagctggaaa	1140
aacattaaag actatgcaga aaagatttat gctgaagata ttaaagtagt agatacgaaa	1200
aaagcataa	1209

<210> SEQ ID NO 46

<211> LENGTH: 1209

<212> TYPE: DNA

<213> ORGANISM: *Bacillus cereus*

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<400> SEQUENCE: 46

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atgacaaaaa aaccttataa agtaatggct ctatcagcac ttatggcagt atttgcagca    60
ggaaatatta tgccgggtca tacgtatgca gctgaaagta cagtgaaca agctccagtt    120
catgcggtag caaaagctta taatgactat gaagaatact cattaggacc agaaggett    180
aaagatgcaa tggaaagaac aggttcaa atgttagtaa tggatctgta cgctttaaca    240
attattaaac aaggaatgt taactttgga aatgtatcgt ctgttgatgc ggctttaaaa    300
gggaaagtaa ttcagcacca agatacagct agaggaaatg cgaagcaatg gttagatgta    360
ttaaaccac agcttatttc aacaaatcaa aatatcatta actacaatac gaaattccaa    420
aactattatg atactttagt tgctgcagtt gatgcaaaag ataaagcgac tcttacgaaa    480
ggcttaacta gattatcaag tagtattaat gaaaataaag cacaagtgga tcagttagta    540
gaagacttga agaaattccg aaataaaaatg acttcggata cgcaaaactt caaggggtgat    600
gcaaatcaaa ttacatctat attagctagt caagatgcag ggattccgct tctgcaaaat    660
caaattacaa cgtacaatga agcaattagt aaatataatg caattattat cggttcacat    720
gttgcgacag ctctaggacc aattgcaatt atcggtggtg cagtagttat tgctacgggc    780
gcaggaacac cgctaggagt agcattaatt gcaggtggtg cagcagctgt aggcgggtgt    840
acagctggaa tcgtattagc gaagaaagag cttgataatg cacaagcaga aattcaaaag    900
ataacaggac aagttacaac tcgcgaatta gaagtagcag gattaacgaa cattaataca    960
caaacagagt atttaacaaa tacaattgat actgcaatta cagcgttaca aaatatttca   1020
aaccaatggt acacaatggg atcaaaatac aattctttac ttcaaatgt agattctatt   1080
agtccaaatg acctagtgtt cattaaagaa gatttaaaaa ttgcgaaaga tagctggaaa   1140
aacattaaag actatgcaga aaagatttat gctgaagata ttaaagtagt agatacgaaa   1200
aaagcataa                                     1209

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<210> SEQ ID NO 47

<211> LENGTH: 1209

<212> TYPE: DNA

<213> ORGANISM: *Bacillus cereus*

<400> SEQUENCE: 47

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atgacaaaaa aaccttataa agtaatggct ctatcagcac ttatggcagt atttgcagca    60
ggaaatatta tgccgggtca tacgtatgca gctgaaagta cagtgaaca agcgcagtt    120
catgcggtag caaaagctta taatgactat gaagaatact cattaggacc agaaggett    180
aaagatgcaa tggaaagaac aggttcaa atgttagtaa tggatctgta cgctttaaca    240
attattaaac aaggaatgt taactttgga aatgtatcgt ctgttgatgc ggctttaaaa    300
gggaaagtaa ttcagcacca agatacagct agaggaaatg cgaagcaatg gttagatgta    360
ttaaaccac agcttatttc aacgagtcaa aatatcatta actacaatac gaaattccaa    420
aactattatg atactttagt tgctgcagtt gatgcaaaag ataaagcaac tcttacgaaa    480
ggcttaacta gattatcaag tagtattaat gaaaataaag cgcaagtgga tcagttagta    540
gaagacttga agaaattccg aaataaaaatg acttcggata cgcaaaactt caaggggtgat    600
gcaaatcaaa ttacatctat attagctagt caagatgcag gaattccgct tctgcaaaat    660
caaattacaa cgtacaatga agcaattagt aaatataatg caattattat cggttcacat    720
gttgcgacag ctctaggacc aattgcaatt atcggtggtg cagtagttat tgctacgggc    780
gcaggaacac cgctaggagt agcattaatt gcaggtggtg cagcagctgt aggcgggtgt    840

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acagctggaa tcgtattagc gaagaaagag cttgataatg cacaagcaga aattcaaaag	900
ataacaggac aagttacaac tgcgcaatta gaagtagcag gattaacgaa cattaaaaca	960
caaacagagt atttaacaaa tacaattgat actgcaatta cagcgttaca aaatatttca	1020
aaccaatggg acacaatggg atcaaaatac aattctttac ttcaaaatgt agattctatt	1080
agtccaaacg acctagtttt cattaaagaa gatttaaaaca ttgcgaaaga tagctggaaa	1140
aacattaaag actatgcaga aaagatttat gctgaagata ttaaagtagt agatacgaaa	1200
aaagcataa	1209

<210> SEQ ID NO 48
 <211> LENGTH: 1208
 <212> TYPE: DNA
 <213> ORGANISM: Bacillus cereus

<400> SEQUENCE: 48

atgacaaaaa aaccttataa agtaatggct ctatcagcac ttatggcagt atttgcagca	60
ggaaatatca tgcgggtca tacgtatgca gcggagagta cagtgaagca agctccagtt	120
catgcggcgc caaaagctta taatgattat gaggaatatt cattaggacc agaaggccta	180
aaagatgcaa tggaagaac gggttcaaac gctttagtaa tggatctgta cgctttaaca	240
attattaaac aaggtaatgt taactttgaa atgtatcgtc tgttgatgcg gctttaaaag	300
ggaaagtgat tcagcaccag gatacagcta gaggaatgc gaagcaatgg ttagatgtac	360
taaagccaca gcttatttca acgaatcaaa atatcattaa ttacaatcgc aaattccaaa	420
actattacga tacttttagtt gctgcggtag atgcaaaaga taaagcgact cttacgaaag	480
gtttaactag attatcaagt agtattaatg aaaataaagc gcaagtagat cagttagtag	540
atgacttgaa gaaattccga aataaaatga cgtccgatac gcaaaacttt aaggggagacg	600
caaatcaaat tacatctatt ttagctagtc aagatgcagg aatcccgctt ctgcaaaatc	660
aaattacaac gtacaatgaa gcaattagta aatataatgc aattattatc ggttcatcag	720
ttgcgacagc tctagggccca attgccatta ttggtgggta agtagtgatt gctacagggtg	780
caggaaacgc gttaggagtc gcgttaattg caggtgggta agcagctgta ggcgggtggca	840
cagctggtat cgtattagcg aagaaagaac ttgataatgc acaagctgaa attcaaaaaa	900
taacaggaca agttacaact gctcaattag aagtagctgg gttacgaac attaagacac	960
aaacggagta tttacaaat acaattgata ctgcaattac agcgttgcaa aacatttcaa	1020
accaatggta cacaatggga tcaaaatata attctttact tcaaaatgta gattcaatta	1080
gtccgaatga ccttgttttc attaaagaag atttaaacat tgcgaaagat agctggaaaa	1140
acattaaaga ctatgcagaa aagatttatg ctgaagatat taaagtagta gatacgaaaa	1200
aagcttaa	1208

<210> SEQ ID NO 49
 <211> LENGTH: 1209
 <212> TYPE: DNA
 <213> ORGANISM: Bacillus cereus

<400> SEQUENCE: 49

atgacaaaaa aaccttataa agtaatggct ctatcagcac tgatggcagt atttgcagca	60
ggaaatatta tgcgggtca tacgtatgca gctgaaagta cagtgaaca agctccagtt	120
catgcggtag caaaagctta taatgactat gaagaatact cattaggacc agaaggcttg	180

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aaagatgcaa tggaaagaac aggttcaaat gcttttagtaa tggatctgta cgctttaaca	240
attattaaac aaggtaatgt taactttgga aatgtatcgt ctgttgatgc ggctttaaaa	300
gggaaagtaa ttcagcacca agatacagct agaggaaatg cgaagcaatg gttagatgta	360
ttaaaaccac agcttatttc aacgaatcaa aatatcatta actacaatac gaaattccaa	420
aactattatg atacttttagt tgcgtcagtt gatgcaaagg ataaagcgac tcttacgaaa	480
ggcttaacaa gattatcaag tagtattaat gaaaataaag cgcaagtgga tcagttagta	540
gaagacttga agaaattccg aaataaaatg acttcggata cgcaaaactt caagggtgat	600
gcaaatcaaa ttacatctat attagctagt caagatgcag gaattccgct tctgcaaaat	660
caaattacaa cgtacaatga agcgattagt aaatataatg caattattat cggttcacat	720
gttgcgacag ctctaggacc aattgcaatt atcggtggtg cagtagttat tgctacgggt	780
gcaggaacac cgctaggagt agcattaatt gcaggtggtg cagcagctgt aggcggtggt	840
acagctggaa tcgtattagc gaagaagag cttgataatg cacaagcaga aattcaaaa	900
ataacaggac aagttacaac tgcgcaatta gaagtagcag gattaacgaa cattaataca	960
caaacagagt atttaacaaa tacaattgat actgcaatta cagcgttaca aaatatttca	1020
aaccaatggt acacaatggg atcaaaaatac aattctttac ttcaaaatgt ggattcaatt	1080
agtccaaacg atcttgtttt cattaaagaa gattttaaaca ttgcgaaaga tagctggaaa	1140
aacattaaag actatgcaga aaagattttat gctgaagata ttaaagtagt agatacgaaa	1200
aaagcataa	1209

<210> SEQ ID NO 50

<211> LENGTH: 1209

<212> TYPE: DNA

<213> ORGANISM: Bacillus cereus

<400> SEQUENCE: 50

atgacaaaaa aaccttataa agtaatggct ctatcagcac ttatggcagt atttcagca	60
gggaatatta tgcgggccca tacgtatgca gctgaaagta cagtgaaca agtccccgta	120
catgcggtcg caaaagctta taatgactat gaagaatact cattaggacc agaaggetta	180
aaagatgcaa tggaaagaac aggttcaaac gcttttagtaa tggatctgta tgctttaaca	240
atcattaaac aaggtaatgt taactttgga aatgtatcga ctgttgatgc tgctttaaaa	300
ggaaaagtga ttcagcacca ggatacagct agaggaaatg cgaagcaatg gttagatgta	360
ttaaagccac agcttatttc aacgaatcaa aatatcatta actataatac gaaattccaa	420
aactattatg atacttttagt tgcgtcgggt gatgcaaaag ataaagcgac acttacgaaa	480
gggttaacta gattatcaag tagtattaat gaaaataaag cgcaagtaga tcagttagta	540
gaagacttga agaaattccg aaataaaatg acgtcggata cccaaaactt caagggtgat	600
gcaaatcaaa ttacatctat tttagctagt caagatgctg gaatccact tctgcaaaat	660
caaattacaa cgtacaatga agcgattagt aaatataatg caattattat cggttcacat	720
gttgcgacag ctctagggcc aattgcaatt atcggtggtg cagtagttat tgctacagg	780
gcaggaacgc cactaggagt cgcattaatt gcaggaggcg cagcggctgt aggcggtggt	840
acagctggaa tcgtattagc gaagaagag cttgataatg cacaagctga aattcaaaaa	900
ataactggac aaattacaac tgcacaatta gaggtagcag gattaacaaa cattaataca	960
caaactgagt atttaacaaa tacaattgat actgcaatta cagcgttgca aaatatttca	1020
aatcaatggt acacaatggg atcaaaaatac aattctctac ttcaaaatgt agattcaatt	1080

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agtccaaacg accttggttt cattaaagaa gatttaaaca ttgcgaaaga tagctggaaa 1140
aacattaaag actatgcaga aaagatttat gctgaagata ttaaagtagt agatacgaaa 1200
aaagcataa 1209

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<210> SEQ ID NO 51
<211> LENGTH: 1209
<212> TYPE: DNA
<213> ORGANISM: Bacillus thuringiensis

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<400> SEQUENCE: 51

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atgacaaaaa aaccttataa agtaatggct ctatcagcac ttatggcagt atttgcggca 60
gggaatatta tgccgacca tacgtatgca gctgaaagta cagtgaaca agctccagtt 120
catgcggtcg caaaagctta taatgactat gaagaatact cattaggacc agaaggccta 180
aaagatgcta tggaaagaac aggttcaaac gctttagtaa tggatctgta tgctttaaca 240
atcattaaac aaggtaatgt taactttgga aatgtatcga ctgttgatgc tgctttaaaa 300
ggaaaagtga ttcagcacca ggatacagct agaggaaatg cgaagcaatg gttagatgta 360
ttaaagccac agcttatttc aacgaatcaa aatatcatta actataatac gaaattccaa 420
aactattatg atactttagt tgctgcggtt gatgcaaaag ataaagcgac acttacgaaa 480
gggttaacta gattatcaag tagtattaat gaaaataaag cgcaagtaga tcagttagta 540
gaagacttga agaaattccg aaataaaatg acgtcggata cgcaaaactt taagggggat 600
gcaaatcaaa ttacatctat tttagctagt caagacgctg gaatcccgtt tctgcaaaat 660
caaattacaa cgtacaatga agcaattagt aaatataatg caattattat cggttcatca 720
gttgcgacag ctctagggcc aattgcaatt atcggtggtg cagtagttat tgctacaggt 780
gcaggaaacg cactaggagt cgcattaatt gcagggggcg cagcggctgt aggtggtggt 840
acagctggaa tcgtattagc gaagaagag cttgataatg cacaagctga gattcaaaaa 900
ataactggac aaattacaac tgctcaatta gaggtagcag gattaacaaa cattaaaaca 960
caaacggagt atttaacaaa tacaattgat actgcaatta cagcgttgca aaatatttca 1020
aatcaatggt acacaatggg atcaaaatac aattctttac ttcaaatgt agattcaatt 1080
agtccaaacg accttggttt cattaaagaa gatttaaaca ttgcgaaaga tagctggaaa 1140
aacattaaag actatgcaga aaagatttat gctgaagata ttaaagtagt agatacgaaa 1200
aaagcataa 1209

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<210> SEQ ID NO 52
<211> LENGTH: 1209
<212> TYPE: DNA
<213> ORGANISM: Bacillus thuringiensis

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<400> SEQUENCE: 52

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atgacaaaaa aaccttataa agtaatggct ctatcagcac ttatggcagt atttgcagca 60
ggaaatatta tgccggtcga tacgtatgca gctgaaagta cagtgaagca agctccagtt 120
catgcggtag caaaagctta taatgactat gaagaatatt cattaggacc agaaggccta 180
aaagatgcaa tggaaagaac aggttcaaat gctttagtaa tggatctgta cgctttaaca 240
attattaaac aaggtaatgt taactttgga aatgtatcgt ctgttgatgc ggctttaaaa 300
gggaaagtaa ttcagcacca agatacagct agaggaaatg cgaagcaatg gttagatgta 360
ttaaaaccac agcttatttc aacgaatcaa aatatcatta actacaatac gaaattccaa 420

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aactattatg atactttagt tgctgcagtt gatgcaaagg ataaagcgac tcttacgaaa	480
ggcttaacta gattatcaag tagtattaat gaaaataaag cacaagtgga tcagttagta	540
gaagacttga agaaattocg aaataaaatg acttcggata cgcaaaactt caagggtgat	600
gcaaatcaaa ttacatctat attagctagt caagatgcag gaattccgct attacaaaat	660
caaattacaa cgtacaatga agcaattagt aaatataatg caattattat cggttcatct	720
gttgcgacag ctctaggacc aattgcaatt atcgggtggtg cagtagttat tgctacgggc	780
gcaggaacac cgctaggagt agcattaatt gcaggtggtg cagcagctgt aggcggtggt	840
acagctggaa tcgtattagc gaagaaagag cttgataatg cacaagcaga aattcaaaag	900
ataacaggac aagttacaac tgcgcaatat gaagtagctg gattaacgaa cattaataca	960
caaacagagt atttaacaaa tacaattgat actgcaatta cagcgttaca aaatatttca	1020
aaccaatggt acacaatggg atcaaaaatat aattctttac ttcaaaatgt ggattcaatt	1080
agtccaaaag accttgtttt cattaaagaa gatttaaaaca ttgcgaaaga tagctggaaa	1140
aatattaaag actatgcaga aaagatttat gctgaagata ttaaagtagt agatacgaaa	1200
aaagcataa	1209

<210> SEQ ID NO 53

<211> LENGTH: 1028

<212> TYPE: DNA

<213> ORGANISM: *Bacillus thuringiensis*

<400> SEQUENCE: 53

atgcagaaac gattttataa aaaatgtctt ttagcggtaa tgattgctgg ggtggcaacg	60
agtaacgcat ttcctttaca tccttttgca gcagaacaaa atgtaacggt gctacaagaa	120
aatgtgaaaa actattctct tggaccagca ggattccaag atgtaatggc acaaacgaca	180
tcaagcatat ttgcaatgga ttcatatgca aaattaattc aaaatcaaca agagacggat	240
ttaagtaaaa taagtctgat taatagtga ttaaaaggga gtatgattca gcatcaaaga	300
gatgcaaaaa ttaatgcagc atattgggta aataatatga agcctcaaat tatgaaaaca	360
gatcaaaaata ttataaatta caataatact tttcaatcgt attataatga catgttaata	420
gcgattgatc aaaaggtagt tggaaaatta aaagcggatt tagaaaagtt gtatgcggat	480
attgtaaaga atcaaaatga ggtagatgga ttattaggaa atttgaaagc ttttcgcat	540
agaatggcga aagatacaaa tagtttcaaa gaggatacaa atcagttaac agcgatattg	600
gcaagtacga atgctggtat tccagctcta gagcaacaaa taaatacata taacgattcg	660
attaataaaga gtaatgatat ggtcattgct ggtggcgtac tttgcgtagc tctaataaca	720
tgtcttgctg gcgggcccga gattgcgggt gcgaaaaaag atatcgcaaa tgcagaaaga	780
gaaatcgcca atttaaaaga tagaatttca ggagcacaag cagaagtcgt aattttgact	840
gatgtaaaaa ataaaacaac aaacatgaca gaaacaattg atgcagcaat tacagcacta	900
caaaacatat caaatcaatg gtatacagta ggtgcaaagt ataataattt attacaaaac	960
gtaaaaggaa ttagtccgga agagtttacg tttataaaag aagatttaca tacagcgaaa	1020
gatagctg	1028

<210> SEQ ID NO 54

<211> LENGTH: 1080

<212> TYPE: DNA

<213> ORGANISM: *Bacillus cereus*

<400> SEQUENCE: 54

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atgcagaaac gattttataa aaaatgtctt ttagcggtaa tgattgctgg ggtggcaacg	60
agtaacgcac ttcctttaca tccttttgca gcagaacaaa atgtaaaggc gctacaagaa	120
aatgtgaaaa actattctct tggaccagct ggattccaag atgtaacggc acaaacgaca	180
tcaagtatat ttgcaatgga ttcatatgca aaattaattc aaaatcaaca agagacggat	240
ttaagtaaaa taagttcgat taatagtga tttaaaggga atatgattca gcatcaaaga	300
gatgcaaaaa ttaatgcagc atattgggta aataaatga agcctcaaat tatgaaaacg	360
gatcaaaaata ttataaatta caataatact tttcaatcgt attataatga catgttaata	420
gcgattgatc aaaaggatag cggaaaatta aaagcggatt tagaaaagtt gtatgcggat	480
attgtaaaga atcaaaatga ggtagatgga ttgttaggaa atttgaaaag ttttcgcgat	540
agaatggcga aagatacaaa tagtttcaaa gaggatacaa atcagttaac agcgatattg	600
gcaagtacga atgctgggat tccagctcta gagcaacaaa taaatacata taacgattcg	660
attaaaaaga gtaatgatat ggtcattgct ggtggcgtac tttgcgtagc tctaataaca	720
tgtcttgctg gtgggcccgc gattgcgggt gcgaaaaaag atatcgcaaa tgcagaaaga	780
gaaatcgcca atttaaaaga tagaatttca ggagcacaag cagaagtcgt aattttgact	840
gatgtaaaaa ataaaaaac aaacatgaca gaaacaattg atgcagcaat tacagcacta	900
caaaacatat caaatcaatg gtatacagta ggtgcaaaat ataataattt actacaaaac	960
gtaaaaggaa ttactccaga agagtttacg tttataaaaag aagatttaca tacagcgaaa	1020
gatagctgga aagatgtaaa ggattataca gaaaaattac atgaaggtgt ggcgaaagtaa	1080

<210> SEQ ID NO 55

<211> LENGTH: 1080

<212> TYPE: DNA

<213> ORGANISM: Bacillus cereus

<400> SEQUENCE: 55

atgcagaaac gattttataa aaaatgtctt ttagcggtag tgattgctgg ggtggcaaca	60
agtaacgcac ttcctttaca tccttttgca gcagaacaaa atgtaaaggc gctacaagaa	120
aatgtgaaaa actattctct tggaccagct ggattccaag atgtaacggc acaaacgaca	180
tcaagtatat ttgcaatgga ttcatatgca aaattaattc aaaatcaaca agagacggat	240
ttaagtaaaa taagttcgat taatagtga tttaaaggga atatgattca gcatcaaaga	300
gatgcaaaaa ttaatgcagc atattgggta aataaatga agcctcaaat tatgaaaacg	360
gatcaaaaata ttataaatta caataatact tttcaatcgt attataatga catgttaata	420
gcgattgatc aaaaggatag cggaaaatta aaagcggatt tagaaaagtt gtatgcggat	480
attgtaaaga atcaaaatga ggtagatgga ttgttaggaa atttgaaaag ttttcgcgat	540
agaatggcga aagatacaaa tagtttcaaa gaggatacaa atcagttaac agcgatattg	600
gcaagtacga atgctgggat tccagctcta gagcaacaaa taaatacata taacgattcg	660
attaaaaaga gtaatgatat ggtcattgct ggtggcgtac tttgcgtagc tctaacaaca	720
tgtcttgctg gtgggcccgc gattgcgggt gcgaaaaaag atatcgcaaa tgcagaagga	780
gaaatcgcca atttaaaaga tagaatttca ggagcacaag cagaagtcgt aattttgact	840
gatgtaaaaa ataaaaaac aaacatgaca gaaacaattg atgcagcaat tacagcacta	900
caaaacatat caaatcaatg gtatacagta ggtgcaaaat ataataattt actacaaaac	960
gtaaaaggaa ttactccaga agagtttacg tttataaaaag aagatttaca tacagcgaaa	1020

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gatagctgga aagatgtaaa ggattataca gaaaaattac atgaaggtgt ggcgaagtaa 1080

<210> SEQ ID NO 56
 <211> LENGTH: 1080
 <212> TYPE: DNA
 <213> ORGANISM: Bacillus cereus

<400> SEQUENCE: 56

atgcagaaaa gattttataa aaagtgtctt ttaacgttaa tgattgctgg ggtggcaacg	60
agtaatgtat ttcctttaca tccttttgca gcagaacaaa acgtaaaaac attgcaagaa	120
agtgcgggaa attattcggt agggccagct ggattccaag atgtaatggc gcaaacgaca	180
tcgagcatat tcgcaatgga ctccatgca aaattaattc aaatcagca agagactgat	240
ttgagtaaaa taagttcgat taatagttag tttaaaggaa atatgattca gcaccaacga	300
gatgcaaaaa ttaacgcggc gtattgggta gatcatatga agccgcaaat tatgaaaacg	360
gatcaaaaata ttattgatta caataatact tttcaagcgt attatagtag catgctaata	420
gcaattgatc aaaaagatag cgtaaagtta aaagcggatt tagaaacatt gtatgcggat	480
attgtaaaga atcaaaatga ggtagatgta ttattaggta atttgaaagc ctttcgcgat	540
agaatggcga aagatacaaa tagcttttaa gcggatacaa atcaactaac ctcgatttta	600
gcaagtacga atgctgggat tccagcttta gagcaacaaa tcaatacata taacgattca	660
attaaaaaga gtaatgatat ggttatcgct ggtggtgtac tttgtgtagc gttaataaca	720
tgccttgctg gcggaccgat gattgcccgt gcgaaaaaag atattgcaaa tgcagaaaga	780
gaaattgcc aatttaaagga tagaatttct ggccgacaag cagaggtcgc aattttgaca	840
gatgtaaaaa ataaaaaac aaacatgact gaaacgattg atgcagcaat tacagcattg	900
caaaatatat cgaatcaatg gtatacagta ggggcaaaat ataataattt actacaaaac	960
gtaaaaggaa ttagtccgga agaatttacc ttcataaaaag aagatttaca tacagcgaaa	1020
gatagctgga aagatgtaaa agattataca gaaaaattac atgaaggtgt ggcgaagtaa	1080

<210> SEQ ID NO 57
 <211> LENGTH: 1080
 <212> TYPE: DNA
 <213> ORGANISM: Bacillus cereus

<400> SEQUENCE: 57

atgcagaaac gattttataa aaaatgtctt ttagcggtaa tgattgctgg ggtggcaacg	60
agtaacgcat ttcctttaca tccttttgca gcagaacaaa atgtaacggt gctacaagaa	120
aatgtgaaaa actattctct tggaccagca ggattccaag atgtaatggc acaaacgaca	180
tcaagcatat ttgcaatgga ttcatatgca aaattaattc aaatcaaca agagacggat	240
ttaagttaaaa taagttcgat taatagttaa tttaaaggaa atatgattca gcatcaaaga	300
gatgcaaaaa ttaatgcagc atattgggta aataatatga agcctcaaat tatgaaaaca	360
gatcaaaaata ttataaatta caataatact tttcaatcgt attataatga catgttaata	420
gcgattgatc aaaaggatag cggaaaatta aaagcggatt tagaaaagtt gtatgcagat	480
attgtaaaga atcaaaatga ggtagatgga ttattaggaa atttgaaagc ttttcgcaat	540
agaatggcga aagatacaaa tagtttcaaa gaagatacaa atcagttaac agcgatattg	600
gcaagtacga atgctgggat tccagctcta gagcaacaaa taaatacata taacgattcg	660
attaaaaaga gtaatgatat ggtcattgct ggtggcgtag tttgtgtagc attaataaca	720
tgtcttgctg gcgggccaat gatcgcggtt gcgaaaaaag atatcgcaaa tgcagaaaga	780

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gaaatcgcta attttaaaga tagaatttca ggagcgcaag cagaagtctt aattttgact	840
gatgtaaaa ataaaaaac aaacatgaca gaaacaattg atgcagcaat tacagcacta	900
caaaacatat caaatcaatg gtatacagta ggtgcaaaat ataataattt actacaaaac	960
gtaaaaggaa ttagtccgga agagtttacg tttataaaag aagatttaca tacagcgaaa	1020
gatagctgga aagatgtaaa ggattataca gaaaaattac atgaaggcgt ggcgaaagtaa	1080

<210> SEQ ID NO 58
 <211> LENGTH: 1080
 <212> TYPE: DNA
 <213> ORGANISM: *Bacillus cereus*

<400> SEQUENCE: 58

atgcagaaac gattttataa gaaatgtctt ttaacattaa tgattgctgg ggtggcaacg	60
agtaacgcat ttcctttaca tacttttgca gcagaacaaa acgtaaaagt actacaagaa	120
aatgcgaaag attattctct tgggccagca ggattccaag atgtaatggc acaacaaca	180
tcgagcatat tcgcaatgga ttcatatgca aagttaatcc aaaatcagca agaaacggat	240
ttaagcaaaa taagttcgat taatagttag tttaaaggaa atatgatgca gcaccaacga	300
gatgcaaaaa ttaacgcggc gtattgggta gatcatatga agccgcaaat tatgaaaacg	360
gatcaaaaata ttattaatta caataatact tttcaagcgt attataatag catgttaata	420
gcaattgatc aaaaagatag cgtaaagtta aaagcggatt tagaaaaatt gtatgcggat	480
attgtaaaga atcaaaatga ggtagatgta ttattaggag atttgaaagc ctttcgtgat	540
agaatggcga aagatacaaa tagctttaaa gaggatacaa atcaactaac ctcgattttg	600
gcaagtacga atgctggaat ccccgctcta gagcaacaaa tcaatacata taatgattca	660
atcaaaaaga gtaatgatat ggttattgct ggtggtgtac tttgcgtagc gttaataaca	720
tgtcttgctg gcggacctat gattgcccgt gcgaaaaaag atattgcaaa tgcagaacga	780
gaaatcgcta attttaaaga tagaatttct ggagcgcaag cagaagtcgc aattttgaca	840
gatgtaaaa ataaaaaac aaatatgact gaaacgattg atgcagcaat tacagcacta	900
caaaacatat caaatcaatg gtatacagta ggtgcaaaat ataataattt actacaaaac	960
gtaaaaggaa ttagtccgga agagtttacg tttataaaag aagatttgaa tacagcgaaa	1020
gatagtggga aagacgtaaa agattataca gaaaaattac atgaaggcgt agcgaaagtaa	1080

<210> SEQ ID NO 59
 <211> LENGTH: 1080
 <212> TYPE: DNA
 <213> ORGANISM: *Bacillus thuringiensis*

<400> SEQUENCE: 59

atgcagaaac gattttataa aaaatgtctt ttaacattaa tgattgctgg agtggcaacg	60
agtaacgcat ttcctttaca tacttttgca gcagaacaaa acgtaaaagt actacaagaa	120
aatgcgaaag attattctct tgggccagca ggattccaag atgtaatggc acaacaaca	180
tcgagcatat tcgcaatgga ttcatatgca aatttaatcc aaaatcagca agaaacggat	240
ttaagcaaaa taagttcgat taatagttag tttaaaggga atatgatgca gcaccaacga	300
gatgcaaaaa ttaacgcggc gtattgggta gatcgatga agccgcaaat tatgaaaacg	360
gatcaaaaata ttattaatta caataatact tttcaaacgt attataatag tatgttaata	420
gcgattgatc aaaaggatag tgtaaaagtta aaagctgatt tagaaaagtt gtatgccgat	480

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attgtaaaga accaaaatga ggtagatgta ttattaaggg atttgaaagc ttttcgtgat	540
agaatggcga aagacacaaa tagttttaag gaagatacaa atcaattaac agcgatttta	600
gcaagtacga atgctgggat tccagcttta gagcaacaaa tcaatacata taatgattca	660
atcaaaaaga gtaatgatat ggtcattgct ggtggtgtac tttgcgtagc gttaataaca	720
tgtcttgctg gcggaccaat gattgcccgc gcgaaaaaag atattgcaa tgcagaaaga	780
gaaatcgcta atttaaagga tagaatttct ggagcacaag cagaagttgc aatttttaact	840
gatgtaaaaa ataaaacaac aaatatgact gaaacgattg atgcagcaat tacagcactg	900
caaaacatat caaatcaatg gtatacggta ggggcaaaat ataataattt actacaaaat	960
gtaaaaggaa tcagctctga agaatttacg tttataaaag aagacttaca tacagcgaaa	1020
gatagctgga aagacgtaaa agattataca gaaaaattac atgaaggtgt ggaaaaataa	1080

<210> SEQ ID NO 60
 <211> LENGTH: 1080
 <212> TYPE: DNA
 <213> ORGANISM: Bacillus thuringiensis

<400> SEQUENCE: 60

atgcagaaaa gattttataa aaaatgtctt ttagcggtaa tgattgctgg ggtggcaacg	60
agtaacgtat ctcctttaca tccttttgca gcagaacaaa atgtaaaggc actacaagaa	120
agtgtgaaaa actattctct tggaccagct ggattccaag atgtaatggc acaaacgaca	180
tcgagtatat ttgcaatgga ttcatatgca aaattaattc aaaatcaaca agagacggat	240
ttaagtaaaa taagttcgat taatagtga tttaaaggga atatgattca gcatcaaaga	300
gatgcaaaaa ttaatgcagc atattgggta aataaatga agcctcaaat tatgaaaacg	360
gatcaaaaata ttataaatta caataatact tttcaatcgt attataacga catgttaata	420
gcgattgacc aaaaggatag cggaaaatta aaagcggatt tagaaaagtt gtatgcggat	480
attgtaaaga atcaaaaatga ggtagatgga ttattaggaa atttgaaagc ttttcgcgat	540
agaatggcga aagatacaaa tagtttcaaa gaggatacaa atcagttaac agcgatattg	600
gcaagtacga atgctgggat tccagctcta gagcaacaaa taaatacata taacgattcg	660
attaaaaaga gtaatgatat ggtcattgct ggtggcgtac tttgcgtagc gctaataaca	720
tgtcttgctg gcgggcccga gattgcggtt gcaaaaaaag atatcgcaa tgcagaaaga	780
gagatagcta atttaaaaga tagaatttca ggagcacaag caaaaatcgt aattttgact	840
gatgtaaaaa ataaaacaac aaacatgacg gaaacaattg atgcagcaat tacagcacta	900
caaaacatat caaaccaatg gtatacagta ggtgcaaaat ataataattt actacaaaac	960
gtaaaaggaa ttagtccgga agagtttacg tttataaaag aagatttaca tacagcgaaa	1020
gatagctgga aagatgtaaa ggattataca gaaaaattgc atgaaggtgt ggcgaagtaa	1080

<210> SEQ ID NO 61
 <211> LENGTH: 1012
 <212> TYPE: DNA
 <213> ORGANISM: Bacillus cereus

<400> SEQUENCE: 61

atgaaacggt ctaaaacata tgtaaaatgt ctcgcattat ctgctgtgtt ggcaagtagt	60
gccctagcaa tgcacacacc ggtgtgcgt gcacaaacaa cttctcaagt tgtaacagat	120
atcgggtcaa atgcaaaaac acatacaagc tacaatacat ttaataatga acaagcagat	180
aatatgacaa tgtcattaaa agtaactttc attgatgatc caagtgtctga taagcaaatt	240

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gcggttatta atacaacagg tagctttatg aaagcaaacc caactcttag tgacgcacct	300
gttgatggat atccaattcc aggggcaagt gtcacattgc gctatccatc acaatatgat	360
attgcaatga atttacaaga taatacgtcg cgattctttc atgtagcacc gacaaatgca	420
gtggaagaaa cgactgtcac atcaagcgtt tcttatcaac ttggcggctc tatcaaagcc	480
tctgtaacac caagcgggcc tagtggcgaa tctggagcaa cagggtcaagt aacttggtct	540
gattccgtca gttataaaca aacaagctat aaaacaaact taattgatca aacaaataaa	600
catgtaaaat ggaacgtatt cttaaatgga tataataatc aaaactgggg catttacact	660
cgcgattctt accatgcttt atatggaaac caattattta tgtattctcg tacgtatcct	720
catgaaacag atgcacgagg caatctagtc ccaatgaatg accttcacgc tctcacaaat	780
agcggtttct ctccaggcat gattgctgtt gtcatttcag aaaaagatac agaacagtct	840
tctatccaag ttgcttatac aaagcatgct gacgattata cacttcgccc tggttttaca	900
ttcggaactg gtaactgggt tggaaataat ataaaagatg tagatcaaaa aacatttaac	960
aaatcatttg tattagattg gaaaaataaa aaactagtag agaagaagta ac	1012

<210> SEQ ID NO 62

<211> LENGTH: 1011

<212> TYPE: DNA

<213> ORGANISM: Bacillus cereus

<400> SEQUENCE: 62

atgaaacggt ctaaaaccta cttaaatgt ttagcattat ccgctgtttt tgctagtagt	60
gctgtaactc tttcaacacc tgctacttac gctcaaacga cgtcacaaagt tgtaacagat	120
atcgggaaaa atgcaaaaac acatacgagc tataatacat ttaataatga tcaagctgat	180
aatatgacaa tgtctttaaa ggtaactttt atcgatgac caagcgcgtga taaacagatt	240
gccgttatta atacaactgg tagttttcta aaagcaaacc ctactataag tgatgcacct	300
attgataact acccaatccc tggcgctagt gcaacattac gttatccttc acaatatgat	360
gttgcaattt accttcaaga taacagcgct cgtttcttta acgtagcgcc tacaaatgct	420
gtagaagaaa cgactgtaac atctagcgta tcttatcaac ttggtggctc tgttaaagct	480
tctgtaacgc ctaatggccc tagcggtgaa gctggtgcaa ctgggtcaagt cacttggtct	540
gactctgtaa gctataaact aactagttat aaaacaaatt taattgacca aacaaacaaa	600
aacgtaaaat ggaacgtatt cttaacgga tataacaatc aaaactgggg tatttacaca	660
cgtgactcct atcattcttt atatggaaac caacttttca tgtactctcg cacataccta	720
tatgaatctg atgcaaaagg taatttaata ccgatggatc aacttcacgc attacaaat	780
agcggtttct ctctggtat gattgctgtt gttatctctg aaaaaatac agatcaatct	840
aacttacaag tcgcttatac aaaacacgcc gacgattacc aacttcgtcc aggtacaca	900
ttcggaactg caaactgggt tggaaacaac gtaaaagacg ttgatcaaaa aacatttaac	960
aaattattca cactagattg gaagaataaa aaattggtag agaaaaata a	1011

<210> SEQ ID NO 63

<211> LENGTH: 1014

<212> TYPE: DNA

<213> ORGANISM: Bacillus cereus

<400> SEQUENCE: 63

atgaaacgct ctaaaacgta ttttaaatgt ttagcattat ccgctgtttt tgctagtagc	60
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gcttttagcac tttcaacacc tgcgtgcttac gctcaaacga cgtcacaaagt tgtaacagat	120
atcgggcaaaa atgcaaaaac acatacgagc tataatacat ttaataatga tcaaactgat	180
aatatgacaaa tgtcttttaaa ggtaactttt atcgatgac cgagcgctga taaacagatt	240
gccgttatta atacaactgg tagttttcta aaagcaaacc ctactataag tagtgcgcct	300
attgataact acccaatccc tggcgctagt gcaacattac gctacccttc acaatatgat	360
attgccttta atcttcaaga taacagcgcc cgtttcttta acgtagcacc tacaaatgct	420
gtagaagaaa cgactgtaac ctctagtgt tcttatcaac ttggcggttc tgtaaagct	480
tctgcaacgc caaatggact tagcgctgaa gcgggtgcaa ctggccaagt aacttggtct	540
gactctgtaa gctataaaca aactagttat aaaacaaact taattgacca aacaaataaa	600
aacgtaaaat ggaacgtatt ctttaacgga tataacaacc aaaactgggg tatttacaca	660
cgtgattcct accattcttt atattgaaac caactgttca tgtactctcg cacatactta	720
tatgaatctg atgcaaaagg taatttaata ccgatggatc aacttcacgc attaacaat	780
agtggtttct ctctggtat gatcgctgtt gttatctctg aaaaaatac agaccaatct	840
aacctacaag tcgcttatac aaaacacgcc gacgactacc aacttcgtcc aggcctcaca	900
ttcggaactg caaactgggt tggaacaac gtaaaagatg ttgatcaaaa aacattta	960
aaatcgttta cattagattg gaagaataag aaattagtag agaaaaatag ataa	1014

<210> SEQ ID NO 64

<211> LENGTH: 1011

<212> TYPE: DNA

<213> ORGANISM: Bacillus cereus

<400> SEQUENCE: 64

atgaaacgct ctaaaacgta tttaaaatgt ttagcattat ccgctgttgt tgctagtagc	60
gcttttagcac tttcaacacc tgcgtgcttac gctcaaacga cgtcacaaagt tgtaacagat	120
atcgggcaaaa atgcaaaaac acatacgagc tataatacat ttaataatga tcaaactgat	180
aatatgacaaa tgtcttttaaa ggtaactttt atcgatgac cgagcgctga taaacagatt	240
gccgttatta atacaactgg tagttttcta aaagcaaacc ctactataag tagtgcgcct	300
attgataact acccaatccc tggcgctagt gcaacattac gctacccttc acaatatgat	360
attgccttta atcttcaaga taacagcgcc cgtttcttta acgtagcacc tacaaatgct	420
gtagaagaaa cgactgtaac ctctagtgt tcttatcaac ttggcggttc tgtaaagct	480
tctgcaacgc caaatggacc tagcgctgaa gcgggtgcaa ctggccaagt aacttggtct	540
gactctgtaa gctataaaca aacaagtatt aaaacaaact taattgacca aacaaataaa	600
aacgtaaaat ggaatgtatt ctttaacgga tataacaacc aaaactgggg tatttacaca	660
cgtgattcct accattcttt atacggaaac caactgttca tgtactctcg cacatactta	720
tatgaatctg atgcaaaagg taatttaata ccgatggatc aacttcacgc attaacaat	780
agcggtttct ctctggtat gatcgctgtt gttatctctg aaaaaatac agaccaatct	840
aacctacaag tcgcttatac aaagcacgcc gacgactacc aacttcgtcc aggcacaca	900
ttcggaactg caaactgggt tggaacaac gtaaaagatg ttgatcaaaa aacattta	960
aaatcgttta cattagattg gaagaataag aaattagtag agaaaaata g	1011

<210> SEQ ID NO 65

<211> LENGTH: 1011

<212> TYPE: DNA

<213> ORGANISM: Bacillus cereus

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<400> SEQUENCE: 65

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atgaaacggt ctaaaccta cttaaaatgt ttagcattat ccgctgtttt tgctagtagt    60
gctgtaactc tttcaacacc tgctacttac gctcaaacga cgtcacaaagt tgtaacagat    120
atcgggcaaa atgcaaaaac acatacgagc tataatacat ttaataatga tcaagctgat    180
aatatgacaa tgtcttttaa ggtaactttt atcgatgata caagcgctga taaacagatt    240
gccgttatta atacaactgg tagttttcta aaagcaaata ctactataag tgatgcacct    300
attgataact acccaatccc tggcgctagt gcaacattac gttatccttc acaatatgat    360
gttgcattha accttcaaga taacagcgct cgtttcttta acgtagcgcc taaaaatgct    420
gtagaagaaa cgactgtaac atctagcgta tcttatcaac ttggtggctc tgttaaagct    480
tctgtaacgc ctaatggccc tagcggtgaa gctggtgcaa ctggtcaagt cacttggtct    540
gactctgtaa gctataaaca aactagttat aaaacaaatt taattgacca aacgaacaaa    600
aacgtaaaat ggaacgtatt ctttaacgga tataacaata aaaactgggg tatttacaca    660
cgtgactcct atcattcttt atatggaaac caacttttca tgtactctcg cacataccta    720
tatgaatctg atgcaaaaagg taatttaata ccaatggata aacttcagc attaacaat    780
agcggtttct ctctggtat gattgtgtt gttatctctg aaaaaatac agatcaatct    840
aacttacaag tcgcttatac aaaacacgcc gatgactacc aacttcgtcc aggttcaca    900
ttcggaactg caaactgggt tggaacaac gtaaaagacg ttgatcaaaa aacatttaat    960
aaattgttca cactagattg gaagaataag aaattggtag agaaaaata a          1011

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<210> SEQ ID NO 66

<211> LENGTH: 1011

<212> TYPE: DNA

<213> ORGANISM: *Bacillus thuringiensis*

<400> SEQUENCE: 66

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atgaaacgct ctaaacgta tttaaaatgt ttagcattat ccgctgtttt tgctagtagc    60
gcttttagcac tttcaacacc tgctgcttac gctcaaacga cgtcacaaagt tgtaacagat    120
atcgggcaaa atgcaaaaac acatacgagc tataatacat ttaataatga tcaaaactgat    180
aatatgacaa tgtcttttaa ggtaactttt atcgatgata caagcgctga taaacagatt    240
gccgttatta atacaactgg tagttttcta aaagcaaata ctactataag tagtgcgcct    300
attgataact acccaatccc tggcgctagt gcaacattac gctatccttc acaatatgat    360
attgccttha atcttcaaga taacagcgct cgtttcttta acgtagcacc taaaaatgct    420
gtagaagaaa cgactgtaac ctctagtgtg tcgtatcaac ttggcggttc tgttaaagct    480
tctgcaacgc caaatggacc tagcgtgtaa ggggtgcaa ctggtcaagt aacttggtct    540
gactctgtaa gctataaaca aactagttat aaaacaaact taattgacca aacaaataaa    600
aacgtaaaat ggaacgtatt ctttaacgga tataacaata aaaactgggg tatttacaca    660
cgtaattcct accattcttt atatggaaac caactgttca tgtactctcg cacatactta    720
tatgaatctg atgcaaaaagg taatttaata ccgatggata aacttcagc gctaacaat    780
agtgttttct ctctggtat gatcgctgtt gttatctctg aaaaaatac agaccaatct    840
aacctacaag tcgcttatac aaaacacgcc gacgactacc aacttcgtcc aggttcaca    900
ttcggaactg caaactgggt tggaacaac gtaaaagatg ttgatcaaaa aacatttaat    960
aagttgttca cactggattg gaagaataag aaattagttg agaaaaata a          1011

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<210> SEQ ID NO 67
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 67

caagagctgt cacgaatc 18

<210> SEQ ID NO 68
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 68

ctgcttgatt agcacgatc 19

<210> SEQ ID NO 69
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 69

cctatcaata ctctcgcaac 20

<210> SEQ ID NO 70
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 70

catcaggtca tactcttggtg 20

<210> SEQ ID NO 71
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 71

cctggtagaa tcgtacaag 19

<210> SEQ ID NO 72
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 72

gagctgcatt ctcaatatgc 20

<210> SEQ ID NO 73
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

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<400> SEQUENCE: 73

gcaagtccga atgtacaac

19

<210> SEQ ID NO 74

<211> LENGTH: 21

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 74

cttcgagttg agttgttaca c

21

<210> SEQ ID NO 75

<211> LENGTH: 19

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 75

ctgctacgaa tggtagtag

19

<210> SEQ ID NO 76

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 76

cttgatccac tgtctgatac

20

<210> SEQ ID NO 77

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 77

cctgacaaca actactgtag

20

<210> SEQ ID NO 78

<211> LENGTH: 18

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 78

gtcttttcgct gcattcag

18

<210> SEQ ID NO 79

<211> LENGTH: 18

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Primer

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (13)..(13)

<223> OTHER INFORMATION: R = A or G

<400> SEQUENCE: 79

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 gttaggatca cartcacc 18

<210> SEQ ID NO 80
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Primer
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (8)..(8)
 <223> OTHER INFORMATION: R = A or G

<400> SEQUENCE: 80

tcggttggtc atctgcag 18

<210> SEQ ID NO 81
 <211> LENGTH: 20
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 81

gatacagcta gaggaaatgc 20

<210> SEQ ID NO 82
 <211> LENGTH: 20
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 82

gatccattg tgtaccattg 20

<210> SEQ ID NO 83
 <211> LENGTH: 19
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Primer
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (5)..(5)
 <223> OTHER INFORMATION: W = T or A

<400> SEQUENCE: 83

cagcwggtt ccaagatgt 19

<210> SEQ ID NO 84
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Primer
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (4)..(4)
 <223> OTHER INFORMATION: R = A or G

<400> SEQUENCE: 84

ccarctatct ttcgctgt 18

<210> SEQ ID NO 85
 <211> LENGTH: 19
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (3)..(6)
<223> OTHER INFORMATION: W = T or A; R = A or G

<400> SEQUENCE: 85

gcwgtргаag aaacgactg                                     19

<210> SEQ ID NO 86
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (12)..(13)
<223> OTHER INFORMATION: W = T or A; S = C or G

<400> SEQUENCE: 86

ccaaccagct twscagttcc                                     20

<210> SEQ ID NO 87
<211> LENGTH: 3551
<212> TYPE: DNA
<213> ORGANISM: Bacillus thuringiensis

<400> SEQUENCE: 87

tcctatcaat actctcgcaa caccaatcgt tcaagcagaa actcaacaag aaaacatgga      60
tattttcttca tcattacgaa aattaggtgc gcattctaaa ttagtcctaaa cgtatattga    120
tcaatcttta atgagtccta atgtacagct agaggaagtc ccagctttaa ataccaatca      180
attcctaate aaacaagata tgaaggaatg gtcacgcgaa ctctatccac agttaattct      240
attaaattca aaaagtaaag gatttgtaac aaaatttaag agttattacc cgacattaaa      300
atcgtttgta gacaataaag aagatagaga aggggttttcg gatagacttg aagtacttca      360
agaaatggct atgacgaatc aagaaaatgc gcaacgacaa atcaatgaat taacagatct      420
taaattacag cttgataaaa aattaaaaga ttttgatact aatgtggcaa ctgcgcaagg      480
catactaagt acagatggaa caggaaaaat agatcagtta aaaaatgaaa tattaaatac      540
caaaaaagca attcaaaatg atttacagca aattgcatta ataccaggag ctttaaatga      600
gcaggggatt gctatattca aagaagttta tagtctttca aaagaaatta ttgaaccggc      660
tgctcaagca ggggtggcag cgtataacaa aggaaaagaa attaacaact ctattctaga      720
agcggagaaa aaagcggcgc aagaagcgac agaacaaggt aaaactgctc tagagattga      780
atcagcaaaa aaagcagctc gtgaagcaat tgagaaaagc aaacaaggtg aaatagcagc      840
cgcagccgca gcaaaaacac aagagtatga cctgatgaaa gccattgata ccgaaaagat      900
taagaaaaca tttggcgttt ttgctgaagt aaataaatta acagcagaac agcgcgcata      960
tttagatgat ttgagaaac aaaatcaaaa aatatatgat ttaacaacga aattatcaat    1020
agctgattta caaaaatcaa tgcttcttct tacacaaaat gatttgcata cgtttgcaaa    1080
tcaagtagat gtagaacttg atctactaaa gcgctataaa gaagatttaa atctaataaa    1140
aaatagcatt acaaaattat ctactaatgt tgatacaact aacgagcagt ctcaaaaaga    1200
tacattaaga caattaaaaa atgtaataag ttaccttgaa gaacaagtat ataaatttta    1260
atattgcgtt ttttgggaat ccataaagat tataagcatt tagcgaaaga aggagaatag    1320

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tcatgaaaaa atttccattc aaagtactaa ctttagctac attagcaact gttataactg	1380
ctactaccgg taacactatt catgcatttg cacaagaaac gaccgctcaa gaacaaaaag	1440
taggcaatta tgcattaggg ccggaaggac tgaagaaagc attagctgaa acaggggtctc	1500
atattctagt aatggattta tacgaaaaa caatgattaa gcaaccaaat gtaaatttat	1560
ctaatacga tttaggctca gaggggggag agttgctcaa aaatattcac cttaatcaag	1620
agctgtcacg aatcaatgcg aattactggg tagatacagc gaagccacag attcaaaaaa	1680
ctgctcgtaa tattgtaaat tacgatgaac aatttcaaaa ttattacgac acattagtag	1740
aaactgtaca aaagaaagat aaggcagggtc taaaagaggg tataaatgat ttaattacta	1800
caatcaatac aaattcaaaa gaagttacag atgtgattaa gatgctacaa gacttcaaa	1860
ggaaattata tcaaaattct acagatttta aaaataatgt tgggtggtcca gatgggaaag	1920
gtggattaac tgcaatatta gcaggccaac aggcacagat tccacaactt caagctgaaa	1980
ttgagcaact tegtctact cagaaaaaac attttgatga tgtattagca tgggtcaattg	2040
gtggtggatt gggagcagct attttagtta ttgcagctat tggaggagcg gtagttattg	2100
ttgtaactgg cggtagacga acaccggctg ttgttggtgg actctcggtc cttggcgag	2160
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atgaaatttc taacaaaatc ggagaattaa gtatgaaagc agatcgtgct aatcaagcag	2280
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atttattgga taatatcgat tctatgcaag accacaaatt ctctttaata ccagatgatt	2460
taaaagcggc taaagaaagt tggaatgata ttcataaaga tgcagaattc atttcaaaag	2520
atattgcttt taaacaggag tagaactgaa atttaaaacc taaattggag gaaaatgaaa	2580
tgataaaaaa aatcccttac aaattactcg ctgtatcgac actattaact attacaactg	2640
ctaattgtagt ttcaccagta acaacttttg caagtgaat tgaacaaacg aataatggag	2700
atacggctct ttctgcaaat gaagcgagaa tgaaagagac cttgcaaaag gctggattat	2760
ttgcaaaatc tatgaatgcc tattcttata tgtaattaa gaatcctgat gtgaattttg	2820
agggaaattac cattaatgga tatgtagatt tacctggtag aatcgtaaa gatcaaaaga	2880
atgcaagggc acatgcggtt acttgggata cgaaagtaaa aaaacagctt ttagatacat	2940
tgaatggtat tgttgaatac gatacaacat ttgataatta ttatgaaaca atgatatagg	3000
cgattaatac aggggatgga gaaactttaa aagaagggat tacagattta cgagggtgaaa	3060
ttcaacaaaa tcaaaagtat gcacaacaac taatagaaga attaaactaaa ttaagagact	3120
ctattggaca cgatgttaga gcatttggaa gtaataaaga gctcttgag tcaattttaa	3180
aaaatcaagg tgcagatggt gatgccgac aaaagcgtct agaagaagta ttaggatcag	3240
taaactatta taaacaatta gaatctgat ggtttaatgt aatgaagggt gctattttgg	3300
gtctaccaat aattggcggg atcatagtgg gagtagcaag ggataattta ggtaagttag	3360
agcctttatt agcagaatta cgtcagaccg tggattataa agtaacctta aatcgtgtag	3420
ttggagttgc ttacagtaat attaataaaa tgcacaaggc gcttgatgat gctattaacg	3480
ctcttactta tatgtccacg cagtggcatg atttagattc tcaatattcg ggcggtctag	3540
ggcatattga g	3551

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<212> TYPE: DNA

<213> ORGANISM: *Bacillus thuringiensis*

<400> SEQUENCE: 88

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actcatttct attaaacaag atatgaaaga gtggtcaccc gaactttatc ctaaattaat    60
tctatttaaat tcaaaaagta aaggatttgt aactaaattt aatagttatt atccaacatt    120
aaaaggattt gtagataata aggaagataa agaagggttt acagatagac tggaagtcct    180
tcaagacatg accatcacia accaagaaaag tgtgcaacgt caaattaatg agttaacaga    240
tctaaaacta caggtagata agaagttgaa aaatcttgat actgatgtgg caaaaacaca    300
gagtgtcctt aattcagagg gaacaggaaa aatagataag ttaaaaaatg aaatgctaga    360
tacaaaaaaa tcaattcaaa atgatttaca gcaaatagcg ttattaccag gagctttaa    420
tgaacaagga ctaaaaggtat tccaagaaat ttatagtcta tcaaaagata tcattgaacc    480
ggctgctcaa acagcagtag tagcgataa caaaggaaaa gaaataaaca atgctattgt    540
agacgcagag aataaagcag agcaagaagc aaaagaaaaa ggaaatcag ctatagaaat    600
tgaggctgcc aaaaaagaag cacgtgaagc gatagagaaa agtaaaaaag gtgaaatcgc    660
tgcagctgca gttacaaaaa cgaaagagta tgatcttatg aaagtaattg atcctgaaaa    720
aattaaaaaa acatataata cttttgctga aattaataaa ctaacagcag agcaacgtgc    780
atattttaaat gatttagaga aacaaaatca gaaattatat gacttaacga ctaaattaac    840
agtagcagat ttacaaaaat caatgattct ttcatgcaa aatgatttgc atacatttgc    900
taaccaagta gatggagaaa ttgagctaag gaaacgttac aaaggaggatt tggatcta    960
aaataaatag attacaaaat tatcgactga agttgatacc aataacaccc agtctcaaaa   1020
agatacatta agacgattaa aaagtgtaac aactcaactc gaagaacaag ttataaatt   1080
ttaatattaa gaaattaggt ttaataaaaa tattataacg caactgaaaa taaggaggag   1140
aatcaaatga tgaattttcc atttaagggt ataactttag ccactttagc aacgggtata   1200
actgctacga atggtagtac tattcatgca cttgcacaag aacagacagc tcaagaacat   1260
aaaatagaaa attatgcgtt aggacctgaa ggggttaaga aagcgttggc tgcaactggc   1320
tctcatatcc ttgtaatgga ttgtacgca aaaactatga ttaagcaacc gaatgtaaat   1380
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gtagatactg taaaaaagaa agataagatg agccttaaag aaggaatagg ggatttaac   1620
gatacaattc atacaaaattc aaatgaagtt actgacgtca ttaagatggt agaggctttc   1680
aaaacaaagt tgtatacaaa tactgtagat tttaaaaata atgttggtgg tcagatgga   1740
cagggaggat tgacggctat attagcggga aaacaagcac tagtcccaca acttcaggcc   1800
gaaattgaga atttacgttc tacacagaaa tcacattttg ataattgtatt agcctggtca   1860
attggcggtg gactaggagc agctatttta gttattggaa cgattgcagg agcggtagta   1920
attgttgtag ctggtggtac agctacacca gctgttggtg gcggtcttac agctctagga   1980
gcagctggta tcggttttagg aacagcagct ggtgtcgagg catctaata tatgaattct   2040
tataatgaaa tttcgaataa aatcgagaa ttaagtatga aagctgatct ggctaataca   2100
gcggttattt cacttactaa tacgaaagac actctaacta atttgatca gacagtggat   2160
caagcaataa tgtctctaac aagtattcag caacaatgga ataaaatggg ggctaattat   2220

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aaagatttat atgataatat cgatcaaatg caagaacata aactttcgtt aatacctgac	2280
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aaagacattg cttttaaaca agaaaaaaca aactaaaaat taatatatat tcataggagg	2400
aattaaagtg aataataaatt ttccttataa actacttgct gtatcgacgt ttttaaccct	2460
gacaacaact actgtagttt caccagtagc tgcttttgca agtgaaagta aaatagaaca	2520
aaccagtagc gaagatatat ctctttctgt aaacagtga aagatgaaaa aagctttgca	2580
agatgctggg gtatttgcaa aatccatgaa tgattactct tatttgtaa ttaataatcc	2640
agatgttaac tttgaaggaa ttgataattaa aggatataca aatctaccta gtcaaattgc	2700
acaagatcaa aagaatgcaa gagagcatgc taaaaaatgg gatgctcaca taaaaaaca	2760
acttttagat acccttacag gaattgtaga gtatgatacc acatttgaca attattacga	2820
tacattagta gaagcaatta atgaaggaga tgcagatata ttaaagaag gcattacaga	2880
tttacaaggt gagattaac aaaaccaagc atatacacag aatttaattc aagaactagc	2940
taagttaaga gatagtattg gagaagatgt ccgagcattt ggaggtcata aagatatctt	3000
gcaatcgatt ttaaaaaatc aagcatctgg aatagatgaa gatgaaaaac gcctaaatga	3060
tgttttagag caaataagac attttaaca agtagaatcg gatggaataa taactgtatc	3120
atatacctca atccctacat ggattgctgg aggtgtgatg ataggggtag caagaaataa	3180
tttaggtacg tttagagcgt tatttagtgca attacgccaa accgtagact ataaataac	3240
atataatcgt gtatgtggag ttgcgtataa taatattact gaaatgcaa atgcaattgg	3300
atcagctatt aatgctctta cctatatgtc agcacaatgg catgatttag attctcaata	3360
ttcaggagtg cttaatcata ttgataaagc atccccaaaa gcagatcaa	3409

<210> SEQ ID NO 89

<211> LENGTH: 3409

<212> TYPE: DNA

<213> ORGANISM: Bacillus thuringiensis

<400> SEQUENCE: 89

tctaattaaa caagatatga aagagtggtc atccgaactt taccctaaat taattctatt	60
aaattcaaaa agtaaggat ttataactaa atttaatagt tattatccaa cattaaaagg	120
attttagatg aataaggag ataaagaagg gtttacagat agactggaag ttcttcaaga	180
catgactata acaaatcaag aaagtgtgca acgtcaaatt aatgagttaa cagatttaaa	240
attactggta gataagaagt tgaaaaacct tgatactgat gtggtaaaag cacaagtgt	300
ccttaattca gagggaaacag gaaaaataga taagttaaaa aatgaaatgc tagatacaaa	360
aaaatctatt caaatgatt tgcagcaaat agcattatta ccaggcgcgt taaatgaaca	420
agggtctaaag gtattccaag aaatttatag tctatcgaaa gatatcattg aaccggctgc	480
tcaaacagca gtagtagcgt ataacaaagg aaaagaaata aacaatgccaa ttgtagacgc	540
agagaagaaa gcagagcaag aagcaaaaga aaagggaata tcagctatag aaattgaagc	600
tgccaaaaaa gaagcacgtg aaacgataga gaaaagtaaa aaagggtgaaa tcgctgcagc	660
tgtagttaca aaacgaaag agtatgatct tatgaaagt attgatcctg aaaaaataaa	720
aaaaacatat aatacttttg ctgaaattaa taaactaaca gctgagcaaa gagcatattt	780
aaatgattta gagaacaaa atcagaaatt atatgactta acaactaaat taacagtagc	840
agatttacaa aaatcaatga ttcttttcat gcaaaatgac ttgcatacat ttactaatca	900
agtagatgga gaaattgagt taatgaaacg ttacaaagag gatttgatc taataaataa	960

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tagtattaca	aaattatoga	ctgaagttga	taccaataat	actcaggctc	aaaaagatat	1020
attaagacga	ttaaaaagtg	taacaattca	acttgaagaa	caagtttata	aattttgata	1080
ttaagaaatt	aggtttatta	aaaaattata	acgaaacgga	aaataaggag	gagaatcaaa	1140
tgatgaaatt	tccattttaa	gttataacct	tagctacttt	agcaacgatt	ataaccgcta	1200
caaatggtag	tactattcat	gcacttgac	aagaacagac	agctcaagaa	cagaaaaatg	1260
aaaattatgc	gttaggacct	gaaggattaa	agaaagcggt	ggctgaaaca	ggctctcata	1320
ttcttgtaat	ggatttgtag	gcaaaaacta	tgattaagca	accgaatgta	aatttatcca	1380
acattgattt	aggttcgggt	ggagaagaat	taatcaaaaa	tattcacctg	aatcaagaac	1440
tgtcacgaat	caatgcaaat	tactggttag	atacagcgaa	gccaaacatt	caaaaaacag	1500
cacgtaatat	tgtaaatat	gatgagcaat	ttcaaaatta	ttacgacaca	ttagtagata	1560
ctgtaaaaaa	gaaggataag	gtgagcctca	aagaaggaat	aggggattta	atctatacaa	1620
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agttgtatac	aaatactgta	gatttttaaaa	ataatgttgg	tggtccagat	ggacagggag	1740
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agaattttacg	ttctacacag	aaaacacatt	ttgataatgt	attagcctgg	tcaattgggtg	1860
gtggattagg	agcagctatt	ttagttattg	gaacgattgc	aggagcggta	gtaattgttg	1920
tgactgggtg	tacagctacg	ccagctggtg	ttggtggtct	tacagctcta	ggagccgctg	1980
gtatcggttt	aggaacagca	gctggcgctg	aggcatctaa	tcatatgaat	tcttataatg	2040
aaatttcgaa	taaaaatgga	gaattaagta	tgaaagctga	tttggctaat	caagcgggta	2100
tttcacttac	taatacgaaa	gacactctaa	catatttgta	tcagacagtg	gatcaagcaa	2160
taatgtctct	aacaagtatt	cagcaacaat	ggaataaaat	gggggctaat	tataaagatt	2220
tatatgataa	tatcgatcaa	atgcaagaac	ataaactttc	gttaataacct	gacgatttaa	2280
aagctgctaa	acaaagttgg	aatgatattc	ataaggatgc	agaattcatt	tcaaaagaca	2340
ttgcttttaa	acaagaaaaa	acaaactaga	aattaatata	tattcatagg	aggaattaaa	2400
gtgaataata	attttcttta	taaactactt	gctgtatcga	cgtttttaac	cctgacaaca	2460
actactgtag	tttcaccagt	agctgctttt	gcaagtgaag	gtaaaataga	acaaaccagt	2520
acggaagata	tatctctttc	tgtaaacagt	gaaaagatga	aaaaagcttt	gcaagatgct	2580
gggggtatttg	caaaatccat	gaatgattac	tcttatttgt	taattaataa	tccagatggt	2640
aactttgaag	gaattgatat	taaaggatat	acaaatctac	ctagtcaaat	tgcaacaagat	2700
caaaagaatg	caagagagca	tgctacaaa	tgggatgcgc	acataaaaaa	acaactttta	2760
gatactctta	caggaattgt	agagtatgat	actacatttg	acaattatta	cgatacatta	2820
gtagaagcaa	ttaatgaagg	agatgcagat	acattaaaag	aaggcattac	agatttacia	2880
ggtgagatta	aaaaaaacca	agcatatata	aagaatttaa	tacaagaact	agctaagtta	2940
agagatagta	ttggagaaga	tgcccgagca	tttgagggtc	ataaagatat	cttgcaatcg	3000
attttaaaaa	atcaagcatc	tggaaatagat	gaagatgaaa	aacgtctaaa	tgatgtttta	3060
gagcaagtaa	gacattttta	acaagtagaa	tcggatggaa	taataactgt	atcagttccc	3120
tcaatcccta	catggattgc	tgagggtgta	atgatagggg	tagcaagaaa	taatttaagt	3180
acgctggaac	cgctattagc	gcaattgcgc	caaacggtag	actataaaat	tacattgaat	3240
cgtgtagttg	gagttgcgta	taataatatt	gctgaaatgc	aaaatgcaat	tgatcagct	3300

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attaatgctc tcacctatat gtcagcaciaa tggcatgatt tagattctca atattcagga	3360
gtacttaatc atattgataa agcatcccaa aaagcagatc aaaataatt	3409

<210> SEQ ID NO 90
 <211> LENGTH: 3345
 <212> TYPE: DNA
 <213> ORGANISM: *Bacillus thuringiensis*

<400> SEQUENCE: 90

atattatttt gcacagccag acattaaggt aaatgcgatg agtagcttag cgaatcatca	60
aaagtttgca aaggcgaatg tacgagagtg gattgatgaa tataatccga agctaattga	120
cttaaatcaa gagatgatga gatacagcac tagattcaat agttattata gtaagctcta	180
tgaactagca ggaaatgtaa atgaagatca gcaagcaaaa acagatttta tgagtgcata	240
tggaaaatta caattgcaag tacagagcat ccaagagagt atggagcaag atttattaga	300
gttaaatcga tttaaaacag tattagacaa agatagtaac aacttatcaa ttaaagccga	360
tgaagcaata aaaacactgc aaggatcaag tggagatatt gtgaaattaa gagaagatat	420
taaaagaatt caaggggaaa ttcaagctga actaactact attttgaata gacctcaaga	480
aataattaaa ggtttctatta atatcggtaa acaagtattt acaatcacia atcaaacctgc	540
acaaacgaaa acaatcgatt ttgtttctat cggtacttta agtaatgaaa ttgtaaatgc	600
tgcagatagt caaacgagag aagcagcttt tcgcattcag caaaagcaaa aagagttatt	660
gccacttatt caaaagttat caaaaactga agcagaggcg actcaaatta cattcgttga	720
agatcaagta aatagcttta cagaattaat tgatcgtcaa attacaactt tagaaacgtt	780
attaacggat tggaaagttt taaataataa tatgattcaa attcaacaa atgttgaaga	840
aggcacgtat acagacagta gtttacttca aaaacatttt aatcaaatta aaaaagtaag	900
tgatgaaatg aataagcaaa caaatcaatt tgaagattac gttacaaacg ttgaagtaca	960
ttaaatagaa aaataattag cgatataggg agagaagaaa aatgacaaaa aaacatata	1020
aagtaatggc tctatcagca cttatggcag tatttgcagc aggaaatatt atgccggctc	1080
atacgtatgc agctgaaagt acagtgaac aagctccagt tcatgcggta gcaaaagctt	1140
ataataacta tgaagaatat tcattaggac cagaaggttt gaaagatgca atggaaagaa	1200
cagggtcaaa tgcttttagta atggatctgt atgctttaac aattattaaa caaggtaatg	1260
ttaactttgg aaatgtatcg actgttgatg cagctttaa aggaaaagtg attcagcacc	1320
aagatacagc tagaggaaat gcgaagcaat ggtagatgt attaaagcca cagcttattt	1380
caacgaatca aaacatcatt aactacaata caaaattcca aaactattat gatactttag	1440
ttgctgcggg agatgcaaaa gataaagcga ctcttacgaa aggcctaact agattatcaa	1500
gtagtattaa tgaataataa gcgcaagtgg atcagttagt agaagacttg aaaaaattcc	1560
gaaataaaat gacgtcggat acgcaaaact tcaagggtga tgcaaatcaa attacatcta	1620
tattagctag tcaagatgca gggattccac ttctgcaaaa tcaaattaca acgtacaatg	1680
aagcaattag taaatataat gcaattatta tcgggttcac tggtgcgaca gctctaggac	1740
caattgcaat tattggtggg gcagtagtta ttgctacggg cgcaggaaca ccgctaggag	1800
tcgcattaat tgcaggtggg gcagcagctg taggcgggtg tacagctggg atcgtattag	1860
cgaagaaaga acttgacaat gcacaagctg aaattcaaaa aataactgga caaattacaa	1920
ctgctcaatt agaagtagct ggggttaacga acattaaaac acaaacctgag tatttaacaa	1980
atacagattga tactgcaatt acagcgttgc aaaacatttc aaaccaatgg tatacaatgg	2040

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gatcaaaata caattcttta cttcaaaatg tggattcaat tagtccaaac gatcttggtt	2100
tcattaaaga agattttaa ac attgcgaaag atagctggaa aaacattaaa gactatgcag	2160
aaaagattta tgctgaagat attaaagtag tagatagcaa aaaagcataa tcgaatacga	2220
atcgtaggg cgtaagtgt tgatgaatga tttgaagctc ctgttcagtt gtgagcagga	2280
gcttttgata tccttataaa gagaataggt gaaaaaatg cagaaacgat ttataaaaa	2340
atgtctttta gcggtaatga ttgctggggt ggcaacgagt aacgcatttc ctttacatcc	2400
ttttgcagca gaacaaaatg taacggtgct acaagaaaat gtgaaaaact attctcttgg	2460
accagcagga ttccaagatg taatggcaca aacgacatca agcatatttg caatggattc	2520
atatgcaaaa ttaattcaaa atcaacaaga gacggattta agtaaaataa gttcgattaa	2580
tagtgaattt aaaggagta tgattcagca tcaaagagat gcaaaaatta atgcagcata	2640
ttggttaaat aatatgaagc ctcaaattat gaaaacagat caaaatatta taaattacaa	2700
taatactttt caatcgtatt ataatgacat gttaatagcg attgatcaaa aggatagtg	2760
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agatggatta ttaggaaatt tgaaagcttt tcgcataga atggcgaaag atacaaatag	2880
tttcaagag gatcaaaatc agttaacagc gatattggca agtacgaatg ctggtattcc	2940
agctctagag caacaaataa atacatataa cgattcgatt aaaaagagta atgatatggt	3000
cattgctggt ggcgtacttt gcgtagctct aataacatgt cttgctggcg ggccgatgat	3060
tgcggttgcg aaaaagata tcgcaaatgc agaaagagaa atcgccaatt taaaagatag	3120
aatttcagga gcacaagcag aagtcgtaat ttgactgat gtaaaaaata aaacaacaaa	3180
catgacagaa acaattgatg cagcaattac agcactacaa aacatatcaa atcaatggta	3240
tacagtaggt gcaaaatata ataatttatt acaaaacgta aaaggaatta gtcggaaga	3300
gtttacgttt ataaaagaag atttacatac agcgaaagat agctg	3345

<210> SEQ ID NO 91

<211> LENGTH: 1107

<212> TYPE: DNA

<213> ORGANISM: Bacillus thuringiensis

<400> SEQUENCE: 91

atgcaattat gcataacat ccattccgtt ttattttcat gttacgatat aaatgaata	60
cgacatatat cgacaaagat aaaaggaagt gattgtatga aacgttctaa aacatactta	120
aaatatattag cattatccgc tgtttttgct agtagtgcta taactctttc aacacctgct	180
gcttacgctc aaacaacatc acaagttgta acagatatcg ggcaaaatgc aaaaacacat	240
acgagctata atacatttaa taatgatcaa gctgataata tgacaatgctc tttaaaggta	300
acttttatcg atgaccctag cgctgataaa cagattgccg ttattaatac aactggtagt	360
tttctaaaag caaatcttac tataagtgat gcacctattg ataactaccc aatccctggc	420
gctagtgcga cattacgtta tccttcacaa tatgatgttg catttaacct tcaagataac	480
agcgtcgtt tctttaacgt agcgcctaca aatgctgtag aagaaacgac tgtaacatct	540
agcgtatctt atcaacttgg tggtctgtt aaagcttctg taacgcctaa tgccctagc	600
ggtagaagctg gtgcaactgg tcaagtcact tggctgact ctgtaagcta taaacaaact	660
agttataaaa caaattta at tgaccaacaa aacaaaaacg taaagtggaa cgtattcttt	720
aacggatata acaatcaaaa ctgggggtatt tatacacgtg actcctatca ttctttatat	780

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ggaaaccaac ttttcatgta ctctcgaca tacctatatg aatctgatgc aaaaggtaat      840
ttaataccga tggatcaact tccagcgcta acaaatagtg gtttctctcc tggtatgatt      900
gctgttggtta tctctgaaaa aaatacagat caatctaact tacaggtcgc ttatacaaaa      960
cacgccgaag actaccaact tcgtccaggc tacacattcg gaactgcaaa ctgggttgga     1020
aacaacgtaa aagacgttga tcaaaaaaca ttaataaat tgttcacact agattggaag     1080
aataagaaat tagtagagaa aaaataa                                         1107

```

```

<210> SEQ ID NO 92
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

```

```

<400> SEQUENCE: 92

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```

gataggatcc gtacagctag aggaagtc                                         28

```

```

<210> SEQ ID NO 93
<211> LENGTH: 38
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

```

```

<400> SEQUENCE: 93

```

```

cttcatttgc atggctttca tcaggtcata ctcttgtg                               38

```

```

<210> SEQ ID NO 94
<211> LENGTH: 39
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

```

```

<400> SEQUENCE: 94

```

```

aaagccatgc aaatgaagcg agaatgaaag agaccttgc                               39

```

```

<210> SEQ ID NO 95
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

```

```

<400> SEQUENCE: 95

```

```

caatggatcc ctgtaagcaa ctccaactac                                         30

```

```

<210> SEQ ID NO 96
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

```

```

<400> SEQUENCE: 96

```

```

ctgtggatcc cagggttatt gggtacagc                                         29

```

```

<210> SEQ ID NO 97
<211> LENGTH: 35
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

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<400> SEQUENCE: 97

atactccgct gcttctctcg ttgactatc tgcag

35

<210> SEQ ID NO 98

<211> LENGTH: 37

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 98

agaagcagcg gagtatgatt cagcatcaaa gagatgc

37

<210> SEQ ID NO 99

<211> LENGTH: 28

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 99

caatggatcc ccagctatct ttgcgtgt

28

<210> SEQ ID NO 100

<211> LENGTH: 30

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 100

cattggatcc gaaagagtgg tcatccgaac

30

<210> SEQ ID NO 101

<211> LENGTH: 37

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 101

tgaaactacg ctcaatttct ccactactt ggtagc

37

<210> SEQ ID NO 102

<211> LENGTH: 38

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 102

aaattgagcg tagtttcacc agtagctgct ttgcaag

38

<210> SEQ ID NO 103

<211> LENGTH: 29

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 103

cttaggatcc gatctgcttt ttgggatgc

29

<210> SEQ ID NO 104

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<211> LENGTH: 37
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 104

ttcttttgat ccttttctct atcgtttcac gtgcttc 37

<210> SEQ ID NO 105
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 105

agaaaaggat caaaagaatg caagagagca tgctac 36

<210> SEQ ID NO 106
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 106

gctgctaaac aaagttggaa t 21

<210> SEQ ID NO 107
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 107

cgtaatacga ctactatag gg 22

<210> SEQ ID NO 108
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 108

ctttctacag ggaaggattt agaa 24

<210> SEQ ID NO 109
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 109

cttaattcag agggaacagg a 21

<210> SEQ ID NO 110
<211> LENGTH: 1722
<212> TYPE: DNA
<213> ORGANISM: Bacillus thuringiensis

<400> SEQUENCE: 110

tcctatcaat actctcgaa caccaatcgt tcaagcagaa actcaacaag aaaacatgga 60

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tattttcttca tcattacgaa aattaggtgc gcattctaaa ttagtcctaaa cgtatattga	120
tcaatcttta atgagtccta atgtacagct agaggaagtc ccagctttaa ataccaatca	180
attcctaadc aaacaagata tgaaggaatg gtcacgga ctctatccac agttaattct	240
atataattca aaaagtaaag gatttgtaac aaaatttaac agttattacc cgacattaaa	300
atcgtttgta gacaataaag aagatagaga agggttttcg gatagacttg aagtacttca	360
agaaatggct atgacgaatc aagaaaatgc gcaacgacaa atcaatgaat taacagatct	420
taaattacag cttgataaaa aattaaaaga ttttgatact aatgtggcaa ctgcgcaagg	480
catactaagt acagatggaa caggaaaaat agatcagtta aaaaatgaaa tattaaatac	540
caaaaaagca attcaaaatg atttacagca aattgcatta ataccaggag ctttaaatga	600
gcagggattt gctatattca aagaagttaa tagtctttca aaagaaatta ttgaaccggc	660
tgctcaagca ggggtggcag cgtataacaa aggaaaagaa attaacaact ctattctaga	720
agcggagaaa aaagcggcgc aagaagcgcac agaacaaggt aaaactgctc tagagattga	780
atcagcaaaa aaagcagctc gtgaagcaat tgagaaaagc aaacaagggtg aaatagcagc	840
cgcagccgca gcaaaaacac aagagtatga cctgatgaaa gccatgcaaa tgaagcgaga	900
atgaagaga ccttgcaaaa ggctggatta tttgcaaaat ctatgaatgc ctattcttat	960
atgttaatta agaactctga tgtgaatttt gagggaaatta ccattaatgg atatgtagat	1020
ttacctggta gaatcgtaca agatcaaaag aatgcaagggt cacatgccgt tacttgggat	1080
acgaaagtaa aaaaacagct tttagatata ttgaatggta ttgttgaata cgatacaaca	1140
tttgataatt attatgaaac aatgatagag gcgattaata caggggatgg agaaacttta	1200
aaagaaggga ttacagattt acgaggtgaa attcaacaaa atcaaaagta tgcacaacaa	1260
ctaatagaag aattaactaa attaagagac tctattggac acgatgttag agcatttgga	1320
agtaataaag agctcttgca gtcaatttta aaaaatcaag gtgcagatgt tgatgccgat	1380
caaaagcgtc tagaagaagt attaggatca gtaaaactatt ataaacaatt agaactctgat	1440
gggtttaatg taatgaagggt tgctattttg ggtctaccaa taattggcgg tatcatagtg	1500
ggagtagcaa gggataattt aggtaaagta gagcctttat tagcagaatt acgtcagacc	1560
gtggattata aagtaacctt aaatcgtgta gttggagttg cttacagtaa tattaatgaa	1620
atgcacaagg cgcttgatga tgctattaac gctcttactt atatgtccac gcagtggcat	1680
gatttagatt ctcaatatct gggcgttcta gggcatattg ag	1722

<210> SEQ ID NO 111

<211> LENGTH: 1862

<212> TYPE: DNA

<213> ORGANISM: Bacillus thuringiensis

<400> SEQUENCE: 111

actcatttct attaaacaag atatgaaaga gtggtcaccc gaactttatc ctaaattaat	60
tctattaaat tcaaaaagta aaggatttgt aactaaattt aatagttatt atccaacatt	120
aaaaggattt gtagataata aggaagataa agaagggttt acagatagac tggaagtcct	180
tcaagacatg accatcacaa accaagaaaag tgtgcaacgt caaattaatg agttaacaga	240
tctaaaacta caggtagata agaagtgaa aaatcttgat actgatgtgg caaaaacaca	300
gagtgctcct aattcagagg gaacaggaaa aatagataag ttaaaaaatg aaatgctaga	360
tacaaaaaaa tcaattcaaa atgatttaca gcaaatagcg ttattaccag gagctttaaa	420

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tgaacaagga ctaaaggtat tccaagaaat ttatagtcta tcaaaagata tcattgaacc	480
ggctgctcaa acagcagtag tagcgtataa caaaggaaaa gaaataaaca atgctattgt	540
agacgcagag aataaagcag agcaagaagc aaaagaaaaa ggaaaatcag ctatagaaat	600
tgaggctgcc aaaaaagaag cacgtgaagc gatagagaaa agtaaaaaag gtgaaatcgc	660
tgcagctgca gttacaaaaa cgaaagagta tgatcttatg aaagtaattg atcctgaaaa	720
aattaaaaaa acatataata cttttgctga aattaataaa ctaacagcag agcaacgtgc	780
atattttaat gatttagaga aacaaaatca gaaattatat gacttaacga ctaaattaac	840
agtagcagat ttacaaaaat caatgattct tttcatgcaa aatgatttgc atacatttgc	900
taaccaagta gatggagaaa ttgagcgtag tttcaccagt agctgctttt gcaagtgaag	960
gtaaaataga acaaacagc acggaagata tatctctttc tgtaaacagt gaaaagatga	1020
aaaaagcttt gcaagatgct ggggtatttg caaaatccat gaatgattac tcttatttgt	1080
taattaataa tccagatggt aactttgaag gaattgatat taaaggatat acaaatctac	1140
ctagtcaaat tgcacaagat caaaagaatg caagagagca tgctacaaaa tgggatgctc	1200
acataaaaaa acaactttta gataccctta caggaattgt agagtatgat accacatttg	1260
acaattatta cgatacatta gtagaagcaa ttaatgaagg agatgcagat acattaaaag	1320
aaggcattac agatttaca ggtgagatta aacaaaacca agcatataga cagaatttaa	1380
ttcaagaact agctaagtta agagatagta ttggagaaga tgtccgagca tttggaggtc	1440
ataaagatat cttgcaatcg attttaaaa atcaagcacc tggaatagat gaagtgaag	1500
aacgcctaaa tgatgtttta gagcaataa gacattttta acaagtagaa tcggatggaa	1560
taataactgt atcatatcct tcaatcccta catggattgc tggagggtgt atgatagggg	1620
tagcaagaaa taatttaggt acgttagagc cgttattagt gcaattacgc caaacgtag	1680
actataaaat aacattaaat cgtgtagttg gagttgcgta taataatatt actgaaatgc	1740
aaaatgcaat tggatcagct attaatgctc ttacctatat gtcagcaca tggcatgatt	1800
tagattctca atattcagga gtgcttaac atattgataa agcatcccaa aaagcagatc	1860
aa	1862

<210> SEQ ID NO 112

<211> LENGTH: 1348

<212> TYPE: DNA

<213> ORGANISM: Bacillus thuringiensis

<400> SEQUENCE: 112

tctaattaaa caagatatga aagagtggc atccgaactt taccctaaat taattctatt	60
aaattcaaaa agtaaggat ttataactaa atttaatagt tattatccaa cattaaaagg	120
attttagat aataaggaag ataagaagg gtttacagat agactggaag ttcttcaaga	180
catgactata acaaatcaag aaagtgtgca acgtcaaatt aatgagttaa cagattttaa	240
attactggta gataagaagt tgaaaaacct tgatactgat gtggtaaaag cacaagtgt	300
ccttaattca gagggaacag gaaaaataga taagttaaaa aatgaaatgc tagatacaaa	360
aaaatctatt caaatgatt tgacagcaat agcattatta ccaggcgcgt taaatgaaca	420
agggtctaaag gtattccaag aaatttatag tctatcgaaa gatatcattg aaccggctgc	480
tcaaacagca gtagtagcgt ataacaaagg aaaagaaata aacaatgcca ttgtagacgc	540
agagaagaaa gcagagcaag aagcaaaaga aaagggaata tcagctatag aaattgaagc	600
tgccaaaaaa gaagcacgtg aaacgataga gaaaaggatc aaaagaatgc aagagagcat	660

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gctacaaagt gggatgcgca cataaaaaaa caacttttag atactcttac aggaattgta	720
gagtatgata ctacatttga caattattac gatacattag tagaagcaat taatgaagga	780
gatgcagata cattaaaaga aggcattaca gatttacaag gtgagattaa aaaaaaccaa	840
gcatatacaa agaatttaaat acaagaacta gctaagttaa gagatagtat tggagaagat	900
gtccgagcat ttggaggta taaagatata ttgcaatcga ttttaaaaaa tcaagcatct	960
ggaatagatg aagatgaaaa acgtctaaat gatgttttag agcaagtaag acattttaaa	1020
caagtagaat cggatggaat aataactgta tcagttccct caatccctac atggattgct	1080
ggagggtgtaa tgataggggt agcaagaaat aatttaagta cgctggaacc gctattagcg	1140
caattgcgcc aaacggtaga ctataaaatt acattgaatc gtgtagtgg agttgcgtat	1200
aataatattg ctgaaatgca aaatgcaatt ggatcagcta ttaatgctct cacctatatg	1260
tcagcacaat ggcatgattt agattctcaa tattcaggag tacttaatca tattgataaa	1320
gcatcccaa aagcagatca aaataatt	1348

<210> SEQ ID NO 113

<211> LENGTH: 1378

<212> TYPE: DNA

<213> ORGANISM: Bacillus thuringiensis

<400> SEQUENCE: 113

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aaagtttgca aaggcgaatg tacgagagtg gattgatgaa tataatccga agctaattga	120
cttaaatcaa gagatgatga gatacagcac tagattcaat agttattata gtaagctcta	180
tgaactagca ggaatgtaa atgaagatca gcaagcaaaa acagatttta tgagtgcata	240
tggaaaatta caattgcaag tacagagcat ccaagagagt atggagcaag atttattaga	300
gttaaatcga tttaaaacag tattagacaa agatagtaac aacttatcaa ttaaagccga	360
tgaagcaata aaaacactgc aaggatcaag tggagatatt gtgaaattaa gagaagatat	420
taaaagaatt caaggggaaa ttcaagctga actaactact attttgaata gacctcaaga	480
aataattaaa ggttctatta atatcggtaa acaagtattt acaatcaca atcaaatgc	540
acaaacgaaa acaatcgatt ttgtttctat cggtacttta agtaatgaaa ttgtaaatgc	600
tgcagatagt caaacgagag aagcagcgga gtatgattca gcatcaaaaga gatgcaaaaa	660
ttaatgcagc atattggtta aataatatga agcctcaaat tatgaaaaca gatcaaaata	720
ttataaatta caataatact tttcaatcgt attataatga catgttaata gcgattgatc	780
aaaaggatag tggaaaatta aaagcggatt tagaaaagtt gtatgcggat attgtaaaga	840
atcaaaatga ggtagatgga ttattaggaa atttgaaagc ttttcgcgat agaatggcga	900
aagatacaaa tagtttcaaa gaggatatac atcagttaac agcgatattg gcaagtacga	960
atgctggtat tccagctcta gagcaacaaa taaatacata taacgattcg attaaaaaga	1020
gtaatgatat ggtcattgct ggtggcgtag tttgcgtagc tctaataaca tgtcttgctg	1080
gcgggccgat gattgcggtt gcgaaaaaag atatcgcaaa tgcagaaaga gaaatcgcca	1140
atttaaaaga tagaatttca ggagcacaag cagaagtcgt aattttgact gatgtaaaaa	1200
ataaaacaac aaacatgaca gaaacaattg atgcagcaat tacagcacta caaaacatat	1260
caaatcaatg gtatacagta ggtgcaaaat ataataattt attacaaaac gtaaaaggaa	1320
ttagtcgga agagtttacg tttataaaag aagatttaca tacagcgaaa gatagctg	1378

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<210> SEQ ID NO 114
<211> LENGTH: 1017
<212> TYPE: DNA
<213> ORGANISM: Bacillus thuringiensis

<400> SEQUENCE: 114
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gaaaaaagct ttgcaagatg ctgggggtatt tgcaaaatcc atgaatgatt actcttattt    120
gttaattaat aatccagatg ttaactttga aggaattgat attaaaggat atacaaatct    180
acctagtcaa attgcacaag atcaaaagaa tgcaagagag catgctacaa agtgggatgc    240
gcacataaaa aaacaacttt tagatactct tacaggaatt gtagagtatg atactacatt    300
tgacaattat tacgatacat tagtagaagc aattaatgaa ggagatgcag atacattaaa    360
agaaggcatt acagatttac aagggtgagat taaaaaaaac caagcatata caaagaattt    420
aatacaagaa ctagctaagt taagagatag tattggagaa gatgtccgag catttggagg    480
tcataaagat atcttgcaat cgattttaaa aaatcaagca tctggaatag atgaagatga    540
aaaacgtcta aatgatgttt tagagcaagt aagacathtt aaacaagtag aatcggatgg    600
aataataact gtatcagttc cctcaatccc tacatggatt gctggagggtg taatgatagg    660
ggtagcaaga aataatttaa gtacgctgga accgctatta gcgcaattgc gccaaacggt    720
agactataaa attacattga atcgtgtagt tggagtgtcg tataataata ttgctgaaat    780
gcaaaatgca attggatcag ctattaatgc tctcacctat atgtcagcac aatggcatga    840
tttagattct caatattcag gagtacttaa tcatattgat aaagcatccc aaaaagcaga    900
tcaaaataaa ttttaattct taaaacctaa tctgaatgca gccaaagaca gctggaaaac    960
attaagagca gatgcgttta cattaaaaga aggaataaaa acattaaaaa tggatcc    1017

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<210> SEQ ID NO 115
<211> LENGTH: 1003
<212> TYPE: DNA
<213> ORGANISM: Bacillus thuringiensis

<400> SEQUENCE: 115
cagacgacgc tcagaacaga aaatagaaaa ttatgcgtta ggacctgaag gattaaagaa    60
agcgttggct gaaacaggct ctcatattct tgtaatggat ttgtacgcaa aaactatgat    120
taagcaaccg aatgtaaatt tatccaacat tgatttaggt tcgggtggag aagaattaat    180
caaaaatatt cacctgaatc aagaactgtc acgaatcaat gcaaattact ggtagatac    240
agcgaagcca aacattcaaa aaacagcacg taatattgta aattatgatg agcaatttca    300
aaattattac gacacattag tagatactgt aaaaaagaag gataaggtga gcctcaaaga    360
aggaataggg gatttaattct atacaattca tacaattca aatgaagtta cggaagtcac    420
taagatgtta gaggctttca aaacaaagt gtatacaaat actgtagatt ttaaaaaata    480
tgttggtggt ccagatggac agggaggatt gacggctata ttagcgggaa aacaagcgct    540
agtccacaaa cttcaggccg aaattgagaa tttacgttct acacagaaaa cacattttga    600
taatgtatta gcctgggtcaa ttggtggtgg attaggagca gctattttag ttattggaac    660
gattgcagga gcggtagtaa ttgtttgac tgggtgtaca gctacgccag ctgttgttgg    720
tggctctaca gctctaggag ccgctgggtat cggtttagga acagcagctg gcgtcgaggc    780
atctaatacat atgaattctt ataataaat ttcgaataaa atcggagaat taagtatgaa    840
agctgatttg gctaatacaag cggttatttc acttactaat acgaaagaca cttaacata    900

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tttgtatcag acagtggatc aagcaataat gtctctaaca agtattcagc aacaatggaa    960
taaaatgggg gctaattata aagatttata tgataaatatc gat                      1003

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<210> SEQ ID NO 116
<211> LENGTH: 1058
<212> TYPE: DNA
<213> ORGANISM: Bacillus thuringiensis

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<400> SEQUENCE: 116

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gcaaacgtat gcaaatcatt tgtgtaagaa gaagcatgat tttgtaaat cagctattga    60
tagtttcgtt gttaaatcat atattttttg attttgttc tctaaatcat ctaaatatgc    120
tcgctgttct gctgttaatt tatttacttc agcaaaaacg ccaaatgttt tcttaatcct    180
ttcggtatca atgaccttca tcaggtcata ctcttggtt tttgctgagg ctgaggctgc    240
tatttcacct tgtttgcttt tctcaattgc ttcacgagct gctttttttg ctgattcaat    300
ctctagagca gttttacctt gttctgtcgc ttcttgccgc gcttttttct ccgcttctag    360
aatagagttg ttaattttct ttcttttgtt atacgctgcc acccctgctt gagcagctgg    420
ttcaataatt tcttttgaaa gactataaac ttctttgaat atagcaaatc cctgctcatt    480
taaagctcct ggtattaatg caatttgctg taaatcattt tgaattgctt ttttggtatt    540
taatatttca ttttttaact gatctatttt tctgttcca tctgtactta gtatgccttg    600
cgcagttgcc acattagtat caaaatcttt taatttttta tcaagctgta atttaagatc    660
tgtaattca ttgatttgct gttgcgcatt ttcttgatc gtcatagcca tttcttgaag    720
tacttcaagt ctatccgaaa acccttctct atcttcttta ttgtctacaa acgattttta    780
tgtcgggtaa taactattaa attttgttac aaatccttta ctttttgaat ttaatagaat    840
taactgtgga tagagtccg atgaccatc ctccatatct tgtttgatta ggaattgatt    900
ggatatttaa gctgggaact cctctagctg tacattagga ctcatataag attgatcaat    960
atacgtttgg attaatntag attgcgcacc taattttcgt aatgaagagg aaatatccat   1020
gcctttctgt tgagtttccg ctggaacgat tgggtgtt                                1058

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<210> SEQ ID NO 117
<211> LENGTH: 1014
<212> TYPE: DNA
<213> ORGANISM: Bacillus thuringiensis

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<400> SEQUENCE: 117

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gcttttaaac aggagtagaa ctgaaattta aaacctaata tggaggaaaa tgaaatgata    60
aaaaaaatcc cttataaatt actcgctgta tcgacgctat taactattac aactgctaatt   120
gtagttttac cagtaacaac ttttgcaagt gaaattgaac aaacgaacaa tggagatacg    180
gctctttctg caaatgaagc gagaatgaaa gagaccttgc aaaaggctgg attatttgca    240
aaatctatga atgcctatc ttatatgtta attaagaatc ctgatgtgaa ttttgagggg    300
attaccatta atggatatgt agattttacct ggtagaatcg tacaagatca aaagaatgca    360
agggcacatg ctgttacttg ggatacgaaa gtaaaaaaac agctttttaga tacattgaat    420
ggattgttg aatacgatac aacatttgac aattattatg aaacaatggt agaagcgatt    480
aatacagggg atggagaaac tttaaaagaa gggattacag atttgcgagg tgaaattcaa    540
caaaatcaaa agtatgcaca acaactaata gaagaattaa ctaaattaag agactctatt    600
ggacatgatg ttagagcttt tggaagtaat aaagagctct tgcagtcatt tttaaaaaat    660

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caaggtgcag atgttgatgc cgatcaaaag cgtctagaag aagtattagg atcagtaaac	720
tattataaac aattagaatc tgatgggttt aatgtaatga agggtgctat tttgggtcta	780
ccaataattg gcggtattat agtgggagta gcaagggata atttaggtaa gttagagcct	840
ttattagcag aattacgtca gactgtggat tataaagtaa ccttaaatcg tgtagttgga	900
gttgcttaca gtaatattaa tgaatgcac aaggcgcttg atgatgctat taacgctctt	960
acttatatgt ccacgcagtg gcatgattta gattctcaat attcgggcgt tcta	1014

<210> SEQ ID NO 118
 <211> LENGTH: 605
 <212> TYPE: DNA
 <213> ORGANISM: *Bacillus thuringiensis*

<400> SEQUENCE: 118

agtaccgata gaaacaaaat cgattgtttt cgtttgtgca gtttgatttg tgattgtaaa	60
tacttgttta ccaatattaa tagaaccttt aatgatttct tgaggctctat tcaaaatagt	120
agttaattca gcttgaattt caccttgaat tcttttaata tcttctctta atttcacaat	180
atctccactt gatccttgca gtgtttttat tgcttcatcg gctttaattg ataagttggt	240
actatctttg tctaatactg ttttaaatcg atttaactct aataaatctt gctccatact	300
ctcttgatg ctttgtaact gcaattgtaa ttttccatat gcactcataa aatctgcttt	360
tgcttgctga tcttcattta cgtttcctgc taattcatag agcttactat aatagctatt	420
aaatctagtg ctgtatctca tcactctctg atttaagtca attagcttcg gattatattc	480
atcaatccat tctcgtaac tcgcctttgc aaacttttga tgattcgta agctactcat	540
cgcatttacc ttaatatctg gctgttgtaa aataaataat ccatatgctt gaataagcgg	600
tgatt	605

<210> SEQ ID NO 119
 <211> LENGTH: 951
 <212> TYPE: DNA
 <213> ORGANISM: *Bacillus thuringiensis*
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (869)..(869)
 <223> OTHER INFORMATION: n is a, c, g, or t

<400> SEQUENCE: 119

cttccggact aattcctttt acgttttgta gtaaattatt atattttgca cctactgtat	60
accattgggt tgatattgtt tgtagtgctg taattgctgc atcaattggt tccgtcatgt	120
ttgttgtttt attttttaca tcagtcacaaa ttacgatttc tgcttggtgt cctgaaattc	180
tatcttttaa attagctatc tctctttctg catttgcat atcttttttt gcaaccgcaa	240
tcacggcccc gccagcaaga catgttatta gcgctacgca aagtagccca ccagcaatga	300
ccatatacatt actcttttta atcgaatcgt tatatgtatt tatttggttc tctagagctg	360
gaataccagc attcgtactt gccaatatcg ctgttaactg atttgatcc tctttgaaac	420
tatttgatc tttcgccatt ctatcgcgaa aacttttcaa atttccaat aatccatcta	480
cctcattttg attctttaca atatccgcat acaacttttc taaatccgct ttttaatttc	540
cgctatcctt ttgatcaac gctattaaca tgctggtata atacgattga aaagtattat	600
tgtaatttat aatattttga tccgttttca taatttgagg cttcatatta ttttaaccaat	660
atgctgcatt aatttttgca tctctttgat gctgaatcat attcccttta aattcactat	720
taatcgaact tattttactt aaatccgtct cttgttgatt ttgaattaat ttgcatatg	780

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aatccattgc aaatatactc gatgtcggtt gtgccattac atcttggaat ccagctgggc	840
caagagaata gtttttcaca tttttctgna gtacctttac atttgtttct gctgcaaaag	900
gatgtaagga gatacggttac tcgttgccac ccagcaatca ttaccgctaa a	951

We claim:

1. A method for obtaining a mutant *Bacillus*, the method comprising the steps of:

mutating at least one enterotoxin-encoding operon of a *Bacillus* that expresses at least one enterotoxin encoded by at least one enterotoxin-encoding operon, the enterotoxin selected from the group consisting of non-hemolytic enterotoxin (NHE), haemolysin BL (HBL), HBL_{a1}, and HBL_{a2}, to produce a mutant *Bacillus* that does not produce any component of wild-type NHE and does not produce at least one of HBL, HBL_{a1}, and HBL_{a2}, wherein the *Bacillus* is selected from the group consisting of *B. cereus* and *B. thuringiensis*; and selecting the mutant *Bacillus*.

2. The method of claim 1, wherein the mutating step introduces a mutation in an operon that encodes NHE and in an operon that encodes at least one of the HBL, HBL_{a1}, and HBL_{a2} enterotoxins.

3. The method of claim 2, wherein the mutation in at least one of the operons yields a polynucleotide that encodes a portion of a first enterotoxin component spliced to a portion of a last enterotoxin component.

4. The method of claim 2, wherein the mutating step deletes a portion of the at least one operon.

5. The method of claim 4, where the mutation leaves about 600-900 nucleotides on either side of the deleted portion available for homologous recombination.

6. The method of claim 1, wherein the mutating step introduces a disabling mutation at locus *nhe* whereby full-length NHE enterotoxin proteins NheA, NheB, and NheC are not produced and a disabling mutation at one or more of loci *hbl*, *hbl_{a2}*, and *hbl_{a1}*, whereby at least one of enterotoxins HBL, HBL_{a2}, and HBL_{a1} is not produced.

7. The method of claim 6, wherein the mutating step introduces at least one disabling mutation in an enterotoxin-encoding sequence selected from the group consisting of SEQ ID NO: 87 at locus *hbl*, SEQ ID NO: 88 at locus *hbl_{a1}*, SEQ ID NO: 89 at locus *hbl_{a2}*, and SEQ ID NO: 90 at locus *nhe*.

8. The method of claim 1, wherein the mutant *Bacillus* is insecticidal.

9. The method of claim 1, wherein the mutant *Bacillus* produces δ -endotoxin.

10. The method of claim 1, wherein the *Bacillus* to be mutated and the mutant *Bacillus* comprise at least one gene that encodes a protein having insecticidal properties.

* * * * *