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

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(51) **Int. Cl.**
***C12N 1/20*** (2006.01)

(52) **U.S. Cl.**
USPC .................................. **435/252.31**; 435/252.5

(58) **Field of Classification Search**
CPC ...................................................... A01N 63/00
See application file for complete search history.

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Rivera (FEMS Microbiology Letters 190:151-155, 2000).*
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*Primary Examiner* — Patricia A Duffy
(74) *Attorney, Agent, or Firm* — Quarles & Brady LLP

(57) **ABSTRACT**

Some HBL and NHE enterotoxins are known to cause foodborne 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.

**4 Claims, 4 Drawing Sheets**

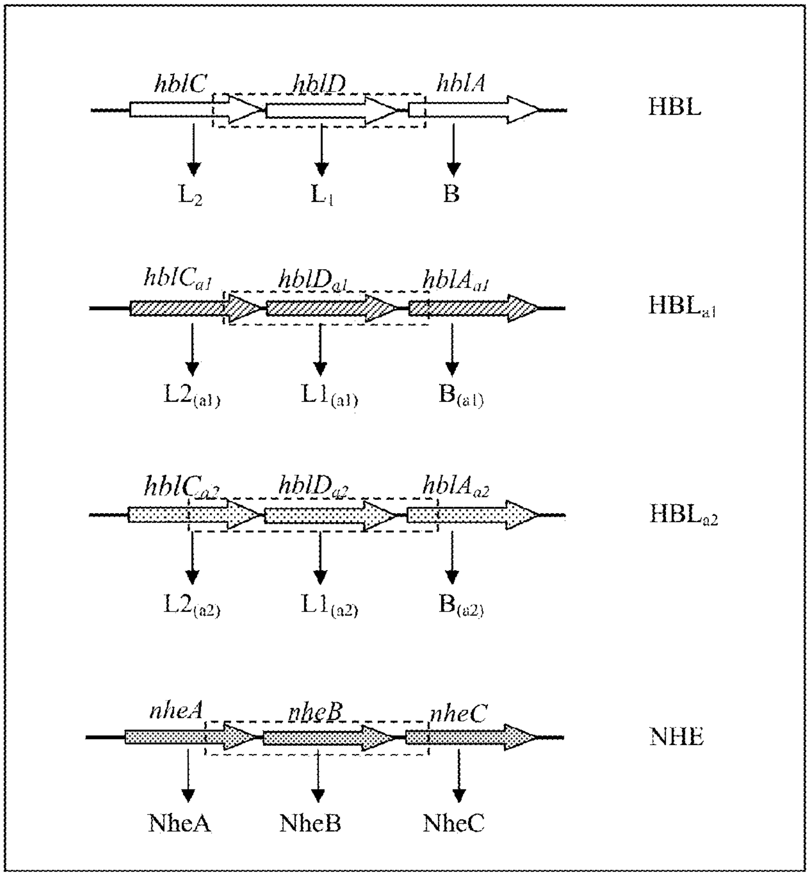
hblC
hblD
hblA
HBL
L2
L1
B
hblCa1
hblDa1
hblAa1
HBLa1
L2(a1)
L1(a1)
B(a1)
hblCa2
hblDa2
hblAa2
HBLa2
L2(a2)
L1(a2)
B(a2)
nheA
nheB
nheC
NHE
NheA
NheB
NheC

Fig. 1

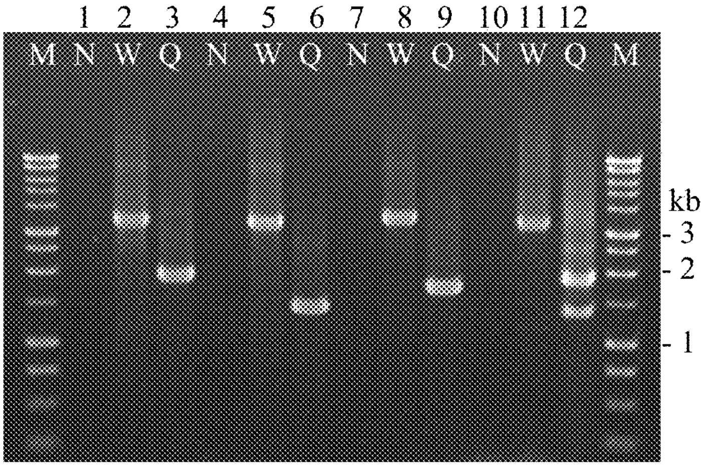

Fig. 2

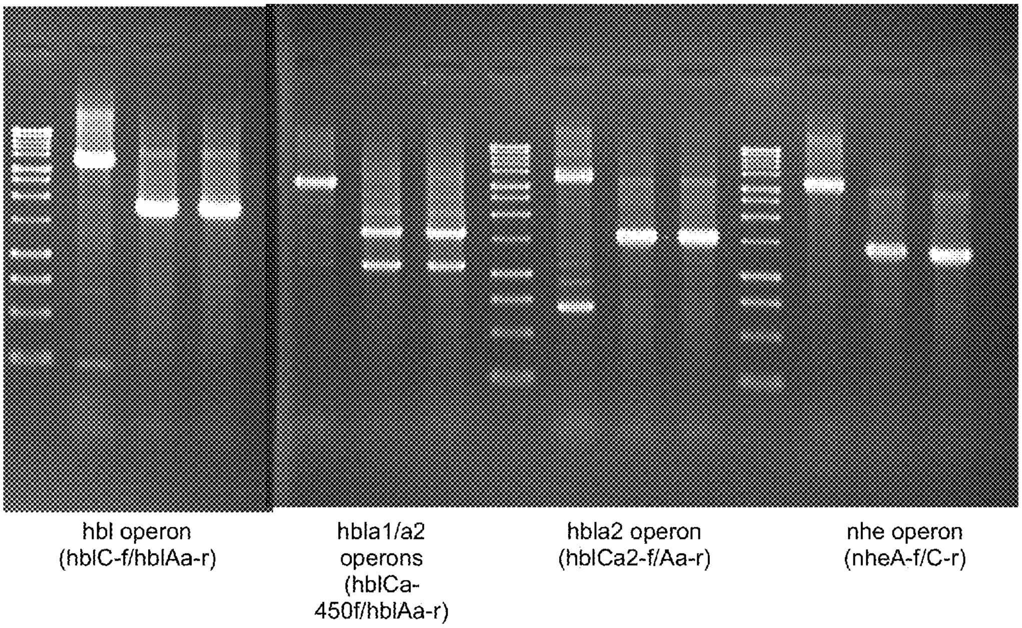
hbl operon
(hblC-f/hblAa-r)
hbla1/a2
operons
(hblCa-
450f/hblAa-r)
hbla2 operon
(hblCa2-f/Aa-r)
nhe operon
(nheA-f/C-r)

Fig. 3

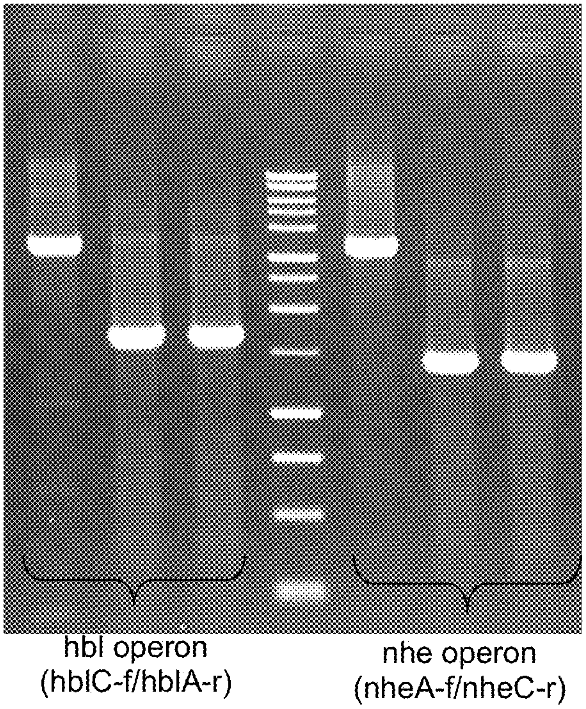

Fig. 4

# CONSTRUCTION OF A QUADRUPLE ENTEROTOXIN-DEFICIENT MUTANT OF *BACILLUS THURINGIENSIS*

## CROSS-REFERENCE TO RELATED APPLICATIONS

This application claims the benefit of U.S. Provisional Patent Application No. 61/353,314, filed Jun. 10, 2010, incorporated herein by reference as if set forth in its entirety.

## STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH OR DEVELOPMENT

This invention was made with United States 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 *Phytopthera* 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., 1997; Lindbäck 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 03BB108 (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 (Ramarao & 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, $hbl_{a1}$, $hbl_{a2}$, 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.

## DESCRIPTION OF PREFERRED EMBODIMENTS

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 enterotoxin-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 | | |
| *Bacillus thuringiensis kurstaki* strain VBTS 2477 | Wild-type | Valent Biosciences Inc. (ATCC Accession Number SD-5811) |
| 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 |
| *E. coli* DH5α | General purpose strain | Hanahan, 1983 |

TABLE 1-continued

Bacterial strains and plasmids used in this study.

| Strain or plasmid | Description | Source or Reference |
|---|---|---|
| *E. coli* GM2929 | dcm-6 dam-13::Tn9, $Cm^r$ | *E. coli* Genetic Stock Center |
| *E. coli* SS1827 | Helper strain for conjugation into *B. thuringiensis*, $Amp^r$ | 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 µl 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, 200Ω, and 25 µF. 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* DH5α were passed through *E. coli* GM2929 (methylation-deficient strain) before being introduced into *B. thuringiensis*. pBKJ236::$\Delta hbl_{a2}$ 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 µl of genomic DNA, 2 µl of 10× Taq buffer, 0.5 µM of each primer, 0.2 mM of each dNTP, 0.2 µl Taq DNA polymerase (Promega, Madison, Wis.) in a final volume of 20 µl. 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 | *B. thuringiensis* subsp. *kurstaki* 2477 (partial) | 1 |
| | *B. cereus* UW85 | 2 |
| | *B. cereus* ATCC 14579 | 3 |
| | *B. cereus* F837-76 | 4 |
| | *B. cereus* G9421 | 5 |
| | *B. thuringiensis* 97-27 serovar *konkukian* | 6 |
| hblD | *B. thuringiensis* subsp. *kurstaki* 2477 | 7 |
| | *B. cereus* UW85 | 8 |
| | *B. cereus* ATCC 14579 | 9 |
| | *B. cereus* F837-76 | 10 |
| | *B. cereus* G9421 | 11 |
| | *B. thuringiensis* serovar *konkukian* 97-27 | 12 |
| hblA | *B. thuringiensis* 2477 subsp. *kurstaki* (partial) | 13 |
| | *B. cereus* UW85 | 14 |
| | *B. cereus* ATCC 14579 | 15 |
| | *B. cereus* F837-76 | 16 |
| | *B. cereus* G9421 | 17 |
| | *B. thuringiensis* serovar *konkukian* 97-27 | 18 |
| hblCa | *B. thuringiensis* subsp. *kurstaki* 2477 hblCa1 (partial) | 19 |
| | *B. thuringiensis* subsp. *kurstaki* 2477 hblCa2 (partial) | 20 |
| | *B. cereus* UW85 | 21 |
| | *B. cereus* AS4-12 (tentative; only have 1-2x coverage) | 22 |
| | *B. cereus* 03BB108 | 23 |
| | *B. weihenstephanensis* KBAB4 | 24 |
| hblDa | *B. thuringiensis* subsp. *kurstaki* 2477 hblDa1 | 25 |
| | *B. thuringiensis* subsp. *kurstaki* 2477 hblDa2 | 26 |
| | *B. cereus* UW85 | 27 |
| | *B. cereus* AS4-12 (tentative; only have 1-2x coverage) | 28 |
| | *B. cereus* 03BB108 | 29 |
| | *B. weihenstephanensis* KBAB4 | 30 |
| hblAa | *B. thuringiensis* subsp. *kurstaki* 2477 hblAa1 (partial) | 31 |
| | *B. thuringiensis* subsp. *kurstaki* 2477 hblAa2 (partial) | 32 |
| | *B. cereus* UW85 | 33 |
| | *B. cereus* AS4-12 (tentative; only have 1-2x coverage) | 34 |
| | *B. cereus* 03BB108 | 35 |
| | *B. weihenstephanensis* KBAB4 | 36 |
| nheA | *B. thuringiensis* subsp. *kurstaki* 2477 (partial) | 37 |
| | *B. cereus* UW85 | 38 |
| | *B. cereus* 1230-88 | 39 |
| | *B. cereus* 10987 | 40 |
| | *B. cereus* ATCC 14579 | 41 |
| | *B. cereus* E3LL | 42 |
| | *B. thuringiensis* serovar *konkukian* 97-27 | 43 |
| | *B. thuringiensis* HD12 | 44 |
| nheB | *B. thuringiensis* subsp. *kurstaki* 2477 | 45 |
| | *B. cereus* UW85 | 46 |
| | *B. cereus* 1230-88 | 47 |

TABLE 2-continued

Gene sequences for HBL, NHE, and cytK used to design PCR primers.

| Gene | Organism | SEQ ID NO. |
|---|---|---|
| | *B. cereus* 10987 | 48 |
| | *B. cereus* ATCC 14579 | 49 |
| | *B. cereus* E3LL | 50 |
| | *B. thuringiensis* serovar *konkukian* 97-27 | 51 |
| | *B. thuringiensis* HD12 | 52 |
| nheC | *B. thuringiensis* subsp. *kurstaki* 2477 (partial) | 53 |
| | *B. cereus* UW85 | 54 |
| | *B. cereus* 1230-88 | 55 |
| | *B. cereus* 10987 | 56 |
| | *B. cereus* ATCC 14579 | 57 |
| | *B. cereus* E3LL | 58 |
| | *B. thuringiensis* serovar *konkukian* 97-27 | 59 |
| | *B. thuringiensis* HD12 | 60 |
| cytK | *B. cereus* 391-98 (cytK-1) | 61 |
| | *B. cereus* 1230-88 (cytK-2) | 62 |
| | *B. cereus* FM-1 (cytK-2) | 63 |
| | *B. cereus* ATCC 10987 (cytK-2) | 64 |
| | *B. cereus* ATCC 14579 (cytK-2) | 65 |
| | *B. thuringiensis* 97-27 (cytK-2) | 66 |

TABLE 3

Primers used for detection of enterotoxin genes in *Bacillus thuringiensis kurstaki* 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 |

TABLE 3-continued

Primers used for detection of enterotoxin genes in *Bacillus thuringiensis kurstaki* strain VBTS 2477.

| Primer | Sequence (5'-3')[a] | Melt Temp. (° C.) | Product size (nt) |
|---|---|---|---|
| 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 | |

[a] Degenerate bases: W = T or A; R = A or G; S = C or G.

### 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 $\Delta$hbl$_{a1}$ 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 μl 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 3730xl 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, 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 $\Delta$hbl$_{a1}$ and $\Delta$hbl$_{a2}$ constructs, the same set of outer primers were used (hblCa_Bam-F (SEQ ID NO:100), hblAa_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: 2477$\Delta$hbl (SEQ ID NO: 110), 2477$\Delta$hbl$_{a1}$ (SEQ ID NO: 111), 2477$\Delta$hbl$_{a2}$ (SEQ ID NO: 112), and 2477$\Delta$nhe (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) | GATA**GGATCC**GTACAGCTAGAGGAAGTC | 58.9 | 735 |
| hblCtail-R (SEQ ID NO: 93) | CTTCATTTGCATGGCTTTCATCAGGTCATACTCTTG TG | 62.8 | |
| hblAtail-F (SEQ ID NO: 94) | AAAGCCATGCAAATGAAGCGAGAATGAAAGAGACCTTGC | 65.3 | 712 |

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) |
|---|---|---|---|
| hblA_Bam-R (SEQ ID NO: 95) | CAAT**GGATCC**CTGTAAGCAACTCCAACTAC | 60.4 | |
| nheA_Bam-F (SEQ ID NO: 96) | CTGT**GGATCC**CAGGGTTATTGGTTACAGC | 62.2 | 815 |
| nheA_tail-R (SEQ ID NO: 97) | ATACTCCGCTGCTTCTCTCGTTTGACTATCTGCAG | 64.3 | |
| nheC_tail-F (SEQ ID NO: 98) | AGAAGCAGCGGAGTATGATTCAGCATCAAAGAGATGC | 64.6 | 744 |
| nheC_Bam-R (SEQ ID NO: 99) | CAAT**GGATCC**CCAGCTATCTTTCGCTGT | 62.1 | |
| hblCa_Bam-F (SEQ ID NO: 100) | CATT**GGATCC**GAAAGAGTGGTCATCCGAAC | 62.1 | 901 |
| hblCa1_tail-R (SEQ ID NO: 101) | TGAAACTACGCTCAATTT CTCCATCTACTTGGTTAGC | 61.9 | |
| hblAa1_tail-F (SEQ ID NO: 102) | AAATTGAGCGTAGTTTCACCAGTAGCTGCTTTTGCAAG | 64.1 | 934 |
| hblAa_Bam-R (SEQ ID NO: 103) | CTTA**GGATCC**GATCTGCTTTTTGGGATGC | 60.9 | |
| hblCa_Bam-F (SEQ ID NO: 100) | CATT**GGATCC**GAAAGAGTGGTCATCCGAAC | 62.1 | 630 |
| hblCa2_tail-R (SEQ ID NO: 104) | TTCTTTTGATCCTTTTCTCTATCGTTTCACGTGCTTC | 61.2 | |
| hblAa2_tail-F (SEQ ID NO: 105) | AGAAAAGGATCAAAAGAATGCAAGAGAGCATGCTAC | 61.5 | 691 |
| hblAa_Bam-R (SEQ ID NO: 103) | CTTA**GGATCC**GATCTGCTTTTTGGGATGC | 60.9 | |

[a] Bam 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 10× Pfu buffer, 0.5 μM 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 Δhbla$_2$ (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 Δhbla$_2$ 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 L$_2$ 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, Bellirica, 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 LC$_{50}$. 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 (LC$_{50}$).

### 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. anthracia* 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 L$_2$ component of HBL (Beecher & Wong, 1994). The triple deletion mutant, in which hbl is deleted, exhibited a negative phenotype, indicating that expression of the L$_2$ 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-L$_2$ 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 L$_2$. 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.

TABLE 6

Detection of HBL and NHE proteins in *B. thuringiensis* subsp. *kurstaki* 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 | Δhbl$_{a1}$ Δnhe | 1024 | 1 |
| Triple mutant | Δhbl$_{a1}$ Δnhe Δhbl | Neg | 1 |
| Quadruple mutant | Δhbl$_{a1}$ Δnhe Δhbl Δhbl$_{a2}$ | Neg | 1 |

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

[b] BDE 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.

TABLE 8

Insecticidal activity against lepidopteran larvae. *B. thuringiensis* cultures from 7.5 L fermentors were fed to 4-day old *T. ni*, 2-day old *S. exigua*, and 4-day old *P. xylostella* larvae. Larval mortality was assessed after 3 days.

| | Insecticidal activity LC$_{50}$* (μg ml$^{-1}$ diet against each lepidopteran species) | | |
|---|---|---|---|
| Strain | *T. ni* (95% CI) | *S. exigua* (95% CI) | *P. xylostella* (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 (Δhbl$_{a1}$ Δnhe Δhbl Δhbl$_{a2}$) was created in *B. thruingiensis* 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::Δ2477hbl, pMAD::Δ2477hbl$_{a1}$, pMAD::Δ2477hbl$_{a2}$, and pMAD::Δ2477nhe. 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 *B. thuringiensis* strains 2478 and 2481.

| Name | Sequence (5' to 3') | Note | SEQ ID NO. |
|---|---|---|---|
| hblCa2-f | CTTTCTACAGGGAAGGATTTAGAA | specific for $\text{hbl}_{a2}$ in strain VBTS 2478* | 108 |
| hblCa-450f | CTTAATTCAGAGGGAACAGGA | Specific for both $\text{hbl}_{a1}$ and $\text{hbl}_{a2}$* | 109 |

*After mutagenesis of $\text{hbl}_{a1}$ in strain 2478, PCR analysis confirmed the existence of a second $\text{hbl}_{a}$ homolog, $\text{hbl}_{a2}$.
The sequencing data of $\text{hbl}_{a2}$ 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 $\text{hblA}_{a2}$ and $\text{hblD}_{a2}$ 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 $L_2$ component of HBL (Beecher & Wong, 1994). The quadruple deletion mutant ($\Delta\text{hbl}_{a1}$ Δnhe Δhbl $\Delta\text{hbl}_{a2}$), 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 $\text{hbl}_{a1}$ and $\text{hbl}_{a2}$ did not yield any products indicating that VBTS 2481 does not contain $\text{hbl}_{a1}$ or $\text{hbl}_{a2}$; 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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actaccggta acactattca tgcatttgca caagaaacga ccgctcaaga acaaaaagta 120

ggcaattatg cattaggccc cgaaggactg aagaaagcat tagctgaaac agggtctcat 180

attctagtaa tggatttata cgcaaaaaca atgattaagc aaccaaatgt aaatttatct 240

aatatcgatt taggctcaga gggggagag ttgctcaaaa atattcacct taatcaagag 300

ctgtcacgaa tcaatgcgaa ttactggtta gatacagcga agccacagat tcaaaaaact 360

gctcgtaata ttgtaaatta cgatgaacaa tttcaaaatt attacgacac attagtagaa 420

actgtacaaa agaaagataa ggcaggtcta aaagagggta taaatgattt aattactaca 480

atcaatacaa attcaaaaga agttacagat gtgattaaga tgctacaaga cttcaaaggg 540

aaattatatc aaaattctac agattttaaa aataatgttg gtggtccaga tgggaaaggt 600

ggattaactg caatattagc aggtcaacag gcaacgattc cacaacttca agctgaaatt 660

gagcaacttc gttctactca gaaaaaacat tttgatgatg tattagcatg gtcaattggt 720

ggtggattgg gagcagctat tttagttatt gcagctattg gaggagcggt agttattgtt 780 gtaactggcg gtacagcaac accggctgtt gttggtggac tctcggctct tggcgcagct 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 cacaaattct ctttaatacc agatgattta 1140

aaagcggcta aagaaagttg gaatgatatt cataaagatg cagaattcat ttcaaaagat 1200

attgctttta aacaggagta g 1221

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

<400> SEQUENCE: 8

atgaaaaaat ttccattcaa agtactaact ttagctacat tagcaactgt tataactgct 60

actaccggta acactattca tgcatttgca caagaaacga ccgctcaaga acaaaaagta 120

ggcaattatg cattaggacc cgaaggactg aagaaagcat tggctgaaac agggtctcat 180

attctagtaa tggatttata tgcaaaaaca atgattaagc aaccaaatgt aaatttatct 240

aatatcgatt tagggtcaga gggggagag ttgctcaaaa atattcacct taatcaagag 300

ctgtcacgaa tcaatgcgaa ttactggtta gatacagcga agccacagat tcaaaaaact 360

gctcgtaata ttgtaaatta cgatgaacaa tttcaaaatt attacgacac attagtagaa 420

actgtacaaa agaaagataa ggcaggtcta aaagagggta taaatgattt aattactaca 480

atcaatacaa attcaaaaga agttacagat gtgattaaga tgctacaaga cttcaaagga 540

aaactatatc aaaattctac agattttaaa aataatgttg gtggtccaga tgggaaaggt 600

ggattaactg caatattagc aggtcaacag gcaacgattc cacaacttca agctgaaatt 660

gagcaacttc gttctactca gaaaaaacat tttgatgatg tattagcatg gtcaattggt 720

ggtggattgg gagcagctat tttagttatt gcagctattg gaggagcggt agttattgtt 780

gtaactggcg gtacagcaac accggctgtt gttggtggac tctcggctct tggtgcagct 840

ggtatcggtc taggaactgc ggctggtgtc acagcatcta agcatatgga ctcctataat 900

gaaatttcta acaaaatcgg agaattaagt atgaaagcag atcgtgctaa tcaagcagtt 960

ctttcactta ctaacgcgaa agaaacattg gcatatttat atcagactgt agatcaagcg 1020

atattgtctc taacaaatat tcaaaagcaa tggaatacaa tgggcgcaaa ttatacagat 1080

ttattggata atatcgattc tatgcaagac cacaaattct ctttaatacc agatgattta 1140

aaagccgcta aagaaagttg gaatgatatt cataaagatg cagaattcat ttcaaaagat 1200

attgctttta aacaggagta g 1221

<210> SEQ ID NO 9
<211> LENGTH: 1221
<212> TYPE: DNA
<213> ORGANISM: Bacillus cereus

<400> SEQUENCE: 9

atgaaaaaat ttccattcaa agtactaact ttagctacat tagcaactgt tataactgct 60

actaccggta acactattca tgcatttgca caagaaacga ccgctcaaga acaaaaagta 120 ggcaattatg cattaggccc cgaaggactg aagaaagcat tagctgaaac agggtctcat 180

attctagtaa tggatttata cgcaaaaaca atgattaagc aaccaaatgt aaatttatct 240

aatatcgatt taggctcaga gggggagag ttgctcaaaa atattcacct taatcaagag 300

ctgtcacgaa tcaatgcgaa ttactggtta gatacagcga agccacagat tcaaaaaact 360

gctcgtaata ttgtaaatta cgatgaacaa tttcaaaatt attacgacac attagtagaa 420

actgtacaaa agaaagataa ggcaggtcta aaagagggta taaatgattt aattactaca 480

atcaatacaa attcaaaaga agttacagat gtgattaaga tgctacaaga cttcaaaggg 540

aaactatatc aaaattctac agattttaaa aataatgttg gtggtccaga tgggaaaggt 600

ggattaactg caatattagc aggtcaacag gcaacgattc cacaacttca agctgaaatt 660

gagcaacttc gttctactca gaaaaaacat tttgatgatg tattagcatg gtcaattggt 720

ggtggattgg gagcagctat tttagttatt gcagctattg gaggagcggt cgttattgtt 780

gtaactggcg gtacagcaac accggctgtt gttggtggac tctcggctct tggtgcagct 840

ggtattggtt taggaacagc ggctggtgtc acagcatcta agcatatgga ctcctataat 900

gaaatttcta acaaaatcgg agaattaagt atgaaagcag atcgtgctaa tcaagcagtt 960

ctttcgctta ctaacgcgaa agaaacattg gcatatttat 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

atgaaaaaat ttccattcaa agtactaact ttagctacat tagcaactgt tataactgct 60

actaccggta acactattca tgcatttgca caagaaacga ccgctcaaga acaaaaagta 120

ggcaattatg cattaggccc cgaaggacta aagaaagcat tggctgaaac agggtctcat 180

attctagtaa tggatttata cgcaaaaaca atgattaagc aaccaaatgt aaatttatct 240

aatatcaatt taggctcaga gggggagag ttgctcaaaa atattcacct taatcaagag 300

ctgtcacgaa tcaatgcgaa ttactggtta gatacagcga agccacagat tcaaaaaact 360

gctcgtaata ttgtaaatta cgatgaacaa tttcaaaatt attacgacac attagtagaa 420

actgtacaaa agaaagataa ggcaggtcta aaagagggca taaatgattt aattactaca 480

atcaatacaa attcaaaaga agttacagat gtgattaaga tgctacaaga cttcaaaggg 540

aaactatatc aaaattctac agattttaaa aataatgttg gtggtccaga tgggaaaggt 600

ggtttaactg caatattagc aggtcaacag gcaacgattc cacaacttca agctgaaatt 660

gagcaacttc gtgctactca gaaaaaacat tttgatgatg tattagcatg gtcaattggt 720

ggtggattgg gagcagctat tttagttatt gcagctattg gaggagcggt agttattgtt 780

gtaactggcg gtacagcaac accggctgtt gttggtggac tctcggctct tggtgcagct 840

ggtattggtt taggaacagc ggctggtgtc acagcatcta agcatatgga ctcctataat 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

caaccaaatg taaatttatc taatatcgat ttaggctcag aggggggaga gttgctcaaa 120

aatattcacc ttaatcaaga gctgtcacga atcaatgcga attactggtt agatacagcg 180

aagccacaga ttcaaaaaac tgctcgtaat attgtaaatt acgatgaaca atttcaaaat 240

tattacgaca cattagtaga aactgtacaa aagaaagata aggcaggtct aaaagagggc 300

ataaatgatt taattactac aatcaataca aattcaaaag aagttacaga tgtgattaag 360

atgctacaag acttcaaagg gaaactatat caaaattcta cagattttaa aaataatgtt 420

ggtggtccag atgggaaagg tggattaact gcaatattag caggtcaaca ggcaaccatt 480

ccacaacttc aagctgaaat tgagcaactt cgttctactc agaaaaaaca ttttgatgat 540

gtattagcat ggtcaattgg tggtggattg ggagcagcta ttttagttat tgcagctatt 600

ggaggagcgg tagttattgt tgtaactggc ggtacagcaa caccagctgt tgttggtgga 660

ctttcagctc ttggagcagc tggtatcggt ctaggaactg cggctggtgt tacagcatct 720

aagcatatgg actcctataa cgaaatttct 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

atgaaaaaat ttccattcaa agtactaact ttagctacat tagcaactgt tataactgct 60

actaccggta acactattca tgcatttgca caagaaacaa ctgctcaaga acaaaaagta 120

ggcaattatg cattaggccc cgaaggactg aagaaagcat tggctgaaac agggtctcat 180

attctagtaa tggatttata cgcaaaaaca atgattaagc aaccaaatgt aaatttatct 240

aatatcgatt taggctcaga ggggggagag ttgctcaaaa atattcacct taatcaagag 300

ctgtcacgaa tcaatgcgaa ttactggtta gatacagcga agccacagat tcaaaaaact 360

gctcgtaata ttgtaaatta cgatgaacaa tttcaaaatt attacgacac attagtagaa 420

actgtacaaa agaaagataa ggcaggtcta aaagagggta taaatgattt aattactaca 480

atcaatacaa attcaaaaga agttacagat gtgattaaga tgctacaaga cttcaaaggg 540

aaactatatc aaaattctac agattttaaa aataatgttg gtggtccaga tgggaaaggt 600

-continued

ggattaactg caatattagc aggtcaacag gcaacgattc cacaacttca agctgaaatt 660

gagcaacttc gttctactca gaaaaaacat tttgatgatg tattagcatg gtcaattggt 720

ggtggattgg gagcagctat tttagttatt gcagctattg gaggagcggt agttattgtt 780

gtaactggcg gtacagcaac accggctgtt gttggtggac tctcggctct tggtgcagct 840

ggtatcggtc taggaactgc ggctggtgtc acagcatcta agcatatgga ctcctataat 900

gaaatttcta acaaaatcgg agaattaagt atgaaagcag atcgtgctaa tcaagcagtt 960

ctttcgctta ctaacgcgaa agaaacattg gcatatttat atcagactgt agatcaagcg 1020

atattgtctc taacaaatat tcaaaagcaa tggaatacaa tgggcgcaaa ttatacagat 1080

ttattggata atatcgattc tatgcaagac cacaaattct ctttaatacc agatgattta 1140

aaagccgcta 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

atgataaaaa aaatccctta caaattactc gctgtatcga cactattaac tattacaact 60

gctaatgtag tttcaccagt aacaactttt gcaagtgaaa ttgaacaaac gaataatgga 120

gatacggctc tttctgcaaa tgaagcgaga atgaaagaga ccttgcaaaa ggctggatta 180

tttgcaaaat ctatgaatgc ctattcttat atgttaatta agaatcctga tgtgaatttt 240

gagggaatta ccattaatgg atatgtagat ttacctggta gaatcgtaca agatcaaaag 300

aatgcaaggg cacatgccgt tacttgggat acgaaagtaa aaaaacagct tttagataca 360

ttgaatggta ttgttgaata cgatacaaca tttgataatt attatgaaac aatgatagag 420

gcgattaata caggggatgg agaaacttta aaagaaggga ttacagattt acgaggtgaa 480

attcaacaaa atcaaaagta tgcacaacaa ctaatagaag aattaactaa attaagagac 540

tctattggac acgatgttag agcatttgga agtaataaag agctcttgca gtcaatttta 600

aaaaatcaag gtgcagatgt tgatgccgat caaaagcgtc tagaagaagt attaggatca 660

gtaaactatt ataaacaatt agaatctgat gggtttaatg taatgaaggg tgctattttg 720

ggtctaccaa taattggcgg tatcatagtg ggagtagcaa gggataattt aggtaagtta 780

gagcctttat tagcagaatt acgtcagacc gtggattata aagtaacctt aaatcgtgta 840

gttggagttg cttacagtaa tattaatgaa atgcacaagg cgcttgatga tgctattaac 900

gctcttactt atatgtccac gcagtggcat gatttagatt ctcaatattc gggcgttcta 960

gggcatattg ag 972

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

<400> SEQUENCE: 14

atgataaaaa aaatccctta caaattactc gctgtatcga cgctattaac tattacaact 60

gctaatgtag tttcaccagt aacaactttt gcaagtgaaa ttgaacaaac gaacaatgga 120

gatacggctc tttctgcaaa tgaagcgaga atgaaagaga ccttgcaaaa ggctggatta 180

tttgcaaaat ctatgaatgc ctattcttat atgttaatta agaatcctga tgtgaatttt 240

-continued

gagggaatta ccattaatgg atatgtagat ttacctggta gaatcgtaca agatcaaaag 300

aatgcaaggg cacatgccgt tacttgggat acgaaagtaa aaaaacagct tttagataca 360

ttgaatggta ttgttgaata cgatacaaca tttgataatt attatgaaac aatgatagag 420

gcgattaata caggggatgg agaaacttta aaagaaggga ttacagattt acgaggtgaa 480

attcaacaaa atcaaaagta tgcacaacaa ctaatagaag aattaactaa attaagagac 540

tctattggac acgatgttag agcatttgga agtaataaag agctcttgca gtcaatttta 600

aaaaatcaag gtgcagatgt tgatgccgat caaaagcgtc tagaagaagt attaggatca 660

gtaaactatt ataaacaatt agaatctgat gggtttaatg taatgaaggg cgctattttg 720

ggtctaccaa taattggcgg tattatagtg ggagtagcaa gggataattt aggtaagtta 780

gagcctttat tagcagaatt acgtcagacc gtggattata aagtaacctt aaatcgtgtg 840

gttggagttg cttacagtaa tattaatgaa atgcacaagg cccttgatga tgctattaac 900

gctcttactt atatgtccac gcagtggcat gatttagatt ctcaatattc gggcgttcta 960

gggcatattg agaatgcagc tcaaaaagcc gatcaaaata aatttaaatt cttaaaacct 1020

aatttaaatg cagcgaaaga cagttggaaa acattacgaa cagatgctgt tacattaaaa 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

atgataaaaa aaatccctta taaattactc gctgtatcga cgctattaac tattacaact 60

gctaatgtag tttcaccagt aacaactttt gcaagtgaaa ttgaacaaac gaacaatgga 120

gatacggctc tttctgcaaa tgaagcgaga atgaaagaga ccttgcaaaa ggctggatta 180

tttgcaaaat ctatgaatgc ctattcttat atgttaatta agaatcctga tgtgaatttt 240

gagggaatta ccattaatgg atatgtagat ttacctggta gaatcgtaca agatcaaaag 300

aatgcaaggg cacatgctgt tacttgggat acgaaagtaa aaaaacagct tttagataca 360

ttgaatggta ttgttgaata cgatacaaca tttgacaatt attatgaaac aatggtagaa 420

gcgattaata caggggatgg agaaacttta aaagaaggga ttacagattt gcgaggtgaa 480

attcaacaaa atcaaaagta tgcacaacaa ctaatagaag aattaactaa attaagagac 540

tctattggac atgatgttag agcttttgga agtaataaag agctcttgca gtcaatttta 600

aaaaatcaag gtgcagatgt tgatgccgat caaaagcgtc tagaagaagt attaggatca 660

gtaaactatt ataaacaatt agaatctgat gggtttaatg taatgaaggg tgctattttg 720

ggtctaccaa taattggcgg tattatagtc ggagtagcaa gggataattt aggtaagtta 780

gagcctttat tagcagaatt acgtcagacc gtggattata aagtaacctt aaatcgtgta 840

gttggagttg cttacagtaa tattaatgaa atgcacaagg cgcttgatga tgctattaac 900

gctcttactt atatgtccac gcagtggcat gatttagatt ctcaatattc gggcgttcta 960

gggcatattg agaatgcagc tcaaaaagcc gatcaaaata aatttaaatt cttaaagcct 1020

aatttaaatg cagcgaaaga cagttggaaa acattacgaa cagatgctgt tacattaaaa 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

atgataaaaa aaatccctta caaattactc gctgtatcga cgttattaac tattacaacc 60

gctaatgtag tttcacctgt agcaactttt gcaagtgaaa ttgaacaaac gaacaatgga 120

gatacggctc tttctgcaaa tgaagcgaag atgaaagaaa ctttgcaaaa ggctggatta 180

tttgcaaaat ctatgaatgc ctattcttat atgttaatta aaaatcctga tgtgaatttt 240

gagggaatta ctattaatgg atatgtagat ttacctggta gaatcgtaca agatcaaaag 300

aatgcaagag cacatgctgt tacttgggat acgaaagtga aaaaacagct tttagataca 360

ttgactggta ttgttgaata tgatacgacg tttgacaatt attatgaaac aatggtagag 420

gcaattaata 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 ataaacaatt agaatctgat gggtttaatg taatgaaggg tgctattttg 720

ggtctaccaa taattggcgg tattatagtg ggagtagcaa gggataattt aggtaagtta 780

gagcctttat tagcagaatt acgtcagacc gtggattata aagtaacctt aaatcgtgta 840

gttggagttg cttacagtaa tattaatgaa atcgacaagg cgcttgatga tgctattaac 900

gctcttactt atatgtccac gcagtggcat gatttagatt ctcaatattc gggcgttcta 960

gggcatattg agaatgcagc tcaaaaagcc gatcaaaata aatttaaatt cttaaaacct 1020

aatttaaatg 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

atgataaaaa aaatccctta caaattactc gctgtatcga cgttattaac tattacaact 60

gctaatgtag tttcaccagt aacaactttt gcaagtgaaa ttgaacaaac gaacaatgaa 120

gatacagctc tttctgcaaa tgaagcgaga atgaaagaga ccttgcaaaa ggctggatta 180

tttgcaaaat ctatgaatgc ctattcttat atgttaatta agaatcctga tgtgaatttt 240

gagggaatta cgattaatgg gtatgtagat ttacctggta gaatcgtaca agatcaaaag 300

aatgcaaggg cacatgctgt tacttgggat acgaaagtaa aaaaacagct tttagataca 360

ttgaatggta ttgttgaata cgatacaaca tttgacaatt attatgaaac aatggtagag 420

gcgattaata caggggatgg agaaacttta aaagaaggga ttacagattt gcgaggtgaa 480

attcaacaaa atcaaaagta tgcacaacaa ctaatagaag aattaactaa attaagagac 540

tctattggac acgatgtgag agcatttgga agtaataaag agctcttgca gtcaatttta 600

aaaaatcaag gtgcagatgt tgatgccgat caaaagcgtc tagaagaagt attaggatca 660

gtaaactatt ataaacaatt agaatctgat gggtttaatg taatgaaggg tgctattttg 720

ggtctaccaa taattggcgg tatcatagtg ggagtagcaa gggataattt aggtaagtta 780

gagcctttat tagcagaatt acgtcagacc gtggattata aagtaacctt aaatcgtgta 840 gttggagttg cttacagtaa tattaatgaa atgcacaagg cgcttgatga tgctattaac 900

gctcttactt atatgtccac gcagtggcat gatttagatt ctcaatattc gggcgttcta 960

gggcatattg agaatgcagc tcaaaaagcc gatcaaaata aatttaaatt cttaaaacct 1020

aatttaaatg cagcgaaaga cagttggaaa acattacgaa cagatgctgt tacattaaaa 1080

gaaggaataa aggaattaaa agtggaaact gttactccac aaaaatag 1128

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

<400> SEQUENCE: 18

atgataaaaa aaatccctta caaattactc gctgtatcga cgctattaac tattacaact 60

gctaatgtag tttcaccagt aacaactttt gcaagtgaaa ttgaacaaac gaacaatgaa 120

gattcagctc tttctgcaaa tgaagcgaga atgaaagaga ccttgcaaaa ggctggatta 180

tttgcaaaat ctatgaatgc ctattcttat atgttaatta aaaatccgga tgtgaatttt 240

gagggaatta ccattaatgg atatgtagat ttacctggta gaatcgtaca agatcaaaag 300

aatgcaagag cacatgctgt tacttgggat acgaaagtaa aaaaacagct tttagataca 360

ttgaatggta ttgttgaata cgatacaaca tttgacaatt 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 ataaacaatt agaatctgat gggtttaatg taatgaaggg tgctattttg 720

ggtctaccaa taattggcgg tatcatagtg ggagtagcaa gagataattt aggtaagtta 780

gagcctttat tagcagaatt acgtcagacc gtggattata aagtaacctt aaatcgtgta 840

gttggagttg cttacagtaa tattaatgaa atgcacaagg cacttgatga tgctattaac 900

gctcttactt atatgtccac gcagtggcat gatttagatt ctcaatattc gggcgttcta 960

gggcatattg agaatgcagc tcaaaaagcc gatcaaaata aatttaaatt cttaaaacct 1020

aatttaaatg 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 gtggtcatcc gaactttatc ctaaattaat 60

tctattaaat tcaaaaagta aaggatttgt aactaaattt aatagttatt atccaacatt 120

aaaaggattt gtagataata aggaagataa agaagggttt acagatagac tggaagtcct 180

tcaagacatg accatcacaa accaagaaag tgtgcaacgt caaattaatg agttaacaga 240

tctaaaacta caggtagata agaagttgaa aaatcttgat actgatgtgg caaaaacaca 300

gagtgtcctt aattcagagg gaacaggaaa aatagataag ttaaaaaatg aaatgctaga 360

tacaaaaaaa tcaattcaaa atgatttaca gcaaatagcg ttattaccag gagctttaaa 420

```
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

atatttaaat gatttagaga aacaaaatca gaaattatat gacttaacga ctaaattaac    840

agtagcagat ttacaaaaat caatgattct tttcatgcaa aatgatttgc atacatttgc    900

taaccaagta gatggagaaa ttgagctaat gaaacgttac aaagaggatt tggatctaat    960

aaataatagt attacaaaat tatcgactga agttgatacc aataacaccc agtctcaaaa   1020

agatacatta agacgattaa aaagtgtaac aactcaactc gaagaacaag tttataaatt   1080

ttaa                                                                1084


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

<400> SEQUENCE: 20

tctaattaaa caagatatga aagagtggtc atccgaactt taccctaaat taattctatt     60

aaattcaaaa agtaaaggat ttataactaa atttaatagt tattatccaa cattaaaagg    120

atttgtagat aataaggaag ataaagaagg gtttacagat agactggaag ttcttcaaga    180

catgactata acaaatcaag aaagtgtgca acgtcaaatt aatgagttaa cagatttaaa    240

attactggta gataagaagt tgaaaaacct tgatactgat gtggtaaaag cacaaagtgt    300

ccttaattca gagggaacag gaaaaataga taagttaaaa aatgaaatgc tagatacaaa    360

aaaatctatt caaaatgatt tgcagcaaat agcattatta ccaggcgcgt taaatgaaca    420

agggctaaag gtattccaag aaatttatag tctatcgaaa gatatcattg aaccggctgc    480

tcaaacagca gtagtagcgt ataacaaagg aaaagaaata aacaatgcca ttgtagacgc    540

agagaagaaa gcagagcaag aagcaaaaga aaagggaaaa tcagctatag aaattgaagc    600

tgccaaaaaa gaagcacgtg aaacgataga gaaaagtaaa aaaggtgaaa tcgctgcagc    660

tgcagttaca aaaacgaaag agtatgatct tatgaaagtg attgatcctg aaaaaataaa    720

aaaaacatat aatacttttg ctgaaattaa taaactaaca gctgagcaaa gagcatattt    780

aaatgattta gagaaacaaa atcagaaatt atatgactta acaactaaat taacagtagc    840

agatttacaa aaatcaatga ttcttttcat gcaaaatgac ttgcatacat ttactaatca    900

agtagatgga gaaattgagt taatgaaacg ttacaaagag gatttggatc taataaataa    960

tagtattaca aaattatcga ctgaagttga taccaataat actcaggctc aaaaagatat   1020

attaagacga ttaaaaagtg 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 caaaacaaga gaatatagat    120
```

atttcctcag cgttacgaaa aataggtgca cactccaaat taacacaaac ctttatcgat 180

ggagccttag caagtccgaa tgtacaactt gaagaagttc catctttaaa tacaactcaa 240

tttctaatta aacaagatat gaaagagtgg tcatccgaac tttatcctaa attaattcta 300

ttaaattcaa aaagtaaagg atttgtaact aaatttaata gttattatcc aatattaaaa 360

gggtttatag ataataggga agataaagaa ggatttacag atagactgga agtccttcaa 420

gacatgacca tcacaaacca agaaagtgtg caacgtcaaa ttaatgagtt aacagatcta 480

aaactacagg tagataagaa gttgaaaaat cttgatactg atgtgacaaa agcacagagt 540

gtccttaatt cagagggaac aggaaaaata gataagttaa aaaatgaaat gctagataca 600

aaaaaatcaa ttcaaaatga tttacagcaa attgcattat taccaggggc tttaaatgaa 660

caagggctaa aggtattcca agaaatttat agtctatcga aagatatcat tgaaccggct 720

gctcaaacag cagtagtagc gtataacaaa ggaaaagaaa taaacaatgc tattgtagac 780

gcagagaata aagcagagca agaagcaaaa gaaaagggaa aatcagctat agaaattgag 840

gctgcaaaaa aagaagcacg tgaagcgata gagaaaagta aaaaaggtga aatcgctgca 900

gctgcagtta caaaaacgaa agagtatgat cttatgaaag tgattgatcc tgaaaaaatt 960

aaaaaaacat ataatacttt tgctgaaatt aataaactaa cagcagagca acgtgcatat 1020

ttaaatgatt tagaaaaaca aaatcagaaa ttatatgact taacaactaa attaacagta 1080

gcagatttac aaaaatcaat gattcttttc atgcaaaatg atttgcatac atttgctaac 1140

caagtagatg gagaaattga gctaatgaaa cgttacaaag aggatttgga tctaataaat 1200

aatagtatta caaaattatc gactgaagtt gataccaata acactcagtc tcaaaaagat 1260

acattaagac gattaaaaag tgtaacaact caactcgaag aacaagttta taaattctaa 1320

<210> SEQ ID NO 22
<211> LENGTH: 1319
<212> TYPE: DNA
<213> ORGANISM: Bacillus cereus

<400> SEQUENCE: 22

atgaagaata aaattatgac aggattttta ataacatcaa ttgctaccgg ggcgactatt 60

cctatcaata ctctcgcaac gccaatcgtc caagcagaaa caaaacaaga gaatatagat 120

atttcctcag cgttacgaaa aataggtgca cactccaaat taacacaaac ctttatcgat 180

ggagccttag caagtccgaa tgtacaactt gaagaagttc catctttaaa tacaactcaa 240

tttctattaa acaagatatg aaagagtggt catccgaact ttatcctaaa ttaattctat 300

taaattcaaa aagtaaagga tttgtaacta aatttaatag ttattatcca atattaaaag 360

ggtttataga taatagggaa gataaagaag gatttacaga tagactggaa gtccttcaag 420

acatgaccat cacaaaccaa gaaagtgtgc aacgtcaaat taatgagtta acagatctaa 480

aactacaggt agataagaag ttgaaaaatc ttgatactga tgtgacaaaa gcacagagtg 540

tccttaattc agagggaaca ggaaaaatag ataagttaaa aaatgaaatg ctagatacaa 600

aaaaatcaat tcaaaatgat ttacagcaaa ttgcattatt accaggggct ttaaatgaac 660

aagggctaaa ggtattccaa gaaatttata gtctatcgaa agatatcatt gaaccggctg 720

ctcaaacagc agtagtagcg tataacaaag gaaaagaaat aaacaatgct attgtagacg 780

cagagaataa agcagagcaa gaagcaaaag aaaagggaaa atcagctata gaaattgagg 840

ctgcaaaaaa agaagcacgt gaagcgatag agaaaagtaa aaaaggtgaa atcgctgcag 900 ctgcagttac aaaaacgaaa gagtatgatc ttatgaaagt gattgatcct gaaaaaatta 960

aaaaaacata taatactttt gctgaaatta ataaactaac agcagagcaa cgtgcatatt 1020

taaatgattt agaaaaacaa aatcagaaat tatatgactt aacaactaaa ttaacagtag 1080

cagatttaca aaaatcaatg attcttttca tgcaaaatga tttgcataca tttgctaacc 1140

aagtagatgg agaaattgag ctaatgaaac gttacaaaga ggatttggat ctaataaata 1200

atagtattac aaaattatcg actgaagttg ataccaataa cactcagtct caaaaagata 1260

cattaagacg attaaaaagt gtaacaactc aactcgaaga acaagtttat aaattctaa 1319

<210> SEQ ID NO 23
<211> LENGTH: 1323
<212> TYPE: DNA
<213> ORGANISM: Bacillus cereus

<400> SEQUENCE: 23

atgaaaaatg atctcactaa aaaatttgta ataacatcag ttgtttttgg attagcaatt 60

tctaactatg tattttcacc tgctatagtc atacaagctg agacacaaca agaacgaata 120

gatatttctt catccttacg caagttaggt gcacaatcta aactaataca aacatatatc 180

gatcaaaatt taataacacc taatatacag ttgaaggaaa tgccatcttt aaatacgaat 240

caatttttaa ttaagcgaga tatgaaagag tggtcatcag 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 aaaggcacaa 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 aaataaacaa 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 cttcgccgaa attaataaac taacggcaga acagcgagcg 1020

catttatatg atttagagaa acaaaaccaa aaattatatg 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

<210> SEQ ID NO 24
<211> LENGTH: 1320
<212> TYPE: DNA
<213> ORGANISM: Bacillus weihenstephanensis

<400> SEQUENCE: 24

atgaagaata aaattatgac aggattttta ataacatcaa tcgttactgg agcgactatt 60

cctatcaata ctctcgcaac gccaatcgtt caggcagaaa tgaaacaaga aaatatagat 120

-continued

atttcctcag cattacgaaa aataggtgca cactccaaat taacacaaac ctttatagat 180

ggagccttag caagtccgaa tgtgcaactt gaagaagttc catctttaaa tacaactcaa 240

tttctaatta aacaagatat gaaagagtgg tcatcagaac tatatccaaa attaattcta 300

ctaaattcaa aaagtaaagg atttgcaacc aaatttaata gctattatcc aacattaaaa 360

ggatttgtag ataataagga agataaagaa gggtttatag atagactgga agttctccaa 420

gatatgacta taacaaacca agaaaacgtg caacgtcaga ttaatgagtt aacagatctt 480

aaactacagg tagataagaa actgaaaaat cttgatacag atgtggtaaa agcacagagt 540

gtacttagtt cagagggaac aggaaaaata gacaagttaa aaaatgaaat gctaaataca 600

aaaaaatcaa ttcaaaatgc tttagagcaa atagcattat taccaggagc tttaaatgaa 660

caagggctaa aggtattcca agaaatttat agcctatcaa aagatatcat tgaaccggct 720

gctcaaacag cggtagtagc gtataacaaa ggaaaagaaa taaataatac tattgtagaa 780

gcagagaaga aagcagagca ggaagcaaca gaaaagggaa aatcagctat agaaattgaa 840

gctgcaaaaa aagaagcacg tgaagcgata gagaaaagta aaaaaggtga gattgctgca 900

gctgcagtta caaaaacgaa agagtatgat cttatgaaag tgattgatcc tgaaaaaatt 960

aaaaaaacat atagtacctt tgccgaaatt aataaactaa cagcagagca aagagtatat 1020

ttaaatgatt tagagaaaca aaatcagaaa ttatatgact taacaactaa attaacagta 1080

gcagatctac aaaaatcaat gattcttttc atgcaaaatg atttgcatac atttgctaat 1140

caagtagatg gagaaattga gctaatgaaa cgttataaag aggatttgaa tctaataaat 1200

aatagtatta aaaaattatt gactgaagtt gatactagta acactcagtc tcaaaaagat 1260

acattaagac gactaaaaaa tgtaacaaat caactcgaag aacaagtcca taaattttaa 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 tgaagggtta aagaaagcgt tggctgcaac tggctctcat 180

attcttgtaa tggatttgta cgcaaaaact atgattaagc aaccgaatgt aaatttatcc 240

aacattgatt taggttcagg aggaggagaa ttaatcaaaa atatccacct gaatcaggaa 300

ctgtcacgaa tcaatgcaaa ttactggtta gatacagcga agccaaacat tcaaaaaaca 360

gctcgtaata ttgtaaatta tgatgagcaa ttccaaaatt attacgacac attagtagat 420

actgtaaaaa agaaagataa gatgagcctt aaagaaggaa taggggattt aatcgataca 480

attcatacaa attcaaatga agttactgac gtcattaaga tgttagaggc tttcaaaaca 540

aagttgtata caaatactgt agattttaaa aataatgttg gtggtccaga tggacaggga 600

ggattgacgg ctatattagc gggaaaacaa gcactagtcc cacaacttca ggccgaaatt 660

gagaatttac gttctacaca gaaatcacat tttgataatg tattagcctg gtcaattggc 720

ggtggactag gagcagctat tttagttatt ggaacgattg caggagcggt agtaattgtt 780

gtgactggtg gtacagctac accagctgtt gttggcggtc ttacagctct aggagcagct 840

ggtatcggtt taggaacagc agctggtgtc gaggcatcta atcatatgaa ttcttataat 900 gaaatttcga ataaaatcgg agaattaagt atgaaagctg atctggctaa tcaagcggtt 960

atttcactta ctaatacgaa agacactcta acatatttgt atcagacagt ggatcaagca 1020

ataatgtctc taacaagtat tcagcaacaa 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
<213> ORGANISM: Bacillus thuringiensis

<400> SEQUENCE: 26

atgatgaaat ttccatttaa agttataacc ttagctactt tagcaacgat tataaccgct 60

acaaatggta gtactattca tgcacttgca caagaacaga cagctcaaga acagaaaata 120

gaaaattatg cgttaggacc tgaaggatta aagaaagcgt tggctgaaac aggctctcat 180

attcttgtaa tggatttgta cgcaaaaact atgattaagc aaccgaatgt aaatttatcc 240

aacattgatt taggttcggg tggagaagaa ttaatcaaaa atattcacct gaatcaagaa 300

ctgtcacgaa tcaatgcaaa ttactggtta gatacagcga agccaaacat tcaaaaaaca 360

gcacgtaata ttgtaaatta tgatgagcaa tttcaaaatt attacgacac attagtagat 420

actgtaaaaa agaaggataa ggtgagcctc aaagaaggaa taggggattt aatctataca 480

attcatacaa attcaaatga agttacggaa gtcattaaga tgttagaggc tttcaaaaca 540

aagttgtata caaatactgt agattttaaa aataatgttg gtggtccaga tggacaggga 600

ggattgacgg ctatattagc gggaaaacaa gcgctagtcc cacaacttca ggccgaaatt 660

gagaatttac gttctacaca gaaaacacat tttgataatg tattagcctg gtcaattggt 720

ggtggattag gagcagctat tttagttatt ggaacgattg caggagcggt agtaattgtt 780

gtgactggtg gtacagctac gccagctgtt gttggtggtc ttacagctct aggagccgct 840

ggtatcggtt taggaacagc agctggcgtc gaggcatcta atcatatgaa ttcttataat 900

gaaatttcga ataaaatcgg agaattaagt atgaaagctg atttggctaa tcaagcggtt 960

atttcactta ctaatacgaa agacactcta acatatttgt atcagacagt ggatcaagca 1020

ataatgtctc taacaagtat tcagcaacaa tggaataaaa tgggggctaa ttataaagat 1080

ttatatgata atatcgatca aatgcaagaa cataaacttt cgttaatacc tgacgattta 1140

aaagctgcta aacaaagttg gaatgatatt cataaggatg cagaattcat ttcaaaagac 1200

attgctttta aacaagaaaa aacaaactag 1230

<210> SEQ ID NO 27
<211> LENGTH: 1215
<212> TYPE: DNA
<213> ORGANISM: Bacillus cereus

<400> SEQUENCE: 27

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 caaaaatatc 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 gaggctttca aaacaaagtt gtatacaaat 540

actgtagatt ttaaaaataa tgttggtggt ccagatggac agggaggatt gacagctata 600

ttagcgggaa aacaagcact agtcccacaa cttcaggccg aaattgagaa tttacgttct 660

acacagaaat cacattttga taatgtatta gcctggttaa ttggcggtgg actaggagca 720

gctattttag ttattggaac gattgcagga gcggtagtaa ttgttgtgac tggtggtaca 780

gctacaccag ctgttgttgg cggtcttaca gctctaggag cagctggtat cggtttagga 840

acagcagctg gtgtcgaggc atctaatcat atgaattctt ataatgaaat ttcgaataaa 900

atcggagaat taagtatgaa agctgatctg gctaatcaag 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 ttttaaacaa 1200

gaaaaaacaa 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 caaaaatatc 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 gaggctttca aaacaaagtt gtatacaaat 540

actgtagatt ttaaaaataa tgttggtggt ccagatggac agggaggatt gacagctata 600

ttagcgggaa aacaagcact agtcccacaa cttcaggccg aaattgagaa tttacgttct 660

acacagaaat cacattttga taatgtatta gcctggttaa ttggcggtgg actaggagca 720

gctattttag ttattggaac gattgcagga gcggtagtaa ttgttgtgac tggtggtaca 780

gctacaccag ctgttgttgg cggtcttaca gctctaggag cagctggtat cggtttagga 840

acagcagctg gtgtcgaggc atctaatcat atgaattctt ataatgaaat ttcgaataaa 900

atcggagaat taagtatgaa agctgatctg gctaatcaag 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 ttttaaacaa 1200

gaaaaaacaa 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 acaaaaaata 120

gaaatttata cattaggacc tgaagggcta aagaaagaat tggctaaaac cggatctaat 180

attctcgtaa tggacttgta cgcaaaaaca atgattaaac agccaaacgt aaacttatcc 240

agtattgatt taggttcagg aggagaagaa ttaatcaaaa acattcaatt gaatcaggaa 300

ttatcacgaa tcaatgcaag ttactggtta gatacagcga agccaaagat tcaaaaaaca 360

gtacgtaaca ttgtaaatta tgatgagcaa tttcaaaatt attacgacac attagtagat 420

actgtaaaaa agaatgataa gatgaacctc aaagaaggaa taggggattt aatccataca 480

attcatacaa attcaaatga agttacggaa gtcattaaga tgttagaggc tttcaaaaca 540

aagttgtata caaatactgt agactttaaa aataatgttg ggggccctga tggtaagggt 600

ggattaacgg ctatactagc cggaaaacag gcattggttc cacaacttca ggctgaaatt 660

gagaatttac gttctacgca gaaattacat tttgataatg tattagcctg gtcaattggt 720

ggtggattag gagcagctat tttagttatt ggagcgattg caggagcggt agtaattgtt 780

gtgactggtg gtacagctac accagctgtt gttggcggtc ttacagctct aggagcagct 840

ggtatcggtt taggaacagc agctggtgtt gaggcatcta atcatatgaa ttcctataat 900

gaaatttcaa ataaaatcgg agaattaagt atgaaagctg atttagctaa ccaagcggtt 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 aacaaactga 1230

<210> SEQ ID NO 30
<211> LENGTH: 1227
<212> TYPE: DNA
<213> ORGANISM: Bacillus weihenstephanensis

<400> SEQUENCE: 30

atgaaatttc catttaaggt cataactttg gccactttag caacggttat aactgctacg 60

aatggtagta ctattcacgc acttgcacaa gaacagacag cacaagaaca gaaaatagaa 120

aattatgcgt taggacctga agggttaaag aaagtgttgg ctaaaacagg ctctcatatt 180

cttgtaatgg atttgtacgc aaaaacaatg attaagcaac cgaatgtaaa tttatccaac 240

attgatttag gttcaggagg gggagaatta atcaaaaaca ttcacctgaa tcaagaactg 300

tcacgaatca atgcaaatta ctggctagat acagcgaagc caaacattca aaagacagca 360

cgtaatattg taaattatga tgaacaattt caaaattatt acgacacact agtagatact 420

gtaaaaaaga aagataaggc gggcctcaaa gaaggaatag gggatttaat cggtacaatt 480

catacaaatt caaatgaagt tacggaaatt attaagatgt tagaagcttt caaaacaaag 540

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ttgtatacaa atactgtaga ttttaaaaat aatgttggag gtccagatgg acaaggggga 600

ttaacggcta tattagcggg aaaacaagca ctagtcccac aacttcaggc cgaaattgag 660

aatttacgtt ctacgcagaa agcacatttt gataatgtat tagcctggtc aattggtggt 720

ggattaggag cagctatttt agttattgga acgattgcag gagcggtagt aattgttgtg 780

accggtggca cagcgacacc agctgttgtt ggtggtctaa cggctctagg ggcagctggt 840

atcggtttag gaacagcagc tggtgttgag gcatctaatc atatgaactc ctataatgaa 900

atttcgaata aaattggaga attaagtatg aaagctgatt tagctaacca agcagttatt 960

tcacttacta atacaaaaga cactttaaca tatttgtatc aaacagttga tcaagcaatt 1020

atgtctctaa caagtattca gcaacaatgg aatacgatgg gagcgaatta taaagatcta 1080

tatgataata tcgaccaaat gcaagaacat aaactttctt taatacctga tgatttaaag 1140

gctgcaaaac aaagttggaa tgatattcat aaggatgcag aattcatttc aaaagacatt 1200

gcttttaaac aagaaaaaac aaattaa 1227

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

<400> SEQUENCE: 31

gtgaataata attttcctta taaactactt gctgtatcga cgtttttaac cctgacaaca 60

actactgtag tttcaccagt agctgctttt gcaagtgaaa gtaaaataga acaaaccagt 120

acggaagata tatctctttc tgtaaacagt gaaaagatga aaaaagcttt gcaagatgct 180

ggggtatttg caaaatccat gaatgattac tcttatttgt taattaataa tccagatgtt 240

aactttgaag gaattgatat taaaggatat acaaatctac ctagtcaaat tgcacaagat 300

caaaagaatg caagagagca tgctacaaaa tgggatgctc acataaaaaa acaactttta 360

gataccctta caggaattgt agagtatgat accacatttg acaattatta cgatacatta 420

gtagaagcaa ttaatgaagg agatgcagat acattaaaag aaggcattac agatttacaa 480

ggtgagatta aacaaaacca agcatataca cagaatttaa ttcaagaact agctaagtta 540

agagatagta ttggagaaga tgtccgagca tttggaggtc ataaagatat cttgcaatcg 600

attttaaaaa atcaagcatc tggaatagat gaagatgaaa aacgcctaaa tgatgtttta 660

gagcaaataa gacattttaa acaagtagaa tcggatggaa taataactgt atcatatcct 720

tcaatcccta catggattgc tggaggtgtg atgatagggg tagcaagaaa taatttaggt 780

acgttagagc cgttattagt gcaattacgc caaaccgtag actataaaat aacattaaat 840

cgtgtagttg gagttgcgta taataatatt actgaaatgc aaaatgcaat tggatcagct 900

attaatgctc ttacctatat gtcagcacaa tggcatgatt tagattctca atattcagga 960

gtgcttaatc atattgataa agcatcccaa aaagcagatc aa 1002

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

<400> SEQUENCE: 32

gtgaataata attttcctta taaactactt gctgtatcga cgtttttaac cctgacaaca 60

actactgtag tttcaccagt agctgctttt gcaagtgaaa gtaaaataga acaaaccagt 120

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acggaagata tatctctttc tgtaaacagt gaaaagatga aaaaagcttt gcaagatgct 180

ggggtatttg caaaatccat gaatgattac tcttatttgt taattaataa tccagatgtt 240

aactttgaag gaattgatat taaaggatat acaaatctac ctagtcaaat tgcacaagat 300

caaaagaatg caagagagca tgctacaaag tgggatgcgc acataaaaaa acaactttta 360

gatactctta caggaattgt agagtatgat actacatttg acaattatta cgatacatta 420

gtagaagcaa ttaatgaagg agatgcagat acattaaaag aaggcattac agatttacaa 480

ggtgagatta aaaaaaacca agcatataca aagaatttaa tacaagaact agctaagtta 540

agagatagta ttggagaaga tgtccgagca tttggaggtc ataaagatat cttgcaatcg 600

attttaaaaa atcaagcatc tggaatagat gaagatgaaa aacgtctaaa tgatgtttta 660

gagcaagtaa gacattttaa 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 gtcagcacaa 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 tccagatgtt 240

aactttgaag gaattgatat taaaggatat acaaatctac ctagtcaaat tgtacaagat 300

caaaagaatg caagagagca tgctacaaaa tgggatgcgc acataaaaaa acaactttta 360

gataccctga caggaattgt agagtatgat accacatttg acaattatta cgatacatta 420

gtagaagcaa ttaatgaagg agatgcagat acattaaaag agggcattac agatttacaa 480

ggtgagatta aacaaaacca agcatataca cagaatttaa tacaagaact agctaagtta 540

agagatagta ttggagaaga tgtccgagca tttggaggtc ataaagatat cttgcaatcg 600

attttaaaaa atcaagcatc tggaatagat gaagatgaaa aacgcctaaa tgatgtttta 660

gagcaaataa gacattttaa acaagtagaa tcggatggaa taataactgt atcatatcct 720

tcaatcccta catggattgc tggaggtgtg atgataggag tagcaagaaa taatttaggt 780

acgttagagc cgttattagc acaattacgc caaacggtag actataaaat aacattaaat 840

cgtgtagttg gagttgcgta taataatatt gctgaaatgc aaaatgcaat tggatcagct 900

attaatgctc ttacctatat gtcagcacaa 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 tccagatgtt 240

aactttgaag gaattgatat taaaggatat acaaatctac ctagtcaaat tgtacaagat 300

caaaagaatg caagagagca tgctacaaaa tgggatgcgc acataaaaaa acaactttta 360

gataccctga caggaattgt agagtatgat accacatttg acaattatta cgatacatta 420

gtagaagcaa ttaatgaagg agatgcagat acattaaaag agggcattac agatttacaa 480

ggtgagatta aacaaaacca agcatataca cagaatttaa tacaagaact agctaagtta 540

agagatagta ttggagaaga tgtccgagca tttggaggtc ataaagatat cttgcaatcg 600

attttaaaaa atcaagcatc tggaatagat gaagatgaaa aacgcctaaa tgatgtttta 660

gagcaaataa gacattttaa acaagtagaa tcggatggaa taataactgt atcatatcct 720

tcaatcccta catggattgc tggaggtgtg atgataggag tagcaagaaa taatttaggt 780

acgttagagc cgttattagc acaattacgc caaacggtag actataaaat aacattaaat 840

cgtgtagttg gagttgcgta taataatatt gctgaaatgc aaaatgcaat tggatcagct 900

attaatgctc ttacctatat gtcagcacaa 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 gcaagtgaaa gtaaaattga acaaacgagt 120

acggaaaata tatctctttc tgtaaacagc gaaaagatga aaaaagcttt gcaagatgct 180

gggggatttg caaaatccat gaatgattac tcttatttgt taattaataa tccaggtgtt 240

aactttgaag gaattgatat taaaggatat acaaatctac ctagtcaaat tatacaagat 300

caaaagaagg caagagagca tgctacaaaa tgggatacgc acataaaaaa acaactttta 360

gatacccttta caggaattgt agagtatgat accacatttg acaattatta cgatacatta 420

gtaaaagcaa ttaatgaagg agatgcagat acattaaaag aaggcattac agatttacaa 480

ggtgatatta aacaaaacca agcatataca cagaatttaa tacaagaact agctaagtta 540

agagatagta ttggagaaga tgtccgagca tttggaggtc ataaagatat cttgcaatcg 600

attttaaaaa atcaagcatc tggaatagat gaagatgaaa aacgcctaaa tgatgtttta 660

gagcaaataa gacattttaa acaagtagaa tcggatggaa taataactac atatgtaccc 720

tcgattccta catggattgc tggtggtata atgatagggg tagcaagaaa taatttaagt 780

acgttagaac cgctattagc gcagttgcgc caaacggtag actataaaat tacattgaat 840

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cgtgtagttg gagttgcgta taataatatt gctgaaatgc agaatgcaat tggatcagct    900

attaatgctc ttacctatat gtcagcacaa 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

<400> SEQUENCE: 36

atgaataaaa actttcctta taaactactt gctgtatcga cgtttttaac tctgacaaca     60

actactgtag tttctccagt ggcagccttc gcaagtgaaa gtaaaatgga acaaactagt    120

accgaagata tatctctttc tgtaaacagc gaaaagatga aaaaagcttt gcaagatgct    180

ggggtatttg caaaatccat gaatgattac tcttatttgt taattaaaaa cccagatgtt    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 agatttacaa    480

ggtgagatta aacaaaatca agcatataca cagaatttaa tacaagaact agctaagtta    540

agagatagta ttggagaaga tgtccgggca tttggaggtc ataaagatat tttgcattcg    600

attctgaaaa accaagcatc tggaattgat gaagatgaaa agcgcctaaa tgaagtttta    660

gagcaagtaa gacattttaa acaagtagaa tcagatggaa taataactgt atcaattccc    720

tcaattccta cgtggattgc tggtggtgta atgatagggg tagcaagaaa taatttaggt    780

acgttagagc cgttgttagc acaattacgt cagactatag attataaagt aacattaaat    840

cgtgtagttg gtgttgcgta taataatatt aatgaaatgc acaatgcgat tggatcggct    900

attaatgcac ttacctatat gtctgcacaa tggcatgatt tagattctca atattcggga    960

gtgcttagtc atattgataa agcatcccaa aaagcggatc aaaataaatt caaattccta   1020

aaacctaatt tgaatgcagc gaaagatagt tggaaaacat tgagagcgga 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

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
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aataattaaa ggttctatta atatcggtaa acaagtattt acaatcacaa atcaaactgc 540

acaaacgaaa acaatcgatt ttgtttctat cggtacttta agtaatgaaa ttgtaaatgc 600

tgcagatagt caaacgagag aagcagcttt tcgcattcag caaaagcaaa aagagttatt 660

gccacttatt caaaagttat cacaaactga agcagaggcg actcaaatta cattcgttga 720

agatcaagta aatagcttta cagaattaat tgatcgtcaa attacaactt tagaaacgtt 780

attaacggat tggaaagttt taaataataa tatgattcaa attcaaacaa atgttgaaga 840

aggcacgtat acagacagta gtttacttca aaaacatttt aatcaaatta aaaaagtaag 900

tgatgaaatg aataagcaaa caaatcaatt tgaagattac gttacaaacg ttgaagtaca 960

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 acactgcaag 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 tgaaatgaat 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 acactgcaag gatccagtgg agatattgtg 600

aaattaagag aagatattaa aagaattcaa ggggaaattc aagctgaact aactactatt 660

ttgaatagac ctcaagaaat tattaaaggt 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 aacggattgg aaagttttaa ataataatat gattcaaatt 1020

caaaagaatg ttgaagaagg cacgtataca gacagtagtt tacttcaaaa acatttcaat 1080

caaattaaaa aagtaagtga tgaaatgaat aagcaaacaa 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 ggaggggcaa ccagaagtga aaacagtata tgcacaaaat 120

gtaattgttc caaatacatt atccaattca attagaatgt taggatcaca gtcaccactt 180

atacaagcat atggactagt gattttacaa cagccagaca twaaggtgaa 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 aaaacggtat tagataagga tagtaacaac 540

ttatcagtta aagctgatga agcaataaaa acactacaag gatcaagtgg agatattgtg 600

aaattaagag aagatattaa aagaattcaa ggggaaattc aagctgaatt aacgactatt 660

ttgaatagac ctcaagaaat tattaaaggt 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 tcgtcaaatc 960

acaactttag aaacgttatt agcagattgg aaagttttaa acagtaatat gatccaaatt 1020

caaaagaatg ttgaagaagg cacatataca gacagtagtt tactacaaaa acatttcaac 1080

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caaattaaaa aagtaagtga tgaaatgaat 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 ggaggggcaa acagaagtga aaacagtata tgcgcaaaat 120

gtaattgctc caaatacatt atccaattca attagaatgt taggatcaca atcaccgctt 180

attcaagcat acggattaat tatcttgcaa cagccagaca ttaaggtaaa tgcgatgagt 240

agcttaacga atcatcaaaa gtttgcaaag gcgaatgtac 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 aaatcgattt aaaacagtat tagacaaaga tagtaacaac 540

ttatcaatta aagccgatga agcaataaaa acactgcaag 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 tacgtataca gacagtagtt tacttcaaaa acatttcaat 1080

caaattaaaa aagtaagtga tgaaatgaat aagcaaacaa 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 agggttattg gttacagcag 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 atcaccaaaa atttgcaaag gcaaatgtaa gagagtggat tgatgaatat 300

aatccgaagt taatcgactt aaatcaagag atgatgaggt atagtactag atttaatagc 360

tattatagta agctctatga actagcagga aaagtcaatg aagatgaaca agcaaaagca 420

gattttacaa atgcatatgg aaaattacaa ttgcaagtac aaagcatcca agagagtatg 480

gagcaagatt tattagagtt aaatcgattt aaatcggtat tagataaaga tagtaataac 540

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ttatcaatta aagctgatga agcaataaaa acactgcaag gatcaagtgg agatattgtg 600

aaattaagag aagatattaa aagaattcaa ggggaaattc aagctgaatt aactactata 660

ttgaatagac ctcaagaaat tattaaaggt tctattaata tcggtaaaca 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 gatccaaatt 1020

caaaagaatg ttgaagaagg cacgtataca gatagtagtt tacttcaaaa acatttcaat 1080

caaattaaaa aagtaagtga tgaaatgaat 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 tgaaatgaat 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

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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

ttatcaatta aagccgatga agcaataaaa acactgcaag gatcaagtgg agatattgtg 600

aaatcaagag aagatattaa aagaattcaa ggtgaaattc aagctgaatt aactactatt 660

ttgaatagac ctcaagaaat cattaaaggt tctattaata ttggtaaaca agtatttaca 720

atcacaaatc aaactgcaca aacgaaaaca atcgattttg tttctatcgg tactttaagt 780

aatgaaattg taaatgctgc agatagtcaa acgagggaag cagctcttcg cattcaacaa 840

aagcaaaagg agttattgcc acttattcaa aagttatcac aaactgaagc agaggcgact 900

caaattacat tcgttgaaga tcaagtaagt agctttacag aattaattga tcgtcaaatt 960

acaactttag aaacgttatt aacggattgg aaagttttaa ataataatat gattcaaatt 1020

caaacaaatg tcgaagaagg cacgtataca gacagtagtt tacttcaaaa acatttcaat 1080

caaattaaaa aagtaagtga tgaaatgaat aagcaaacaa atcaatttga 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 atttgcagca 60

ggaaatatta tgccggctca tacgtatgca gctgaaagta cagtgaaaca 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 tgctgcggta 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 attggtggtg cagtagttat tgctacgggc 780

gcaggaacac cgctaggagt cgcattaatt gcaggtggtg cagcagctgt aggcggtggt 840

acagctggta tcgtattagc gaagaaagaa cttgacaatg cacaagctga aattcaaaaa 900

ataactggac aaattacaac tgctcaatta gaagtagctg ggttaacgaa cattaaaaca 960 caaactgagt atttaacaaa tacgattgat actgcaatta cagcgttgca aaacatttca 1020

aaccaatggt atacaatggg atcaaaatac aattctttac ttcaaaatgt ggattcaatt 1080

agtccaaacg atcttgtttt cattaaagaa gatttaaaca 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

<400> SEQUENCE: 46

atgacaaaaa aaccttataa agtaatggct ctatcagcac ttatggcagt atttgcagca 60

ggaaatatta tgccggctca tacgtatgca gctgaaagta cagtgaaaca agctccagtt 120

catgcggtag caaaagctta taatgactat gaagaatact cattaggacc agaaggcttg 180

aaagatgcaa tggaaagaac aggttcaaat gctttagtaa tggatctgta cgctttaaca 240

attattaaac aaggtaatgt taactttgga aatgtatcgt ctgttgatgc ggctttaaaa 300

gggaaagtaa ttcagcacca agatacagct agaggaaatg cgaagcaatg gttagatgta 360

ttaaaaccac agcttatttc aacaaatcaa aatatcatta actacaatac gaaattccaa 420

aactattatg atactttagt tgctgcagtt gatgcaaaag ataaagcgac tcttacgaaa 480

ggcttaacta gattatcaag tagtattaat gaaaataaag cacaagtgga tcagttagta 540

gaagacttga agaaattccg aaataaaatg acttcggata cgcaaaactt caagggtgat 600

gcaaatcaaa ttacatctat attagctagt caagatgcag ggattccgct tctgcaaaat 660

caaattacaa cgtacaatga agcaattagt aaatataatg caattattat cggttcatct 720

gttgcgacag ctctaggacc aattgcaatt atcggtggtg cagtagttat tgctacgggc 780

gcaggaacac cgctaggagt agcattaatt gcaggtggtg cagcagctgt aggcggtggt 840

acagctggaa tcgtattagc gaagaaagag cttgataatg cacaagcaga aattcaaaag 900

ataacaggac aagttacaac tgcgcaatta gaagtagcag gattaacgaa cattaaaaca 960

caaacagagt atttaacaaa tacaattgat actgcaatta cagcgttaca aaatatttca 1020

aaccaatggt acacaatggg atcaaaatac aattctttac ttcaaaatgt agattctatt 1080

agtccaaatg acctagtttt cattaaagaa gatttaaaca ttgcgaaaga tagctggaaa 1140

aacattaaag actatgcaga aaagatttat gctgaagata ttaaagtagt agatacgaaa 1200

aaagcataa 1209

<210> SEQ ID NO 47
<211> LENGTH: 1209
<212> TYPE: DNA
<213> ORGANISM: Bacillus cereus

<400> SEQUENCE: 47

atgacaaaaa aaccttataa agtaatggct ctatcagcac ttatggcagt atttgcagca 60

ggaaatatta tgccggctca tacgtatgca gctgaaagta cagtgaaaca agcgccagtt 120

catgcggtag caaaagctta taatgactat gaagaatact cattaggacc agaaggcttg 180

aaagatgcaa tggaaagaac aggttcaaat gctttagtag tggatctgta cgctttaaca 240

attattaaac aaggtaatgt taactttgga aatgtatcgt ctgttgatgc ggctttaaaa 300

gggaaagtaa ttcagcacca agatacagct agaggaaatg cgaagcaatg gttagatgta 360

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ttaaaaccac agcttatttc aacgagtcaa aatatcatta actacaatac gaaattccaa    420

aactattatg atactttagt tgctgcagtt gatgcaaagg ataaagcaac tcttacgaaa    480

ggcttaacta gattatcaag tagtattaat gaaaataaag cgcaagtgga tcagttagta    540

gaagacttga agaaattccg aaataaaatg acttcggata cgcaaaactt caagggtgat    600

gcaaatcaaa ttacatctat attagctagt caagatgcag gaattccgct tctgcaaaat    660

caaattacaa cgtacaatga agcaattagt aaatataatg caattattat cggttcatct    720

gttgcgacag ctctaggacc aattgcaatt atcggtggtg cagtagttat tgctacgggc    780

gcaggaacac cgctaggagt agcattaatt gcaggtggtg cagcagctgt aggcggtggt    840

acagctggaa tcgtattagc gaagaaagag cttgataatg cacaagcaga aattcaaaag    900

ataacaggac aagttacaac tgcgcaatta gaagtagcag gattaacgaa cattaaaaca    960

caaacagagt atttaacaaa tacaattgat actgcaatta cagcgttaca aaatatttca   1020

aaccaatggt acacaatggg atcaaaatac aattctttac ttcaaaatgt agattctatt   1080

agtccaaacg acctagtttt cattaaagaa gatttaaaca ttgcgaaaga tagctggaaa   1140

aacattaaag actatgcaga aaagatttat gctgaagata ttaaagtagt agatacgaaa   1200

aaagcataa                                                           1209
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<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 tgccggctca tacgtatgca gcggagagta cagtgaagca agctccagtt    120

catgcggccg caaaagctta taatgattat gaggaatatt cattaggacc agaaggccta    180

aaagatgcaa tggaaagaac gggttcaaac gctttagtaa tggatctgta cgctttaaca    240

attattaaac aaggtaatgt taactttgaa atgtatcgtc tgttgatgcg gctttaaaag    300

ggaaagtgat tcagcaccag gatacagcta gaggaaatgc gaagcaatgg ttagatgtac    360

taaagccaca gcttatttca acgaatcaaa atatcattaa ttacaatacg aaattccaaa    420

actattacga tactttagtt gctgcggtag atgcaaaaga taaagcgact cttacgaaag    480

gtttaactag attatcaagt agtattaatg aaaataaagc gcaagtagat cagttagtag    540

atgacttgaa gaaattccga aataaaatga cgtccgatac gcaaaacttt aagggagacg    600

caaatcaaat tacatctatt ttagctagtc aagatgcagg aatcccgctt ctgcaaaatc    660

aaattacaac gtacaatgaa gcaattagta aatataatgc aattattatc ggttcatcag    720

ttgcgacagc tctagggcca attgccatta ttggtggtgc agtagtgatt gctacaggtg    780

caggaacgcc gttaggagtc gcgttaattg caggtggtgc agcagctgta ggcggtggca    840

cagctggtat cgtattagcg aagaaagaac ttgataatgc acaagctgaa attcaaaaaa    900

taacaggaca agttacaact gctcaattag aagtagctgg gttaacgaac attaagacac    960

aaacggagta tttaacaaat acaattgata ctgcaattac agcgttgcaa aacatttcaa   1020

accaatggta cacaatggga tcaaaataca 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 tgccggctca tacgtatgca gctgaaagta cagtgaaaca agctccagtt 120

catgcggtag caaaagctta taatgactat gaagaatact cattaggacc agaaggcttg 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

aactattatg atactttagt tgctgcagtt 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 cggttcatct 720

gttgcgacag ctctaggacc aattgcaatt atcggtggtg cagtagttat tgctacgggt 780

gcaggaacac cgctaggagt agcattaatt gcaggtggtg cagcagctgt aggcggtggt 840

acagctggaa tcgtattagc gaagaaagag cttgataatg cacaagcaga aattcaaaag 900

ataacaggac aagttacaac tgcgcaatta gaagtagcag gattaacgaa cattaaaaca 960

caaacagagt atttaacaaa tacaattgat actgcaatta cagcgttaca aaatatttca 1020

aaccaatggt acacaatggg atcaaaatac aattctttac ttcaaaatgt ggattcaatt 1080

agtccaaacg atcttgtttt cattaaagaa gatttaaaca ttgcgaaaga tagctggaaa 1140

aacattaaag actatgcaga aaagatttat 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 atttgcagca 60

gggaatatta tgccggccca tacgtatgca gctgaaagta cagtgaaaca agctcccgta 120

catgcggtcg caaaagctta taatgactat gaagaatact cattaggacc agaaggctta 180

aaagatgcaa 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 cccaaaactt caagggtgat 600 gcaaatcaaa ttacatctat tttagctagt caagatgctg gaatcccact tctgcaaaat 660

caaattacaa cgtacaatga agcgattagt aaatataatg caattattat cggttcatca 720

gttgcgacag ctctagggcc aattgcaatt atcggtggtg cagtagttat tgctacaggt 780

gcaggaacgc cactaggagt cgcattaatt gcaggaggcg cagcggctgt aggcggtggt 840

acagctggaa tcgtattagc gaagaaagag cttgataatg cacaagctga aattcaaaaa 900

ataactggac aaattacaac tgctcaatta gaggtagcag gattaacaaa cattaaaaca 960

caaactgagt atttaacaaa tacaattgat actgcaatta cagcgttgca aaatatttca 1020

aatcaatggt acacaatggg atcaaaatac aattctctac ttcaaaatgt agattcaatt 1080

agtccaaacg accttgtttt cattaaagaa gatttaaaca ttgcgaaaga tagctggaaa 1140

aacattaaag actatgcaga aaagatttat gctgaagata ttaaagtagt agatacgaaa 1200

aaagcataa 1209

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

<400> SEQUENCE: 51

atgacaaaaa aaccttataa agtaatggct ctatcagcac ttatggcagt atttgcggca 60

gggaatatta tgccgaccca tacgtatgca gctgaaagta cagtgaaaca 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 gaatcccgct tctgcaaaat 660

caaattacaa cgtacaatga agcaattagt aaatataatg caattattat cggttcatca 720

gttgcgacag ctctagggcc aattgcaatt atcggtggtg cagtagttat tgctacaggt 780

gcaggaacgc cactaggagt cgcattaatt gcagggggcg cagcggctgt aggtggtggt 840

acagctggaa tcgtattagc gaagaaagag cttgataatg cacaagctga gattcaaaaa 900

ataactggac aaattacaac tgctcaatta gaggtagcag gattaacaaa cattaaaaca 960

caaacggagt atttaacaaa tacaattgat actgcaatta cagcgttgca aaatatttca 1020

aatcaatggt acacaatggg atcaaaatac aattctttac ttcaaaatgt agattcaatt 1080

agtccaaacg accttgtttt cattaaagaa gatttaaaca ttgcgaaaga tagctggaaa 1140

aacattaaag actatgcaga aaagatttat gctgaagata ttaaagtagt agatacgaaa 1200

aaagcataa 1209

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

<400> SEQUENCE: 52

atgacaaaaa aaccttataa agtaatggct ctatcagcac ttatggcagt atttgcagca 60

ggaaatatta tgccggctca 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

aactattatg atactttagt tgctgcagtt gatgcaaagg ataaagcgac tcttacgaaa 480

ggcttaacta gattatcaag tagtattaat gaaaataaag cacaagtgga tcagttagta 540

gaagacttga agaaattccg aaataaaatg acttcggata cgcaaaactt caagggtgat 600

gcaaatcaaa ttacatctat attagctagt caagatgcag gaattccgct attacaaaat 660

caaattacaa cgtacaatga agcaattagt aaatataatg caattattat cggttcatct 720

gttgcgacag ctctaggacc aattgcaatt atcggtggtg cagtagttat tgctacgggc 780

gcaggaacac cgctaggagt agcattaatt gcaggtggtg cagcagctgt aggcggtggt 840

acagctggaa tcgtattagc gaagaaagag cttgataatg cacaagcaga aattcaaaag 900

ataacaggac aagttacaac tgcgcaatat gaagtagctg gattaacgaa cattaaaaca 960

caaacagagt atttaacaaa tacaattgat actgcaatta cagcgttaca aaatatttca 1020

aaccaatggt acacaatggg atcaaaatat aattctttac ttcaaaatgt ggattcaatt 1080

agtccaaacg accttgtttt cattaaagaa gatttaaaca 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 taagttcgat taatagtgaa tttaaaggga gtatgattca gcatcaaaga 300

gatgcaaaaa ttaatgcagc atattggtta aataatatga agcctcaaat tatgaaaaca 360

gatcaaaata ttataaatta caataatact tttcaatcgt attataatga catgttaata 420

gcgattgatc aaaaggatag tggaaaatta aaagcggatt tagaaaagtt gtatgcggat 480

attgtaaaga atcaaaatga ggtagatgga ttattaggaa atttgaaagc ttttcgcgat 540

agaatggcga aagatacaaa tagtttcaaa gaggatacaa atcagttaac agcgatattg 600

gcaagtacga atgctggtat tccagctcta gagcaacaaa taaatacata taacgattcg 660

attaaaaaga gtaatgatat ggtcattgct ggtggcgtac tttgcgtagc tctaataaca 720

tgtcttgctg gcgggccgat gattgcggtt 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

atgcagaaac gattttataa aaaatgtctt ttagcggtaa tgattgctgg ggtggcaacg 60

agtaacgcat ttcctttaca tccttttgca gcagaacaaa atgtaaaggt gctacaagaa 120

aatgtgaaaa actattctct tggaccagct ggattccaag atgtaatggc acaaacgaca 180

tcaagtatat ttgcaatgga ttcatatgca aaattaattc aaaatcaaca agagacggat 240

ttaagtaaaa taagttcgat taatagtgaa tttaaaggga atatgattca gcatcaaaga 300

gatgcaaaaa ttaatgcagc atattggtta aataatatga agcctcaaat tatgaaaacg 360

gatcaaaata 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 atgctggtat tccagctcta gagcaacaaa taaatacata taacgattcg 660

attaaaaaga gtaatgatat ggtcattgct ggtggcgtac tttgcgtagc tctaataaca 720

tgtcttgctg gtgggccgat gattgcggtt gcgaaaaaag atatcgcaaa tgcagaaaga 780

gaaatcgcca atttaaaaga tagaatttca ggagcacaag cagaagtcgt aattttgact 840

gatgtaaaaa ataaaacaac aaacatgaca gaaacaattg atgcagcaat tacagcacta 900

caaaacatat caaatcaatg gtatacagta ggtgcaaaat ataataattt actacaaaac 960

gtaaaaggaa ttactccaga agagtttacg tttataaaag aagatttaca tacagcgaaa 1020

gatagctgga aagatgtaaa ggattataca gaaaaattac atgaaggtgt ggcgaagtaa 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

agtaacgcat ttcctttaca tccttttgca gcagaacaaa atgtaaaggt gctacaagaa 120

aatgtgaaaa actattctct tggaccagct ggattccaag atgtaacggc acaaacgaca 180

tcaagtatat ttgcaatgga ttcatatgca aaattaattc aaaatcaaca agagacggat 240

ttaagtaaaa taagttcgat taatagtgaa tttaaaggga atatgattca gcatcaaaga 300

gatgcaaaaa ttaatgcagc atattggtta aataatatga agcctcaaat tatgaaaacg 360

gatcaaaata ttataaatta caataatact tttcaatcgt attataatga catgttaata 420

gcgattgatc aaaaggatag cggaaaatta aaagcggatt tagaaaagtt gtatgcggat 480

attgtaaaga atcaaaatga ggtagatgga ttgttaggaa atttgaaaag ttttcgcgat 540

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agaatggcga aagatacaaa tagtttcaaa gaggatacaa atcagttaac agcgatattg 600

gcaagtacga atgctggtat tccagctcta gagcaacaaa taaatacata taacgattcg 660

attaaaaaga gtaatgatat ggtcattgct ggtggcgtac tttgcgtagc tctaacaaca 720

tgtcttgctg gtgggccgat gattgcggtt gcgaaaaaag atatcgcaaa tgcagaagga 780

gaaatcgcca atttaaaaga tagaatttca ggagcacaag cagaagtcgt aattttgact 840

gatgtaaaaa ataaaacaac aaacatgaca gaaacaattg atgcagcaat tacagcacta 900

caaaacatat caaatcaatg gtatacagta ggtgcaaaat ataataattt actacaaaac 960

gtaaaaggaa ttactccaga agagtttacg tttataaaag aagatttaca tacagcgaaa 1020

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 attattcgtt agggccagct ggattccaag atgtaatggc gcaaacgaca 180

tcgagcatat tcgcaatgga ctcctatgca aaattaattc aaaatcagca agagactgat 240

ttgagtaaaa taagttcgat taatagtgag tttaaaggaa atatgattca gcaccaacga 300

gatgcaaaaa ttaacgcggc gtattggtta gatcatatga agccgcaaat tatgaaaacg 360

gatcaaaata ttattgatta caataatact tttcaagcgt attatagtag catgctaata 420

gcaattgatc aaaaagatag cgtaaagtta aaagcggatt tagaaacatt gtatgcggat 480

attgtaaaga atcaaaatga ggtagatgta ttattaggta atttgaaagc ctttcgcgat 540

agaatggcga aagatacaaa tagctttaaa gcggatacaa atcaactaac ctcgatttta 600

gcaagtacga atgctggtat tccagcttta gagcaacaaa tcaatacata taacgattca 660

attaaaaaga gtaatgatat ggttatcgct ggtggtgtac tttgtgtagc gttaataaca 720

tgccttgctg gcggaccgat gattgccgtt gcgaaaaaag atattgcaaa tgcagaaaga 780

gaaattgcca atttaaagga tagaatttct ggcgcacaag cagaggtcgc aattttgaca 840

gatgtaaaaa ataaaacaac aaacatgact gaaacgattg atgcagcaat tacagcattg 900

caaaatatat cgaatcaatg gtatacagta ggggcaaaat ataataattt actacaaaac 960

gtaaaaggaa ttagtccgga agaatttacc ttcataaaag 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 aaaatcaaca agagacggat 240

ttaagtaaaa taagttcgat taatagtgaa tttaaaggaa atatgattca gcatcaaaga 300

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gatgcaaaaa ttaatgcagc atattggtta aataatatga agcctcaaat tatgaaaaca 360

gatcaaaata 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 atgctggtat tccagctcta gagcaacaaa taaatacata taacgattcg 660

attaaaaaga gtaatgatat ggtcattgct ggtggcgtac tttgtgtagc attaataaca 720

tgtcttgctg gcgggccaat gatcgcggtt gcgaaaaaag atatcgcaaa tgcagaaaga 780

gaaatcgcta atttaaaaga tagaatttca ggagcgcaag cagaagtctt aattttgact 840

gatgtaaaaa ataaaacaac aaacatgaca gaaacaattg atgcagcaat tacagcacta 900

caaaacatat caaatcaatg gtatacagta ggtgcaaaat ataataattt actacaaaac 960

gtaaaaggaa ttagtccgga agagtttacg tttataaaag aagatttaca tacagcgaaa 1020

gatagctgga aagatgtaaa ggattataca gaaaaattac atgaaggcgt ggcgaagtaa 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 tggtccagca ggattccaag atgtaatggc acaaacaaca 180

tcgagcatat tcgcaatgga ttcatatgca aagttaatcc aaaatcagca agaaacggat 240

ttaagcaaaa taagttcgat taatagtgag tttaaaggaa atatgatgca gcaccaacga 300

gatgcaaaaa ttaacgcggc gtattggtta gatcatatga agccgcaaat tatgaaaacg 360

gatcaaaata 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 gattgccgtt gcgaaaaaag atattgcaaa tgcagaacga 780

gaaatcgcta atttaaaaga tagaatttct ggagcgcaag cagaagtcgc aattttgaca 840

gatgtaaaaa ataaaacaac aaatatgact gaaacgattg atgcagcaat tacagcacta 900

caaaacatat caaatcaatg gtatacagta ggtgcaaaat ataataattt actacaaaac 960

gtaaaaggaa ttagtccgga agagtttacg tttataaaag aagatttgaa tacagcgaaa 1020

gatagttgga aagacgtaaa agattataca gaaaaattac atgaaggcgt agcgaagtaa 1080

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

<400> SEQUENCE: 59

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atgcagaaac gattttataa aaaatgtctt ttaacattaa tgattgctgg agtggcaacg 60

agtaacgcat ttcctttaca tacttttgca gcagaacaaa acgtaaaagt actacaagaa 120

aatgcgaaag attattctct tggtccagca ggattccaag atgtaatggc acaaacaaca 180

tcgagcatat tcgcaatgga ttcatatgca aatttaatcc aaaatcagca agaaacggat 240

ttaagcaaaa taagttcgat taatagtgag tttaaaggga atatgatgca gcaccaacga 300

gatgcaaaaa ttaacgcggc gtattggtta gatcgtatga agccgcaaat tatgaaaacg 360

gatcaaaata ttattaatta caataatact tttcaaacgt attataatag tatgttaata 420

gcgattgatc aaaaggatag tgtaaagtta aaagctgatt tagaaaagtt gtatgccgat 480

attgtaaaga accaaaatga ggtagatgta ttattaaggg atttgaaagc ttttcgtgat 540

agaatggcga aagacacaaa tagttttaag gaagatacaa atcaattaac agcgatttta 600

gcaagtacga atgctggtat tccagcttta gagcaacaaa tcaatacata taatgattca 660

atcaaaaaga gtaatgatat ggtcattgct ggtggtgtac tttgcgtagc gttaataaca 720

tgtcttgctg gcggaccaat gattgccgtc gcgaaaaaag atattgcaaa tgcagaaaga 780

gaaatcgcta atttaaagga tagaatttct ggagcacaag cagaagttgc aattttaact 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 atgtaaaggt actacaagaa 120

agtgtgaaaa actattctct tggaccagct ggattccaag atgtaatggc acaaacgaca 180

tcgagtatat ttgcaatgga ttcatatgca aaattaattc aaaatcaaca agagacggat 240

ttaagtaaaa taagttcgat taatagtgaa tttaaaggga atatgattca gcatcaaaga 300

gatgcaaaaa ttaatgcagc atattggtta aataatatga agcctcaaat tatgaaaacg 360

gatcaaaata ttataaatta caataatact tttcaatcgt attataacga catgttaata 420

gcgattgacc aaaaggatag cggaaaatta aaagcggatt tagaaaagtt gtatgcggat 480

attgtaaaga atcaaaatga ggtagatgga ttattaggaa atttgaaagc ttttcgcgat 540

agaatggcga aagatacaaa tagtttcaaa gaggatacaa atcagttaac agcgatattg 600

gcaagtacga atgctggtat tccagctcta gagcaacaaa taaatacata taacgattcg 660

attaaaaaga gtaatgatat ggtcattgct ggtggcgtac tttgcgtagc gctaataaca 720

tgtcttgctg gcgggccgat gattgcggtt gcaaaaaaag atatcgcaaa 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

atgaaacgtt ctaaaacata tgtaaaatgt ctcgcattat ctgctgtgtt ggcaagtagt 60

gccctagcaa tgcacacacc ggttgtcgct gcacaaacaa cttctcaagt tgtaacagat 120

atcggtcaaa atgcaaaaac acatacaagc tacaatacat ttaataatga acaagcagat 180

aatatgacaa tgtcattaaa agtaactttc attgatgatc caagtgctga taagcaaatt 240

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 caagcggtcc tagtggcgaa tctggagcaa caggtcaagt aacttggtct 540

gattccgtca gttataaaca aacaagctat aaaacaaact taattgatca aacaaataaa 600

catgtaaaat ggaacgtatt ctttaatgga tataataatc aaaactgggg catttacact 660

cgcgattctt accatgcttt atatggaaac caattattta tgtattctcg tacgtatcct 720

catgaaacag atgcacgagg caatctagtc ccaatgaatg accttccagc tctcacaaat 780

agcggtttct ctccaggcat gattgctgtt gtcatttcag aaaaagatac agaacagtct 840

tctatccaag ttgcttatac aaagcatgct gacgattata cacttcgccc tggctttaca 900

ttcggaactg gtaactgggt tggaaataat ataaaagatg tagatcaaaa aacatttaat 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

atgaaacgtt ctaaaaccta cttaaaatgt ttagcattat ccgctgtttt tgctagtagt 60

gctgtaactc tttcaacacc tgctacttac gctcaaacga cgtcacaagt tgtaacagat 120

atcgggaaaa atgcaaaaac acatacgagc tataatacat ttaataatga tcaagctgat 180

aatatgacaa tgtctttaaa ggtaactttt atcgatgatc caagcgctga taaacagatt 240

gccgttatta atacaactgg tagttttcta aaagcaaatc ctactataag tgatgcacct 300

attgataact acccaatccc tggcgctagt gcaacattac gttatccttc acaatatgat 360

gttgcattta accttcaaga taacagcgct cgtttcttta acgtagcgcc tacaaatgct 420

gtagaagaaa cgactgtaac atctagcgta tcttatcaac ttggtggctc tgttaaagct 480

tctgtaacgc ctaatggccc tagcggtgaa gctggtgcaa ctggtcaagt cacttggtct 540

gactctgtaa gctataaact aactagttat aaaacaaatt taattgacca aacaaacaaa 600

aacgtaaagt ggaacgtatt ctttaacgga tataacaatc aaaactgggg tatttacaca 660

cgtgactcct atcattcttt atatggaaac caacttttca tgtactctcg cacataccta 720

tatgaatctg atgcaaaagg taatttaata ccgatggatc aacttccagc attaacaaat 780

agcggtttct ctcctggtat gattgctgtt gttatctctg aaaaaaatac agatcaatct 840 aacttacaag tcgcttatac aaaacacgcc gacgattacc aacttcgtcc aggctacaca 900

ttcggaactg caaactgggt tggaaacaac gtaaaagacg ttgatcaaaa aacatttaac 960

aaattattca cactagattg gaagaataaa aaattggtag agaaaaaata a 1011

<210> SEQ ID NO 63
<211> LENGTH: 1014
<212> TYPE: DNA
<213> ORGANISM: Bacillus cereus

<400> SEQUENCE: 63

atgaaacgct ctaaaacgta tttaaaatgt ttagcattat ccgctgtttt tgctagtagc 60

gctttagcac tttcaacacc tgctgcttac gctcaaacga cgtcacaagt tgtaacagat 120

atcgggcaaa atgcaaaaac acatacgagc tataatacat ttaataatga tcaaactgat 180

aatatgacaa tgtctttaaa ggtaactttt atcgatgatc cgagcgctga taaacagatt 240

gccgttatta atacaactgg tagttttcta aaagcaaatc ctactataag tagtgcgcct 300

attgataact acccaatccc tggcgctagt gcaacattac gctacccttc acaatatgat 360

attgccttta atcttcaaga taacagcgcc cgtttcttta acgtagcacc tacaaatgct 420

gtagaagaaa cgactgtaac ctctagtgta tcttatcaac ttggcggttc tgttaaagct 480

tctgcaacgc caaatggact tagcgctgaa gcgggtgcaa ctggccaagt aacttggtct 540

gactctgtaa gctataaaca aactagttat aaaacaaact taattgacca aacaaataaa 600

aacgtaaaat ggaacgtatt ctttaacgga tataacaatc aaaactgggg tatttacaca 660

cgtgattcct accattcttt atatggaaac caactgttca tgtactctcg cacatactta 720

tatgaatctg atgcaaaagg taatttaata ccgatggatc aacttccagc attaacaaat 780

agtggtttct ctcctggtat gatcgctgtt gttatctctg aaaaaaatac agaccaatct 840

aacctacaag tcgcttatac aaaacacgcc gacgactacc aacttcgtcc aggcttcaca 900

ttcggaactg caaactgggt tggaaacaac gtaaaagatg ttgatcaaaa aacatttaat 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

gctttagcac tttcaacacc tgctgcttac gctcaaacga cgtcacaagt tgtaacagat 120

atcgggcaaa atgcaaaaac acatacgagc tataatacat ttaataatga tcaaactgat 180

aatatgacaa tgtctttaaa ggtaactttt atcgatgatc cgagcgctga taaacagatt 240

gccgttatta atacaactgg tagttttcta aaagcaaatc ctactataag tagtgcgcct 300

attgataact acccaatccc tggcgctagt gcaacattac gctacccttc acaatatgat 360

attgccttta atcttcaaga taacagcgcc cgtttcttta acgtagcacc tacaaatgct 420

gtagaagaaa cgactgtaac ctctagtgta tcttatcaac ttggcggttc tgttaaagct 480

tctgcaacgc caaatggacc tagcgctgaa gcgggtgcaa ctggccaagt aacttggtct 540

gactctgtaa gctataaaca aacaagttat aaaacaaact taattgacca aacaaataaa 600

aacgtaaaat ggaatgtatt ctttaacgga tataacaatc aaaactgggg tatttacaca 660

cgtgattcct accattcttt atacggaaac caactgttca tgtactctcg cacatactta 720

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tatgaatctg atgcaaaagg taatttaata ccgatggatc aacttccagc attaacaaat 780

agcggtttct ctcctggtat gatcgctgtt gttatctctg aaaaaaatac agaccaatct 840

aacctacaag tcgcttatac aaagcacgcc gacgactacc aacttcgtcc aggctacaca 900

ttcggaactg caaactgggt tggaaacaac gtaaaagatg ttgatcaaaa aacatttaat 960

aaatcgttta cattagattg gaagaataag aaattagtag agaaaaaata g 1011

<210> SEQ ID NO 65
<211> LENGTH: 1011
<212> TYPE: DNA
<213> ORGANISM: Bacillus cereus

<400> SEQUENCE: 65

atgaaacgtt ctaaaaccta cttaaaatgt ttagcattat ccgctgtttt tgctagtagt 60

gctgtaactc tttcaacacc tgctacttac gctcaaacga cgtcacaagt tgtaacagat 120

atcgggcaaa atgcaaaaac acatacgagc tataatacat ttaataatga tcaagctgat 180

aatatgacaa tgtctttaaa ggtaactttt atcgatgatc caagcgctga taaacagatt 240

gccgttatta atacaactgg tagttttcta aaagcaaatc ctactataag tgatgcacct 300

attgataact acccaatccc tggcgctagt gcaacattac gttatccttc acaatatgat 360

gttgcattta accttcaaga taacagcgct cgtttcttta acgtagcgcc tacaaatgct 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 tataacaatc aaaactgggg tatttacaca 660

cgtgactcct atcattcttt atatggaaac caacttttca tgtactctcg cacataccta 720

tatgaatctg atgcaaaagg taatttaata ccaatggatc aacttccagc attaacaaat 780

agcggtttct ctcctggtat gattgctgtt gttatctctg aaaaaaatac agatcaatct 840

aacttacaag tcgcttatac aaaacacgcc gatgactacc aacttcgtcc aggcttcaca 900

ttcggaactg caaactgggt tggaaacaac gtaaaagacg ttgatcaaaa aacatttaat 960

aaattgttca cactagattg gaagaataag aaattggtag agaaaaaata a 1011

<210> SEQ ID NO 66
<211> LENGTH: 1011
<212> TYPE: DNA
<213> ORGANISM: Bacillus thuringiensis

<400> SEQUENCE: 66

atgaaacgct ctaaaacgta tttaaaatgt ttagcattat ccgctgtttt tgctagtagc 60

gctttagcac tttcaacacc tgctgcttac gctcaaacga cgtcacaagt tgtaacagat 120

atcgggcaaa atgcaaaaac acatacgagc tataatacat ttaataatga tcaaactgat 180

aatatgacaa tgtctttaaa ggtaactttt atcgatgatc caagcgctga taaacagatt 240

gccgttatta atacaactgg tagttttcta aaagcaaatc ctactataag tagtgcgcct 300

attgataact acccaatccc tggcgctagt gcaacattac gctatccttc acaatatgat 360

attgccttta atcttcaaga taacagcgct cgtttcttta acgtagcacc tacaaatgct 420

gtagaagaaa cgactgtaac ctctagtgta tcgtatcaac ttggcggttc tgttaaagct 480

tctgcaacgc caaatggacc tagcgctgaa gcgggtgcaa ctggtcaagt aacttggtct 540

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gactctgtaa gctataaaca aactagttat aaaacaaact taattgacca aacaaataaa 600

aacgtaaaat ggaacgtatt ctttaacgga tataacaatc aaaactgggg tatttacaca 660

cgtaattcct accattcttt atatggaaac caactgttca tgtactctcg cacatactta 720

tatgaatctg atgcaaaagg taatttaata ccgatggatc aacttccagc gctaacaaat 780

agtggtttct ctcctggtat gatcgctgtt gttatctctg aaaaaaatac agaccaatct 840

aacctacaag tcgcttatac aaaacacgcc gacgactacc aacttcgtcc aggcttcaca 900

ttcggaactg caaactgggt tggaaacaac gtaaaagatg ttgatcaaaa aacatttaat 960

aagttgttca cactggattg gaagaataag aaattagttg agaaaaaata a 1011

<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 tactcttgtg 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

<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 tggtagtac                                                   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
```

```
gtctttcgct 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

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

tcgtttgrct 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

gatcccattg 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

cagcwggatt ccaagatgt                                                 19


<210> SEQ ID NO 84
<211> LENGTH: 18
<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: (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
<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

gcwgtrgaag 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

ccaacccagt 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

tatttcttca tcattacgaa aattaggtgc gcattctaaa ttagtccaaa cgtatattga   120

tcaatcttta atgagtccta atgtacagct agaggaagtc ccagctttaa ataccaatca   180

attcctaatc aaacaagata tgaaggaatg gtcatcggaa ctctatccac agttaattct   240

attaaattca aaaagtaaag gatttgtaac aaaatttaat 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 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
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cgcagccgca gcaaaaacac aagagtatga cctgatgaaa gccattgata ccgaaaagat    900

taagaaaaca tttggcgttt ttgctgaagt aaataaatta acagcagaac agcgagcata    960

tttagatgat ttagagaaac 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

tcatgaaaaa atttccattc aaagtactaa ctttagctac attagcaact gttataactg   1380

ctactaccgg taacactatt catgcatttg cacaagaaac gaccgctcaa gaacaaaaag   1440

taggcaatta tgcattaggc cccgaaggac tgaagaaagc attagctgaa acagggtctc   1500

atattctagt aatggattta tacgcaaaaa caatgattaa gcaaccaaat gtaaatttat   1560

ctaatatcga tttaggctca gagggggag agttgctcaa aaatattcac cttaatcaag   1620

agctgtcacg aatcaatgcg aattactggt tagatacagc gaagccacag attcaaaaaa   1680

ctgctcgtaa tattgtaaat tacgatgaac aatttcaaaa ttattacgac acattagtag   1740

aaactgtaca aaagaaagat aaggcaggtc taaaagaggg tataaatgat ttaattacta   1800

caatcaatac aaattcaaaa gaagttacag atgtgattaa gatgctacaa gacttcaaag   1860

ggaaattata tcaaaattct acagatttta aaaataatgt tggtggtcca gatgggaaag   1920

gtggattaac tgcaatatta gcaggtcaac aggcaacgat tccacaactt caagctgaaa   1980

ttgagcaact tcgttctact cagaaaaaac attttgatga tgtattagca tggtcaattg   2040

gtggtggatt gggagcagct attttagtta ttgcagctat tggaggagcg gtagttattg   2100

ttgtaactgg cggtacagca acaccggctg ttgttggtgg actctcggct cttggcgcag   2160

ctggtatcgg tctaggaact gcggctggtg tcacagcatc taagcatatg gattcctata   2220

atgaaatttc taacaaaatc ggagaattaa gtatgaaagc agatcgtgct aatcaagcag   2280

ttctttcgct tactaacgcg aaagaaacat tggcatattt ataccagact gtagatcaag   2340

cgatattgtc tctaacaaat attcaaaagc aatggaatac aatgggcgca aattatacag   2400

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

ctaatgtagt ttcaccagta acaactttg caagtgaaat tgaacaaacg aataatggag   2700

atacggctct ttctgcaaat gaagcgagaa tgaaagagac cttgcaaaag gctggattat   2760

ttgcaaaatc tatgaatgcc tattcttata tgttaattaa gaatcctgat gtgaattttg   2820

agggaattac cattaatgga tatgtagatt tacctggtag aatcgtacaa gatcaaaaga   2880

atgcaagggc acatgccgtt acttgggata cgaaagtaaa aaaacagctt ttagatacat   2940

tgaatggtat tgttgaatac gatacaacat ttgataatta ttatgaaaca atgatagagg   3000

cgattaatac aggggatgga gaaactttaa aagaagggat tacagattta cgaggtgaaa   3060

ttcaacaaaa tcaaaagtat gcacaacaac taatagaaga attaactaaa ttaagagact   3120

ctattggaca cgatgttaga gcatttggaa gtaataaaga gctcttgcag tcaattttaa   3180

aaaatcaagg tgcagatgtt gatgccgatc aaaagcgtct agaagaagta ttaggatcag   3240
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taaactatta taaacaatta gaatctgatg ggtttaatgt aatgaagggt gctattttgg 3300

gtctaccaat aattggcggt atcatagtgg gagtagcaag ggataattta ggtaagttag 3360

agcctttatt agcagaatta cgtcagaccg tggattataa agtaacctta aatcgtgtag 3420

ttggagttgc ttacagtaat attaatgaaa tgcacaaggc gcttgatgat gctattaacg 3480

ctcttactta tatgtccacg cagtggcatg atttagattc tcaatattcg ggcgttctag 3540

ggcatattga g 3551

<210> SEQ ID NO 88
<211> LENGTH: 3409
<212> TYPE: DNA
<213> ORGANISM: Bacillus thuringiensis

<400> SEQUENCE: 88

actcatttct attaaacaag atatgaaaga gtggtcatcc gaactttatc ctaaattaat 60

tctattaaat tcaaaaagta aaggatttgt aactaaattt aatagttatt atccaacatt 120

aaaaggattt gtagataata aggaagataa agaagggttt acagatagac tggaagtcct 180

tcaagacatg accatcacaa accaagaaag tgtgcaacgt caaattaatg agttaacaga 240

tctaaaacta caggtagata agaagttgaa aaatcttgat actgatgtgg caaaaacaca 300

gagtgtcctt aattcagagg gaacaggaaa aatagataag ttaaaaaatg aaatgctaga 360

tacaaaaaaa tcaattcaaa atgatttaca gcaaatagcg ttattaccag gagctttaaa 420

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

atatttaaat gatttagaga aacaaaatca gaaattatat gacttaacga ctaaattaac 840

agtagcagat ttacaaaaat caatgattct tttcatgcaa aatgatttgc atacatttgc 900

taaccaagta gatggagaaa ttgagctaat gaaacgttac aaagaggatt tggatctaat 960

aaataatagt attacaaaat tatcgactga agttgatacc aataacaccc agtctcaaaa 1020

agatacatta agacgattaa aaagtgtaac aactcaactc gaagaacaag tttataaatt 1080

ttaatattaa gaaattaggt ttaataaaaa tattataacg caactgaaaa taaggaggag 1140

aatcaaatga tgaaatttcc atttaaggtt ataactttag ccactttagc aacggttata 1200

actgctacga atggtagtac tattcatgca cttgcacaag aacagacagc tcaagaacat 1260

aaaatagaaa attatgcgtt aggacctgaa gggttaaaga aagcgttggc tgcaactggc 1320

tctcatattc ttgtaatgga tttgtacgca aaaactatga ttaagcaacc gaatgtaaat 1380

ttatccaaca ttgatttagg ttcaggagga ggagaattaa tcaaaaatat ccacctgaat 1440

caggaactgt cacgaatcaa tgcaaattac tggttagata cagcgaagcc aaacattcaa 1500

aaaacagctc gtaatattgt aaattatgat gagcaattcc aaaattatta cgacacatta 1560

gtagatactg taaaaaagaa agataagatg agccttaaag aaggaatagg ggatttaatc 1620

gatacaattc atacaaattc aaatgaagtt actgacgtca ttaagatgtt agaggctttc 1680

aaaacaaagt tgtatacaaa tactgtagat tttaaaaata atgttggtgg tccagatgga 1740

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cagggaggat tgacggctat attagcggga aaacaagcac tagtcccaca acttcaggcc 1800

gaaattgaga atttacgttc tacacagaaa tcacattttg ataatgtatt agcctggtca 1860

attggcggtg gactaggagc agctatttta gttattggaa cgattgcagg agcggtagta 1920

attgttgtga ctggtggtac agctacacca gctgttgttg gcggtcttac agctctagga 1980

gcagctggta tcggtttagg aacagcagct ggtgtcgagg catctaatca tatgaattct 2040

tataatgaaa tttcgaataa aatcggagaa ttaagtatga aagctgatct ggctaatcaa 2100

gcggttattt cacttactaa tacgaaagac actctaacat atttgtatca gacagtggat 2160

caagcaataa tgtctctaac aagtattcag caacaatgga ataaaatggg ggctaattat 2220

aaagatttat atgataatat cgatcaaatg caagaacata aactttcgtt aatacctgac 2280

gatttaaaag ctgctaaaca aagttggaat gacattcata aggacgcaga attcatttca 2340

aaagacattg cttttaaaca agaaaaaaca aactaaaaat taatatatat tcataggagg 2400

aattaaagtg aataataatt ttccttataa actacttgct gtatcgacgt ttttaaccct 2460

gacaacaact actgtagttt caccagtagc tgcttttgca agtgaaagta aaatagaaca 2520

aaccagtacg gaagatatat ctctttctgt aaacagtgaa aagatgaaaa aagctttgca 2580

agatgctggg gtatttgcaa aatccatgaa tgattactct tatttgttaa ttaataatcc 2640

agatgttaac tttgaaggaa ttgatattaa aggatataca aatctaccta gtcaaattgc 2700

acaagatcaa aagaatgcaa gagagcatgc tacaaaatgg gatgctcaca taaaaaaaca 2760

acttttagat acccttacag gaattgtaga gtatgatacc acatttgaca attattacga 2820

tacattagta gaagcaatta atgaaggaga tgcagataca ttaaaagaag gcattacaga 2880

tttacaaggt gagattaaac aaaaccaagc atatacacag aatttaattc aagaactagc 2940

taagttaaga gatagtattg gagaagatgt ccgagcattt ggaggtcata aagatatctt 3000

gcaatcgatt ttaaaaaatc aagcatctgg aatagatgaa gatgaaaaac gcctaaatga 3060

tgttttagag caaataagac attttaaaca agtagaatcg gatggaataa taactgtatc 3120

atatccttca atccctacat ggattgctgg aggtgtgatg atagggggtag caagaaataa 3180

tttaggtacg ttagagccgt tattagtgca attacgccaa accgtagact ataaaataac 3240

attaaatcgt gtagttggag ttgcgtataa taatattact gaaatgcaaa atgcaattgg 3300

atcagctatt aatgctctta cctatatgtc agcacaatgg catgatttag attctcaata 3360

ttcaggagtg cttaatcata ttgataaagc atcccaaaaa 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 agtaaaggat ttataactaa atttaatagt tattatccaa cattaaaagg 120

atttgtagat aataaggaag ataaagaagg gtttacagat agactggaag ttcttcaaga 180

catgactata acaaatcaag aaagtgtgca acgtcaaatt aatgagttaa cagatttaaa 240

attactggta gataagaagt tgaaaaacct tgatactgat gtggtaaaag cacaaagtgt 300

ccttaattca gagggaacag gaaaaataga taagttaaaa aatgaaatgc tagatacaaa 360

aaaatctatt caaaatgatt tgcagcaaat agcattatta ccaggcgcgt taaatgaaca 420

agggctaaag gtattccaag aaatttatag tctatcgaaa gatatcattg aaccggctgc 480

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```
tcaaacagca gtagtagcgt ataacaaagg aaaagaaata aacaatgcca ttgtagacgc    540

agagaagaaa gcagagcaag aagcaaaaga aaagggaaaa tcagctatag aaattgaagc    600

tgccaaaaaa gaagcacgtg aaacgataga gaaaagtaaa aaaggtgaaa tcgctgcagc    660

tgcagttaca aaaacgaaag agtatgatct tatgaaagtg attgatcctg aaaaaataaa    720

aaaaacatat aatacttttg ctgaaattaa taaactaaca gctgagcaaa gagcatattt    780

aaatgattta gagaaacaaa atcagaaatt atatgactta acaactaaat taacagtagc    840

agatttacaa aaatcaatga ttcttttcat gcaaaatgac ttgcatacat ttactaatca    900

agtagatgga gaaattgagt taatgaaacg ttacaaagag gatttggatc taataaataa    960

tagtattaca aaattatcga ctgaagttga taccaataat actcaggctc aaaaagatat   1020

attaagacga ttaaaaagtg taacaattca acttgaagaa caagtttata aattttgata   1080

ttaagaaatt aggtttatta aaaaattata acgaaacgga aaataaggag gagaatcaaa   1140

tgatgaaatt tccatttaaa gttataacct tagctacttt agcaacgatt ataaccgcta   1200

caaatggtag tactattcat gcacttgcac aagaacagac agctcaagaa cagaaaatag   1260

aaaattatgc gttaggacct gaaggattaa agaaagcgtt ggctgaaaca ggctctcata   1320

ttcttgtaat ggatttgtac gcaaaaacta tgattaagca accgaatgta aatttatcca   1380

acattgattt aggttcgggt ggagaagaat taatcaaaaa tattcacctg aatcaagaac   1440

tgtcacgaat caatgcaaat tactggttag atacagcgaa gccaaacatt caaaaaacag   1500

cacgtaatat tgtaaattat gatgagcaat ttcaaaatta ttacgacaca ttagtagata   1560

ctgtaaaaaa gaaggataag gtgagcctca aagaaggaat aggggattta atctatacaa   1620

ttcatacaaa ttcaaatgaa gttacggaag tcattaagat gttagaggct ttcaaaacaa   1680

agttgtatac aaatactgta gattttaaaa ataatgttgg tggtccagat ggacagggag   1740

gattgacggc tatattagcg ggaaaacaag cgctagtccc acaacttcag gccgaaattg   1800

agaatttacg ttctacacag aaaacacatt ttgataatgt attagcctgg tcaattggtg   1860

gtggattagg agcagctatt ttagttattg gaacgattgc aggagcggta gtaattgttg   1920

tgactggtgg tacagctacg ccagctgttg ttggtggtct tacagctcta ggagccgctg   1980

gtatcggttt aggaacagca gctggcgtcg aggcatctaa tcatatgaat tcttataatg   2040

aaatttcgaa taaaatcgga gaattaagta tgaaagctga tttggctaat caagcggtta   2100

tttcacttac taatacgaaa gacactctaa catatttgta tcagacagtg gatcaagcaa   2160

taatgtctct aacaagtatt cagcaacaat ggaataaaat gggggctaat tataaagatt   2220

tatatgataa tatcgatcaa atgcaagaac ataaactttc gttaatacct gacgatttaa   2280

aagctgctaa acaaagttgg aatgatattc ataaggatgc agaattcatt tcaaaagaca   2340

ttgcttttaa acaagaaaaa acaaactaga aattaatata tattcatagg aggaattaaa   2400

gtgaataata attttcctta taaactactt gctgtatcga cgtttttaac cctgacaaca   2460

actactgtag tttcaccagt agctgctttt gcaagtgaaa gtaaaataga acaaaccagt   2520

acggaagata tatctctttc tgtaaacagt gaaaagatga aaaaagcttt gcaagatgct   2580

ggggtatttg caaaatccat gaatgattac tcttatttgt taattaataa tccagatgtt   2640

aactttgaag gaattgatat taaaggatat acaaatctac ctagtcaaat tgcacaagat   2700

caaaagaatg caagagagca tgctacaaag tgggatgcgc acataaaaaa acaactttta   2760

gatactctta caggaattgt agagtatgat actacatttg acaattatta cgatacatta   2820
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gtagaagcaa ttaatgaagg agatgcagat acattaaaag aaggcattac agatttacaa 2880

ggtgagatta aaaaaaacca agcatataca aagaatttaa tacaagaact agctaagtta 2940

agagatagta ttggagaaga tgtccgagca tttggaggtc ataaagatat cttgcaatcg 3000

attttaaaaa atcaagcatc tggaatagat gaagatgaaa aacgtctaaa tgatgtttta 3060

gagcaagtaa gacattttaa acaagtagaa tcggatggaa taataactgt atcagttccc 3120

tcaatcccta catggattgc tggaggtgta atgataggg tagcaagaaa taatttaagt 3180

acgctggaac cgctattagc gcaattgcgc caaacggtag actataaaat tacattgaat 3240

cgtgtagttg gagttgcgta taataatatt gctgaaatgc aaaatgcaat tggatcagct 3300

attaatgctc tcacctatat gtcagcacaa 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 ggttctatta atatcggtaa acaagtattt acaatcacaa atcaaactgc 540

acaaacgaaa acaatcgatt ttgtttctat cggtacttta agtaatgaaa ttgtaaatgc 600

tgcagatagt caaacgagag aagcagcttt tcgcattcag caaaagcaaa aagagttatt 660

gccacttatt caaaagttat cacaaactga agcagaggcg actcaaatta cattcgttga 720

agatcaagta aatagcttta cagaattaat tgatcgtcaa attacaactt tagaaacgtt 780

attaacggat tggaaagttt taaataataa tatgattcaa attcaaacaa atgttgaaga 840

aggcacgtat acagacagta gtttacttca aaaacatttt aatcaaatta aaaaagtaag 900

tgatgaaatg aataagcaaa caaatcaatt tgaagattac gttacaaacg ttgaagtaca 960

ttaaatagaa aaataattag cgatataggg agagaagaaa aatgacaaaa aaaccatata 1020

aagtaatggc tctatcagca cttatggcag tatttgcagc aggaaatatt atgccggctc 1080

atacgtatgc agctgaaagt acagtgaaac aagctccagt tcatgcggta gcaaaagctt 1140

ataataacta tgaagaatat tcattaggac cagaaggttt gaaagatgca atggaaagaa 1200

caggttcaaa tgctttagta atggatctgt atgctttaac aattattaaa caaggtaatg 1260

ttaactttgg aaatgtatcg actgttgatg cagctttaaa aggaaaagtg attcagcacc 1320

aagatacagc tagaggaaat gcgaagcaat ggttagatgt attaaagcca cagcttattt 1380

caacgaatca aaacatcatt aactacaata caaaattcca aaactattat gatactttag 1440

ttgctgcggt agatgcaaaa gataaagcga ctcttacgaa aggcctaact agattatcaa 1500

gtagtattaa tgaaaataaa gcgcaagtgg atcagttagt agaagacttg aaaaaattcc 1560

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gaaataaaat gacgtcggat acgcaaaact tcaagggtga tgcaaatcaa attacatcta 1620

tattagctag tcaagatgca gggattccac ttctgcaaaa tcaaattaca acgtacaatg 1680

aagcaattag taaatataat gcaattatta tcggttcatc tgttgcgaca gctctaggac 1740

caattgcaat tattggtggt gcagtagtta ttgctacggg cgcaggaaca ccgctaggag 1800

tcgcattaat tgcaggtggt gcagcagctg taggcggtgg tacagctggt atcgtattag 1860

cgaagaaaga acttgacaat gcacaagctg aaattcaaaa aataactgga caaattacaa 1920

ctgctcaatt agaagtagct gggttaacga acattaaaac acaaactgag tatttaacaa 1980

atacgattga tactgcaatt acagcgttgc aaaacatttc aaaccaatgg tatacaatgg 2040

gatcaaaata caattcttta cttcaaaatg tggattcaat tagtccaaac gatcttgttt 2100

tcattaaaga agatttaaac attgcgaaag atagctggaa aaacattaaa gactatgcag 2160

aaaagattta tgctgaagat attaaagtag tagatacgaa aaaagcataa tcgaatacga 2220

atcgttaggg cgttaagtgt tgatgaatga tttgaagctc ctgttcagtt gtgagcagga 2280

gcttttgata tccttataaa gagaataggt gaaaaatatg cagaaacgat tttataaaaa 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 aaagggagta tgattcagca tcaaagagat gcaaaaatta atgcagcata 2640

ttggttaaat aatatgaagc ctcaaattat gaaaacagat caaaatatta taaattacaa 2700

taatactttt caatcgtatt ataatgacat gttaatagcg attgatcaaa aggatagtgg 2760

aaaattaaaa gcggatttag aaaagttgta tgcggatatt gtaaagaatc aaaatgaggt 2820

agatggatta ttaggaaatt tgaaagcttt tcgcgataga atggcgaaag atacaaatag 2880

tttcaaagag gatacaaatc agttaacagc gatattggca agtacgaatg ctggtattcc 2940

agctctagag caacaaataa atacatataa cgattcgatt aaaaagagta atgatatggt 3000

cattgctggt ggcgtacttt gcgtagctct aataacatgt cttgctggcg ggccgatgat 3060

tgcggttgcg aaaaaagata tcgcaaatgc agaaagagaa atcgccaatt taaaagatag 3120

aatttcagga gcacaagcag aagtcgtaat tttgactgat gtaaaaaata aaacaacaaa 3180

catgacagaa acaattgatg cagcaattac agcactacaa aacatatcaa atcaatggta 3240

tacagtaggt gcaaagtata ataatttatt acaaaacgta aaggaatta gtccggaaga 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 gcataaccat ccattccgtt ttattttcat gttacgatat aaatgtaata 60

cgacatatat cgacaaagat aaaaggaagt gattgtatga aacgttctaa aacatactta 120

aaatatttag cattatccgc tgtttttgct agtagtgcta taactctttc aacacctgct 180

gcttacgctc aaacaacatc acaagttgta acagatatcg ggcaaaatgc aaaaacacat 240

acgagctata atacatttaa taatgatcaa gctgataata tgacaatgtc tttaaaggta 300

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acttttatcg atgaccctag cgctgataaa cagattgccg ttattaatac aactggtagt 360

tttctaaaag caaatcctac tataagtgat gcacctattg ataactaccc aatccctggc 420

gctagtgcaa cattacgtta tccttcacaa tatgatgttg catttaacct tcaagataac 480

agcgctcgtt tctttaacgt agcgcctaca aatgctgtag aagaaacgac tgtaacatct 540

agcgtatctt atcaacttgg tggctctgtt aaagcttctg taacgcctaa tggccctagc 600

ggtgaagctg gtgcaactgg tcaagtcact tggtctgact ctgtaagcta taaacaaact 660

agttataaaa caaatttaat tgaccaaaca aacaaaaacg taaagtggaa cgtattcttt 720

aacggatata acaatcaaaa ctggggtatt tatacacgtg actcctatca ttctttatat 780

ggaaaccaac ttttcatgta ctctcgcaca tacctatatg aatctgatgc aaaaggtaat 840

ttaataccga tggatcaact tccagcgcta acaaatagtg gtttctctcc tggtatgatt 900

gctgttgtta tctctgaaaa aaatacagat caatctaact tacaggtcgc ttatacaaaa 960

cacgccgacg actaccaact tcgtccaggc tacacattcg gaactgcaaa ctgggttgga 1020

aacaacgtaa aagacgttga tcaaaaaaca tttaataaat 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

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 ggttacagc                                        29


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

<400> SEQUENCE: 97

atactccgct gcttctctcg tttgactatc 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 ttcgctgt                                         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 ccatctactt ggttagc                               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
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```
aaattgagcg tagtttcacc agtagctgct tttgcaag                        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
<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 ctcactatag 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
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<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 actctcgcaa caccaatcgt tcaagcagaa actcaacaag aaaacatgga     60

tatttcttca tcattacgaa aattaggtgc gcattctaaa ttagtccaaa cgtatattga    120

tcaatcttta atgagtccta atgtacagct agaggaagtc ccagctttaa ataccaatca    180

attcctaatc aaacaagata tgaaggaatg gtcatcggaa ctctatccac agttaattct    240

attaaattca aaaagtaaag gatttgtaac aaaatttaat 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 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 gccatgcaaa tgaagcgaga    900

atgaaagaga ccttgcaaaa ggctggatta tttgcaaaat ctatgaatgc ctattcttat    960

atgttaatta agaatcctga tgtgaatttt gagggaatta ccattaatgg atatgtagat   1020

ttacctggta gaatcgtaca agatcaaaag aatgcaaggg cacatgccgt tacttgggat   1080

acgaaagtaa aaaaacagct tttagataca 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 gtaaactatt ataaacaatt agaatctgat   1440

gggtttaatg taatgaaggg tgctattttg ggtctaccaa taattggcgg tatcatagtg   1500

ggagtagcaa gggataattt aggtaagtta gagcctttat tagcagaatt acgtcagacc   1560

gtggattata aagtaacctt aaatcgtgta gttggagttg cttacagtaa tattaatgaa   1620

atgcacaagg cgcttgatga tgctattaac gctcttactt atatgtccac gcagtggcat   1680

gatttagatt ctcaatattc gggcgttcta gggcatattg ag                      1722


<210> SEQ ID NO 111
<211> LENGTH: 1862
<212> TYPE: DNA
<213> ORGANISM: Bacillus thuringiensis
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<400> SEQUENCE: 111

actcatttct attaaacaag atatgaaaga gtggtcatcc gaactttatc ctaaattaat     60

tctattaaat tcaaaaagta aaggatttgt aactaaattt aatagttatt atccaacatt    120

aaaaggattt gtagataata aggaagataa agaagggttt acagatagac tggaagtcct    180

tcaagacatg accatcacaa accaagaaag tgtgcaacgt caaattaatg agttaacaga    240

tctaaaacta caggtagata agaagttgaa aaatcttgat actgatgtgg caaaaacaca    300

gagtgtcctt aattcagagg gaacaggaaa aatagataag ttaaaaaatg aaatgctaga    360

tacaaaaaaa tcaattcaaa atgatttaca gcaaatagcg ttattaccag gagctttaaa    420

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

atatttaaat gatttagaga aacaaaatca gaaattatat gacttaacga ctaaattaac    840

agtagcagat ttacaaaaat caatgattct tttcatgcaa aatgatttgc atacatttgc    900

taaccaagta gatggagaaa ttgagcgtag tttcaccagt agctgctttt gcaagtgaaa    960

gtaaaataga acaaaccagt acggaagata tatctctttc tgtaaacagt gaaaagatga   1020

aaaaagcttt gcaagatgct ggggtatttg caaaatccat gaatgattac tcttatttgt   1080

taattaataa tccagatgtt 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 agatttacaa ggtgagatta aacaaaacca agcatataca cagaatttaa   1380

ttcaagaact agctaagtta agagatagta ttggagaaga tgtccgagca tttggaggtc   1440

ataaagatat cttgcaatcg attttaaaaa atcaagcatc tggaatagat gaagatgaaa   1500

aacgcctaaa tgatgtttta gagcaaataa gacattttaa acaagtagaa tcggatggaa   1560

taataactgt atcatatcct tcaatcccta catggattgc tggaggtgtg atgatagggg   1620

tagcaagaaa taatttaggt acgttagagc cgttattagt gcaattacgc caaaccgtag   1680

actataaaat aacattaaat cgtgtagttg gagttgcgta taataatatt actgaaatgc   1740

aaaatgcaat tggatcagct attaatgctc ttacctatat gtcagcacaa tggcatgatt   1800

tagattctca atattcagga gtgcttaatc 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 aagagtggtc atccgaactt taccctaaat taattctatt     60

aaattcaaaa agtaaaggat ttataactaa atttaatagt tattatccaa cattaaaagg    120

atttgtagat aataaggaag ataaagaagg gtttacagat agactggaag ttcttcaaga    180
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catgactata acaaatcaag aaagtgtgca acgtcaaatt aatgagttaa cagatttaaa 240

attactggta gataagaagt tgaaaaacct tgatactgat gtggtaaaag cacaaagtgt 300

ccttaattca gagggaacag gaaaaataga taagttaaaa aatgaaatgc tagatacaaa 360

aaaatctatt caaaatgatt tgcagcaaat agcattatta ccaggcgcgt taaatgaaca 420

agggctaaag gtattccaag aaatttatag tctatcgaaa gatatcattg aaccggctgc 480

tcaaacagca gtagtagcgt ataacaaagg aaaagaaata aacaatgcca ttgtagacgc 540

agagaagaaa gcagagcaag aagcaaaaga aaagggaaaa tcagctatag aaattgaagc 600

tgccaaaaaa gaagcacgtg aaacgataga gaaaaggatc aaaagaatgc aagagagcat 660

gctacaaagt gggatgcgca cataaaaaaa caacttttag atactcttac aggaattgta 720

gagtatgata ctacatttga caattattac gatacattag tagaagcaat taatgaagga 780

gatgcagata cattaaaaga aggcattaca gatttacaag gtgagattaa aaaaaaccaa 840

gcatatacaa agaatttaat acaagaacta gctaagttaa gagatagtat tggagaagat 900

gtccgagcat ttggaggtca taaagatatc ttgcaatcga ttttaaaaaa tcaagcatct 960

ggaatagatg aagatgaaaa acgtctaaat gatgttttag agcaagtaag acattttaaa 1020

caagtagaat cggatggaat aataactgta tcagttccct caatccctac atggattgct 1080

ggaggtgtaa tgataggggt agcaagaaat aatttaagta cgctggaacc gctattagcg 1140

caattgcgcc aaacggtaga ctataaaatt acattgaatc gtgtagttgg agttgcgtat 1200

aataatattg ctgaaatgca aaatgcaatt ggatcagcta ttaatgctct cacctatatg 1260

tcagcacaat ggcatgattt agattctcaa tattcaggag tacttaatca tattgataaa 1320

gcatcccaaa aagcagatca aaataatt 1348

<210> SEQ ID NO 113
<211> LENGTH: 1378
<212> TYPE: DNA
<213> ORGANISM: Bacillus thuringiensis

<400> SEQUENCE: 113

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 ggttctatta atatcggtaa acaagtattt acaatcacaa atcaaactgc 540

acaaacgaaa acaatcgatt ttgtttctat cggtacttta agtaatgaaa ttgtaaatgc 600

tgcagatagt caaacgagag aagcagcgga gtatgattca gcatcaaaga 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

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aagatacaaa tagtttcaaa gaggatacaa atcagttaac agcgatattg gcaagtacga    960

atgctggtat tccagctcta gagcaacaaa taaatacata taacgattcg attaaaaaga   1020

gtaatgatat ggtcattgct ggtggcgtac 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 ggtgcaaagt ataataattt attacaaaac gtaaaaggaa   1320

ttagtccgga agagtttacg tttataaaag aagatttaca tacagcgaaa gatagctg     1378


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

<400> SEQUENCE: 114

gaagtaaata gaacaaacca gtacggaaga tatatctctt tctgtaaaca gtgaaaagat     60

gaaaaaagct ttgcaagatg ctggggtatt 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 aaggtgagat taaaaaaaac caagcatata caaagaattt    420

aatacaagaa ctagctaagt taagagatag tattggagaa gatgtccgag catttggagg    480

tcataaagat atcttgcaat cgattttaaa aaatcaagca tctggaatag atgaagatga    540

aaaacgtcta aatgatgttt tagagcaagt aagacatttt aaacaagtag aatcggatgg    600

aataataact gtatcagttc cctcaatccc tacatggatt gctggaggtg taatgatagg    660

ggtagcaaga aataatttaa gtacgctgga accgctatta gcgcaattgc gccaaacggt    720

agactataaa attacattga atcgtgtagt tggagttgcg tataataata ttgctgaaat    780

gcaaaatgca attggatcag ctattaatgc tctcacctat atgtcagcac aatggcatga    840

tttagattct caatattcag gagtacttaa tcatattgat aaagcatccc aaaaagcaga    900

tcaaaataaa tttaaattct taaaacctaa tctgaatgca gccaaagaca gctggaaaac    960

attaagagca gatgcgttta cattaaaaga aggaataaaa acattaaaaa tggatcc      1017


<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 ggttagatac    240

agcgaagcca aacattcaaa aaacagcacg taatattgta aattatgatg agcaatttca    300

aaattattac gacacattag tagatactgt aaaaaagaag gataaggtga gcctcaaaga    360

aggaataggg gatttaatct atacaattca tacaaattca aatgaagtta cggaagtcat    420
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taagatgtta gaggctttca aaacaaagtt gtatacaaat actgtagatt ttaaaaataa 480

tgttggtggt ccagatggac agggaggatt gacggctata ttagcgggaa aacaagcgct 540

agtcccacaa cttcaggccg aaattgagaa tttacgttct acacagaaaa cacattttga 600

taatgtatta gcctggtcaa ttggtggtgg attaggagca gctattttag ttattggaac 660

gattgcagga gcggtagtaa ttgttgtgac tggtggtaca gctacgccag ctgttgttgg 720

tggtcttaca gctctaggag ccgctggtat cggtttagga acagcagctg gcgtcgaggc 780

atctaatcat atgaattctt ataatgaaat ttcgaataaa atcggagaat taagtatgaa 840

agctgatttg gctaatcaag cggttatttc acttactaat acgaaagaca ctctaacata 900

tttgtatcag acagtggatc aagcaataat gtctctaaca agtattcagc aacaatggaa 960

taaaatgggg gctaattata aagatttata tgataatatc gat 1003

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

<400> SEQUENCE: 116

gcaaacgtat gcaaatcatt tgtgtaagaa gaagcatgat tttgtaaat cagctattga 60

tagtttcgtt gttaaatcat atattttttg attttgtttc tctaaatcat ctaaatatgc 120

tcgctgttct gctgttaatt tatttacttc agcaaaaacg ccaaatgttt tcttaatctt 180

ttcggtatca atgaccttca tcaggtcata ctcttgtgtt tttgctgcgg ctgcggctgc 240

tatttcacct tgtttgcttt tctcaattgc ttcacgagct gcttttttg ctgattcaat 300

ctctagagca gttttacctt gttctgtcgc ttcttgcgcc gctttttct ccgcttctag 360

aatagagttg ttaatttctt ttcctttgtt atacgctgcc acccctgctt gagcagctgg 420

ttcaataatt tcttttgaaa gactataaac ttctttgaat atagcaaatc cctgctcatt 480

taaagctcct ggtattaatg caatttgctg taaatcattt tgaattgctt ttttggtatt 540

taatatttca ttttttaact gatctatttt tcctgttcca tctgtactta gtatgccttg 600

cgcagttgcc acattagtat caaaatcttt taattttta tcaagctgta atttaagatc 660

tgttaattca ttgatttgtc gttgcgcatt ttcttgattc gtcatagcca tttcttgaag 720

tacttcaagt ctatccgaaa acccttctct atcttcttta ttgtctacaa acgattttaa 780

tgtcgggtaa taactattaa attttgttac aaatccttta ctttttgaat ttaatagaat 840

taactgtgga tagagttccg atgaccattc cttcatatct tgtttgatta ggaattgatt 900

ggtatttaaa gctgggactt cctctagctg tacattagga ctcattaaag attgatcaat 960

atacgtttgg attaatttag attgcgcacc taattttcgt aatgaagagg aaatatccat 1020

gcctttctgt tgagtttccg cttgaacgat tggtgttg 1058

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

<400> SEQUENCE: 117

gcttttaaac aggagtagaa ctgaaattta aaacctaaat tggaggaaaa tgaaatgata 60

aaaaaaatcc cttataaatt actcgctgta tcgacgctat taactattac aactgctaat 120

gtagttttac cagtaacaac ttttgcaagt gaaattgaac aaacgaacaa tggagatacg 180 gctctttctg caaatgaagc gagaatgaaa gagaccttgc aaaaggctgg attatttgca 240

aaatctatga atgcctattc ttatatgtta attaagaatc ctgatgtgaa ttttgaggga 300

attaccatta atggatatgt agatttacct ggtagaatcg tacaagatca aaagaatgca 360

agggcacatg ctgttacttg ggatacgaaa gtaaaaaaac agcttttaga tacattgaat 420

ggtattgttg aatacgatac aacatttgac aattattatg aaacaatggt agaagcgatt 480

aatacagggg atggagaaac tttaaaagaa gggattacag atttgcgagg tgaaattcaa 540

caaaatcaaa agtatgcaca acaactaata gaagaattaa ctaaattaag agactctatt 600

ggacatgatg ttagagcttt tggaagtaat aaagagctct tgcagtcaat tttaaaaaat 660

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 tgaaatgcac 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 tgaggtctat tcaaaatagt 120

agttaattca gcttgaattt caccttgaat tcttttaata tcttctctta atttcacaat 180

atctccactt gatccttgca gtgtttttat tgcttcatcg gctttaattg ataagttgtt 240

actatctttg tctaatactg ttttaaatcg atttaactct aataaatctt gctccatact 300

ctcttggatg ctttgtactt gcaattgtaa ttttccatat gcactcataa aatctgcttt 360

tgcttgctga tcttcattta cgtttcctgc taattcatag agcttactat aatagctatt 420

aaatctagtg ctgtatctca tcatctcttg atttaagtca attagcttcg gattatattc 480

atcaatccat tctcgtacat tcgcctttgc aaactttga tgattcgtta agctactcat 540

cgcatttacc ttaatatctg gctgttgtaa aataattaat 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

accattggtt tgatatgttt tgtagtgctg taattgctgc atcaattgtt tccgtcatgt 120

ttgttgtttt attttttaca tcagtcaaaa ttacgatttc tgcttgtgct cctgaaattc 180

tatcttttaa attagctatc tctctttctg catttgcgat atcttttttt gcaaccgcaa 240

tcatcggccc gccagcaaga catgttatta gcgctacgca aagtacgcca ccagcaatga 300

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ccatatcatt actcttttta atcgaatcgt tatatgtatt tatttgttgc tctagagctg    360

gaataccagc attcgtactt gccaatatcg ctgttaactg atttgtatcc tctttgaaac    420

tatttgtatc tttcgccatt ctatcgcgaa aacttttcaa atttcctaat aatccatcta    480

cctcattttg attctttaca atatccgcat acaacttttc taaatccgct tttaattttc    540

cgctatcctt ttgatcaatc gctattaaca tgtcgttata atacgattga aaagtattat    600

tgtaatttat aatattttga tccgttttca taatttgagg cttcatatta tttaaccaat    660

atgctgcatt aatttttgca tctctttgat gctgaatcat attcccttta aattcactat    720

taatcgaact tattttactt aaatccgtct cttgttgatt ttgaattaat tttgcatatg    780

aatccattgc aaatatactc gatgtcgttt gtgccattac atcttggaat ccagctggtc    840

caagagaata gtttttcaca ttttcttgna gtacctttac attttgttct gctgcaaaag    900

gatgtaagga gatacgttac tcgttgccac ccagcaatca ttaccgctaa a             951
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We claim:

**1**. An isolated *Bacillus thuringiensis* strain comprising a disabling mutation at locus nhe whereby NHE enterotoxin is not produced, a disabling mutation at locus hbl$_{a2}$ whereby enterotoxin HBL$_{a2}$ is not produced, and a disabling mutation at one or more of loci hbl and hbl$_{a1}$, whereby at least one of enterotoxins HBL and HBL$_{a1}$ is not produced.

**2**. A *Bacillus thuringiensis* strain as claimed in claim **1**, wherein the disabling mutation at locus nhe comprises the disabling mutation of SEQ ID NO:111; wherein the disabling mutation at locus hbla$_2$ comprises the disabling mutation of SEQ ID NO:110; and wherein the one or more of the hbl and hbl$_{a1}$ loci comprise the disabling mutation of SEQ ID NO: 112 and SEQ ID NO: 113, respectively.

**3**. A *Bacillus thuringiensis* strain as claimed in claim **1** that is insecticidal.

**4**. A *Bacillus thuringiensis* strain as claimed in claim **1** that produces δ-endotoxin.

* * * * *