



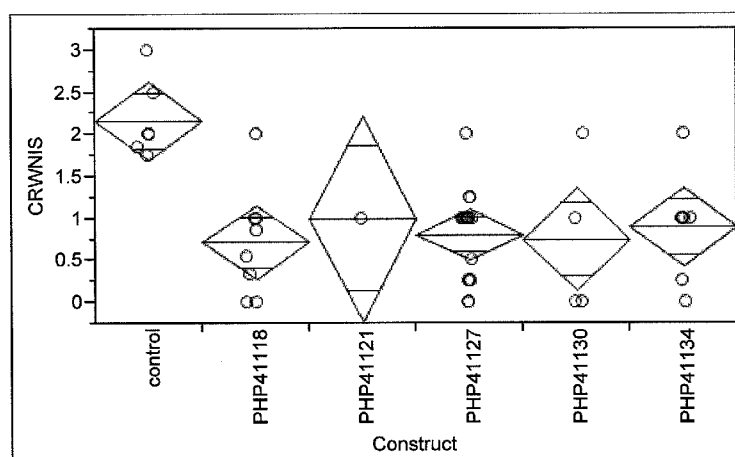
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(19) **United States**(12) **Patent Application Publication**
Broglie et al.(10) **Pub. No.: US 2011/0054007 A1**(43) **Pub. Date: Mar. 3, 2011**(54) **COMPOSITIONS AND METHODS TO
CONTROL INSECT PESTS**(75) Inventors: **Karen E. Broglie**, Landenberg, PA
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Company**, Wilmington, DE (US)(21) Appl. No.: **12/868,994**(22) Filed: **Aug. 26, 2010****Related U.S. Application Data**(60) Provisional application No. 61/330,484, filed on May
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C07H 21/02 (2006.01)**A01H 5/00** (2006.01)**A01H 5/10** (2006.01)**A01P 7/04** (2006.01)**C12N 5/10** (2006.01)**C12N 15/63** (2006.01)(52) **U.S. Cl. 514/44 A**; 536/24.5; 800/302; 435/419;
435/320.1; 435/412; 435/415; 435/416; 435/414(57) **ABSTRACT**

Methods and compositions are provided which employ a silencing element that, when ingested by a pest, such as a Coleopteran plant pest or a *Diabrotica* plant pest, decrease the expression of a target sequence in the pest. In specific embodiments, the decrease in expression of the target sequence controls the pest and thereby the methods and compositions are capable of limiting damage to a plant. The present invention provides various target polynucleotides set forth in any one of SEQ ID NOS: 1-236 or active variants and fragments thereof, wherein a decrease in expression of one or more the sequences in the target pest controls the pest (i.e., has insecticidal activity). Further provided are silencing elements which when ingested by the pest decrease the level of the target polypeptide and thereby control the pest. In specific embodiment, the pest is *D. virgifera virgifera*, *D. barberi*, *D. speciosa*, or *D. undecimpunctata howardi*. Plants, plant part, bacteria and other host cells comprising the silencing elements or an active variant or fragment thereof of the invention are also provided.

Figure 1

T0 Test of first RNAi candidates in SFX germplasm

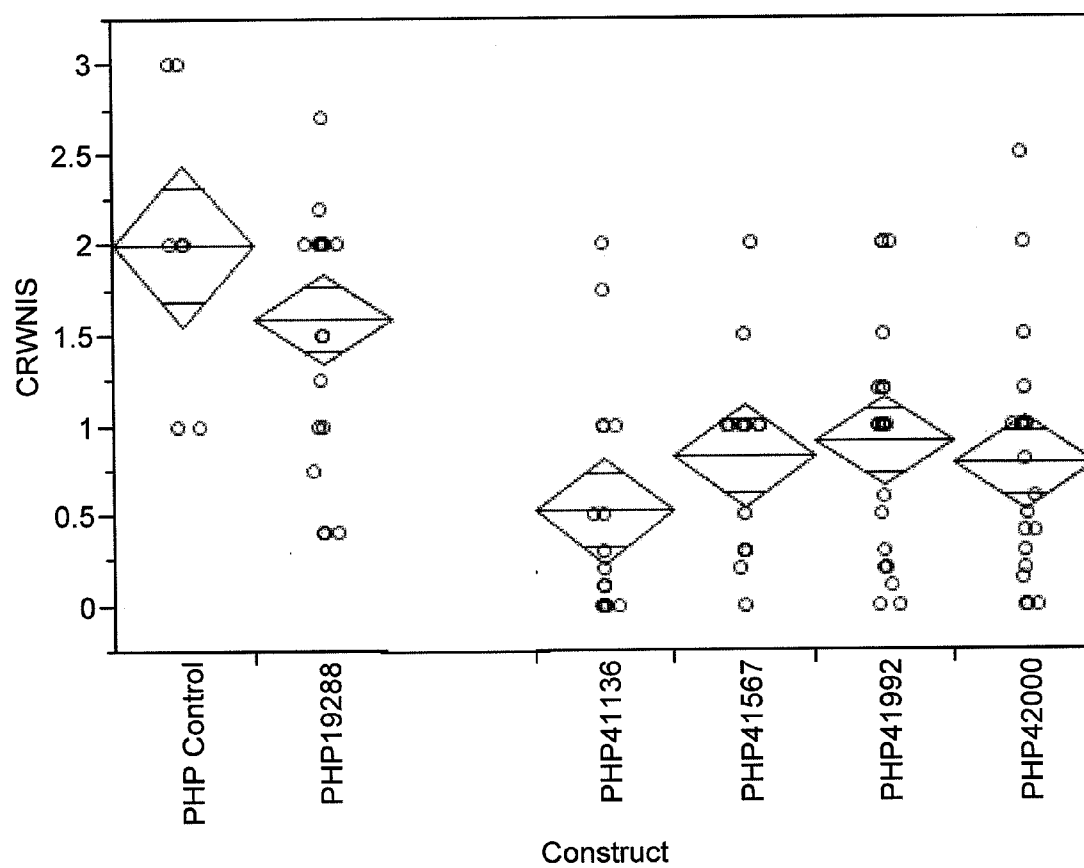


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Means Comparisons**Comparisons for all pairs using Tukey-Kramer HSD**

Construct	Gene	# events	Priority	Grouping	mean
Control		6		A	2.16
PHP41121	SEQ ID NO: 8 RIBOSOMAL PROTEIN S10E	1	17	AB	1
PHP41134	SEQ ID NO: 26 RIBOSOMAL PROTEIN	7	29	B	0.89
PHP41127	SEQ ID NO: 17 27kD PROTEINASE	22	44	B	0.81
PHP41130	SEQ ID NO: 28 Nucleoplasmin-like	4	12	B	0.75
PHP41118	SEQ ID NO: 10 NO HITS	8	26	B	0.72

Figure 2



COMPOSITIONS AND METHODS TO CONTROL INSECT PESTS

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of U.S. Provisional Application No. 61/330,484, filed on May 3, 2010 and U.S. Provisional Application No. 61/237,880, filed Aug. 28, 2009, the contents of which are herein incorporated by reference in their entirety.

FIELD OF THE INVENTION

[0002] The present invention relates generally to methods of molecular biology and gene silencing to control pests.

REFERENCE TO A SEQUENCE LISTING SUBMITTED AS A TEXT FILE VIA EFS-WEB

[0003] The official copy of the sequence listing is submitted concurrently with the specification as a text file via EFS-Web, in compliance with the American Standard Code for Information Interchange (ASCII), with a file name of 391924SEQLIST.txt, a creation date of Aug. 25, 2010 and a size of 306 Kb. The sequence listing filed via EFS-Web is part of the specification and is hereby incorporated in its entirety by reference herein.

BACKGROUND OF THE INVENTION

[0004] Insect pests are a serious problem in agriculture. They destroy millions of acres of staple crops such as corn, soybeans, peas, and cotton. Yearly, these pests cause over \$100 billion dollars in crop damage in the U.S. alone. In an ongoing seasonal battle, farmers must apply billions of gallons of synthetic pesticides to combat these pests. Other methods employed in the past delivered insecticidal activity by microorganisms or genes derived from microorganisms expressed in transgenic plants. For example, certain species of microorganisms of the genus *Bacillus* are known to possess pesticidal activity against a broad range of insect pests including Lepidoptera, Diptera, Coleoptera, Hemiptera, and others. In fact, microbial pesticides, particularly those obtained from *Bacillus* strains, have played an important role in agriculture as alternatives to chemical pest control. Agricultural scientists have developed crop plants with enhanced insect resistance by genetically engineering crop plants to produce insecticidal proteins from *Bacillus*. For example, corn and cotton plants genetically engineered to produce Cry toxins (see, e.g., Aronson (2002) *Cell Mol. Life Sci.* 59(3):417-425; Schnepf et al. (1998) *Microbiol. Mol. Biol. Rev.* 62(3):775-806) are now widely used in American agriculture and have provided the farmer with an alternative to traditional insect-control methods. However, these Bt insecticidal proteins only protect plants from a relatively narrow range of pests. Moreover, these modes of insecticidal activity provided varying levels of specificity and, in some cases, caused significant environmental consequences. Thus, there is an immediate need for alternative methods to control pests.

BRIEF SUMMARY OF THE INVENTION

[0005] Methods and compositions are provided which employ a silencing element that, when ingested by a pest, such as Coleopteran plant pest including a *Diabrotica* plant pest, is capable of decreasing the expression of a target

sequence in the pest. In specific embodiments, the decrease in expression of the target sequence controls the pest and thereby the methods and compositions are capable of limiting damage to a plant. The present invention provides various target polynucleotides as set forth in SEQ ID NOS: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236 or active variants or fragments thereof, wherein a decrease in expression of one or more the sequences in the target pest controls the pest (i.e., has insecticidal activity). Further provided are silencing elements, which when ingested by the pest, decrease the level of expression of one or more of the target polynucleotides. Plants, plant parts, plant cells, bacteria and other host cells comprising the silencing elements or an active variant or fragment thereof are also provided.

[0006] In another embodiment, a method for controlling a pest, such as a Coleopteran plant pest or a *Diabrotica* plant pest, is provided. The method comprises feeding to a pest a composition comprising a silencing element, wherein the silencing element, when ingested by the pest, reduces the level of a target sequence in the pest and thereby controls the pest. Further provided are methods to protect a plant from a pest. Such methods comprise introducing into the plant or plant part a silencing element of the invention. When the plant expressing the silencing element is ingested by the pest, the level of the target sequence is decreased and the pest is controlled.

BRIEF DESCRIPTION OF THE DRAWINGS

[0007] FIG. 1 shows a corn rootworm whole plant assay. The data demonstrates that expression of SEQ ID NO: 8 (clone idvlc.pk001.e9.f); SEQ ID NO: 26 (clone idvlc.pk003.p13.f); SEQ ID NO:17 (clone idvlc.pk003.f9.f); SEQ ID NO:28 (clone idvlc.pk004.d17.p); and SEQ ID NO:10 (clone idvlc.pk001.n1.f) as a hairpin in a maize plant produces a maize plant, which when ingested by corn root worm, has insecticidal activity. CRWNIS refers to corn root worm nodal injury score.

[0008] FIG. 2 shows a corn rootworm whole plant assay. The data demonstrates that expression of SEQ ID NO: 13 (clone idvlc.pk002.j171); SEQ ID NO: 40 (clone idvlc.pk013.h1.f); SEQ ID NO:72 (clone idvlc.pk017.d14.f); and SEQ ID NO:73 (clone idvlc.pk017.e22.f) as a hairpin in a maize plant produces a maize plant, which when ingested by corn root worm, has insecticidal activity. CRWNIS refers to

corn root worm nodal injury score. PHP19288 is a control plasmid lacking the silencing element.

DETAILED DESCRIPTION OF THE INVENTION

[0009] The present inventions now will be described more fully hereinafter with reference to the accompanying drawings, in which some, but not all embodiments of the inventions are shown. Indeed, these inventions may be embodied in many different forms and should not be construed as limited to the embodiments set forth herein; rather, these embodiments are provided so that this disclosure will satisfy applicable legal requirements. Like numbers refer to like elements throughout.

[0010] Many modifications and other embodiments of the inventions set forth herein will come to mind to one skilled in the art to which these inventions pertain having the benefit of the teachings presented in the foregoing descriptions and the associated drawings. Therefore, it is to be understood that the inventions are not to be limited to the specific embodiments disclosed and that modifications and other embodiments are intended to be included within the scope of the appended claims. Although specific terms are employed herein, they are used in a generic and descriptive sense only and not for purposes of limitation.

I. Overview

[0011] Frequently, RNAi discovery methods rely on evaluation of known classes of sensitive genes (transcription factors, housekeeping genes etc.). In contrast, the target polynucleotide set forth herein were identified based solely on high throughput screens of all singletons and representatives of all gene clusters from a cDNA library of neonate western corn rootworms. This screen allowed for the discovery of many novel sequences, many of which have extremely low or no homology to known sequences. This method provided the advantage of having no built in bias to genes that are frequently highly conserved across taxa. As a result, many novel targets for RNAi as well as known genes not previously shown to be sensitive to RNAi have been identified.

[0012] As such, methods and compositions are provided which employ a silencing element that, when ingested by a pest, such as a Coleopteran plant pest or a *Diabrotica* plant pest, is capable of decreasing the expression of a target sequence in the pest. In specific embodiments, the decrease in expression of the target sequence controls the pest and thereby the methods and compositions are capable of limiting damage to a plant or plant part. The present invention provides target polynucleotides as set forth in SEQ ID NOS: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212,

213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, or 236, or active variants and fragments thereof, including, for example, nucleotides 1-380 of SEQ ID NO: 45; nucleotides 1-266 of SEQ ID NO:50; SEQ ID NO:50; nucleotides 1-675 of SEQ ID NO:37; and nucleotides 1-132 of SEQ ID NO: 40. Silencing elements designed in view of these target polynucleotides are provided which, when ingested by the pest, decrease the expression of one or more of the target sequences and thereby controls the pest (i.e., has insecticidal activity).

[0013] As used herein, by “controlling a pest” or “controls a pest” is intended any affect on a pest that results in limiting the damage that the pest causes. Controlling a pest includes, but is not limited to, killing the pest, inhibiting development of the pest, altering fertility or growth of the pest in such a manner that the pest provides less damage to the plant, decreasing the number of offspring produced, producing less fit pests, producing pests more susceptible to predator attack, or deterring the pests from eating the plant.

[0014] Reducing the level of expression of the target polynucleotide or the polypeptide encoded thereby, in the pest results in the suppression, control, and/or killing the invading pathogenic organism. Reducing the level of expression of the target sequence of the pest will reduce the disease symptoms resulting from pathogen challenge by at least about 2% to at least about 6%, at least about 5% to about 50%, at least about 10% to about 60%, at least about 30% to about 70%, at least about 40% to about 80%, or at least about 50% to about 90% or greater. Hence, the methods of the invention can be utilized to control pests, particularly, Coleopteran plant pest or a *Diabrotica* plant pest.

[0015] Assays that measure the control of a pest are commonly known in the art, as are methods to quantitate disease resistance in plants following pathogen infection. See, for example, U.S. Pat. No. 5,614,395, herein incorporated by reference. Such techniques include, measuring over time, the average lesion diameter, the pathogen biomass, and the overall percentage of decayed plant tissues. See, for example, Thomma et al. (1998) *Plant Biology* 95:15107-15111, herein incorporated by reference. See, also Baum et al. (2007) *Nature Biotech* 11:1322-1326 and WO 2007/035650 which proved both whole plant feeding assays and corn root feeding assays. Both of these references are herein incorporated by reference in their entirety. See, also the examples below.

[0016] The invention is drawn to compositions and methods for protecting plants from a plant pest, such as Coleopteran plant pests or *Diabrotica* plant pests or inducing resistance in a plant to a plant pest, such as Coleopteran plant pests or *Diabrotica* plant pests. As used herein “Coleopteran plant pest” is used to refer to any member of the Coleoptera order.

[0017] As used herein, the term “*Diabrotica* plant pest” is used to refer to any member of the *Diabrotica* genus. Accordingly, the compositions and methods are also useful in protecting plants against any *Diabrotica* plant pest including, for example, *Diabrotica adelpha*; *Diabrotica amecameca*; *Diabrotica balteata*; *Diabrotica barberi*; *Diabrotica biannularis*; *Diabrotica cristata*; *Diabrotica decempunctata*; *Diabrotica dissimilis*; *Diabrotica lemniscata*; *Diabrotica limitata* (including, for example, *Diabrotica limitata quindecimpunctata*); *Diabrotica longicornis*; *Diabrotica nummularis*; *Diabrotica porracea*; *Diabrotica scutellata*; *Diabrotica sexmaculata*; *Diabrotica speciosa* (including, for example, *Diabrotica speciosa speciosa*); *Diabrotica tibialis*;

Diabrotica undecimpunctata (including, for example, *Diabrotica undecimpunctata duodecimnotata*; *Diabrotica undecimpunctata howardi* (spotted cucumber beetle); *Diabrotica undecimpunctata undecimpunctata* (western spotted cucumber beetle)); *Diabrotica virgifera* (including, for example, *Diabrotica virgifera virgifera* (western corn rootworm) and *Diabrotica virgifera zea* (Mexican corn rootworm)); *Diabrotica viridula*; *Diabrotica wartensis*; *Diabrotica* sp. JJG335; *Diabrotica* sp. JJG336; *Diabrotica* sp. JJG341; *Diabrotica* sp. JJG356; *Diabrotica* sp. JJG362; and, *Diabrotica* sp. JJG365.

[0018] In specific embodiments, the *Diabrotica* plant pest comprises *D. virgifera virgifera*, *D. barberi*, *D. speciosa* or *D. undecimpunctata howardi*.

II. Target Sequences

[0019] As used herein, a “target sequence” or “target polynucleotide” comprises any sequence in the pest that one desires to reduce the level of expression. In specific embodiments, decreasing the level of the target sequence in the pest controls the pest. For instance, the target sequence can be essential for growth and development. While the target sequence can be expressed in any tissue of the pest, in specific embodiments, the sequences targeted for suppression in the pest are expressed in cells of the gut tissue of the pest, cells in the midgut of the pest, and cells lining the gut lumen or the midgut. Such target sequences can be involved in, for example, gut cell metabolism, growth or differentiation. Non-limiting examples of target sequences of the invention include a polynucleotide set forth in SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, or 236 or variants and fragments thereof, including, for example, nucleotides 1-380 of SEQ ID NO: 45; nucleotides 1-266 of SEQ ID NO: 50; SEQ ID NO: 50; nucleotides 1-675 of SEQ ID NO: 37; and nucleotides 1-132 of SEQ ID NO: 40. As exemplified elsewhere herein, decreasing the level of expression of one or more of these target sequences in a Coleopteran plant pest or a *Diabrotica* plant pest controls the pest.

III. Silencing Elements

[0020] By “silencing element” is intended a polynucleotide which when ingested by a pest, is capable of reducing or eliminating the level or expression of a target polynucleotide or the polypeptide encoded thereby. The silencing element employed can reduce or eliminate the expression level of the target sequence by influencing the level of the target RNA transcript or, alternatively, by influencing translation and

thereby affecting the level of the encoded polypeptide. Methods to assay for functional silencing elements that are capable of reducing or eliminating the level of a sequence of interest are disclosed elsewhere herein. A single polynucleotide employed in the methods of the invention can comprise one or more silencing elements to the same or different target polynucleotides. The silencing element can be produced in vivo (i.e., in a host cell such as a plant or microorganism) or in vitro.

[0021] In specific embodiments, the target sequence is not endogenous to the plant. In other embodiments, while the silencing element controls pests, preferably the silencing element has no effect on the normal plant or plant part.

[0022] As discussed in further detail below, silencing elements can include, but are not limited to, a sense suppression element, an antisense suppression element, a double stranded RNA, a siRNA, a amiRNA, a miRNA, or a hairpin suppression element. Non-limiting examples of silencing elements that can be employed to decrease expression of these target Coleopteran plant pest sequences or *Diabrotica* plant pest sequences comprise fragments and variants of the sense or antisense sequence or consists of the sense or antisense sequence of the sequence set forth in SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236 or a biologically active variant or fragment thereof, including, for example, nucleotides 1-380 of SEQ ID NO: 45; nucleotides 1-266 of SEQ ID NO: 50; SEQ ID NO: 50; nucleotides 1-675 of SEQ ID NO: 37; and nucleotides 1-132 of SEQ ID NO: 40. The silencing element can further comprise additional sequences that advantageously effect transcription and/or the stability of a resulting transcript. For example, the silencing elements can comprise at least one thymine residue at the 3' end. This can aid in stabilization. Thus, the silencing elements can have at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more thymine residues at the 3' end. As discussed in further detail below, enhancer suppressor elements can also be employed in conjunction with the silencing elements disclosed herein.

[0023] By “reduces” or “reducing” the expression level of a polynucleotide or a polypeptide encoded thereby is intended to mean, the polynucleotide or polypeptide level of the target sequence is statistically lower than the polynucleotide level or polypeptide level of the same target sequence in an appropriate control pest which is not exposed to (i.e., has not ingested) the silencing element. In particular embodiments of the invention, reducing the polynucleotide level and/or the polypeptide level of the target sequence in a pest according to the invention results in less than 95%, less than 90%, less than 80%, less than 70%, less than 60%, less than 50%, less than

40%, less than 30%, less than 20%, less than 10%, or less than 5% of the polynucleotide level, or the level of the polypeptide encoded thereby, of the same target sequence in an appropriate control pest. Methods to assay for the level of the RNA transcript, the level of the encoded polypeptide, or the activity of the polynucleotide or polypeptide are discussed elsewhere herein.

[0024] i. Sense Suppression Elements

[0025] As used herein, a “sense suppression element” comprises a polynucleotide designed to express an RNA molecule corresponding to at least a part of a target messenger RNA in the “sense” orientation. Expression of the RNA molecule comprising the sense suppression element reduces or eliminates the level of the target polynucleotide or the polypeptide encoded thereby. The polynucleotide comprising the sense suppression element may correspond to all or part of the sequence of the target polynucleotide, all or part of the 5' and/or 3' untranslated region of the target polynucleotide, all or part of the coding sequence of the target polynucleotide, or all or part of both the coding sequence and the untranslated regions of the target polynucleotide.

[0026] Typically, a sense suppression element has substantial sequence identity to the target polynucleotide, typically greater than about 65% sequence identity, greater than about 85% sequence identity, about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity. See, U.S. Pat. Nos. 5,283,184 and 5,034,323; herein incorporated by reference. The sense suppression element can be any length so long as it allows for the suppression of the targeted sequence. The sense suppression element can be, for example, 15, 16, 17, 18, 19, 20, 22, 25, 30, 50, 100, 150, 200, 250, 300, 350, 400, 450, 500, 600, 700, 900, 1000, 1100, 1200, 1300 nucleotides or longer of the target polynucleotides set forth in any of SEQ ID NO:1-106. In other embodiments, the sense suppression element can be, for example, about 15-25, 19-35, 19-50, 25-100, 100-150, 150-200, 200-250, 250-300, 300-350, 350-400, 450-500, 500-550, 550-600, 600-650, 650-700, 700-750, 750-800, 800-850, 850-900, 900-950, 950-1000, 1000-1050, 1050-1100, 1100-1200, 1200-1300, 1300-1400, 1400-1500, 1500-1600, 1600-1700, 1700-1800 nucleotides or longer of the target polynucleotides set forth in any of SEQ ID NO:1-236.

[0027] ii. Antisense Suppression Elements

[0028] As used herein, an “antisense suppression element” comprises a polynucleotide which is designed to express an RNA molecule complementary to all or part of a target messenger RNA. Expression of the antisense RNA suppression element reduces or eliminates the level of the target polynucleotide. The polynucleotide for use in antisense suppression may correspond to all or part of the complement of the sequence encoding the target polynucleotide, all or part of the complement of the 5' and/or 3' untranslated region of the target polynucleotide, all or part of the complement of the coding sequence of the target polynucleotide, or all or part of the complement of both the coding sequence and the untranslated regions of the target polynucleotide. In addition, the antisense suppression element may be fully complementary (i.e., 100% identical to the complement of the target sequence) or partially complementary (i.e., less than 100% identical to the complement of the target sequence) to the target polynucleotide. In specific embodiments, the antisense suppression element comprises at least 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence complementarity to the target polynucleotide. Antisense sup-

pression may be used to inhibit the expression of multiple proteins in the same plant. See, for example, U.S. Pat. No. 5,942,657. Furthermore, the antisense suppression element can be complementary to a portion of the target polynucleotide. Generally, sequences of at least 15, 16, 17, 18, 19, 20, 22, 25, 50, 100, 200, 300, 400, 450 nucleotides or greater of the sequence set forth in any of SEQ ID NO:1-236 may be used. Methods for using antisense suppression to inhibit the expression of endogenous genes in plants are described, for example, in Liu et al (2002) *Plant Physiol.* 129:1732-1743 and U.S. Pat. Nos. 5,759,829 and 5,942,657, each of which is herein incorporated by reference.

[0029] iii. Double Stranded RNA Suppression Element

[0030] A “double stranded RNA silencing element” or “dsRNA” comprises at least one transcript that is capable of forming a dsRNA either before or after ingestion by a pest. Thus, a “dsRNA silencing element” includes a dsRNA, a transcript or polyribonucleotide capable of forming a dsRNA or more than one transcript or polyribonucleotide capable of forming a dsRNA. “Double stranded RNA” or “dsRNA” refers to a polyribonucleotide structure formed either by a single self-complementary RNA molecule or a polyribonucleotide structure formed by the expression of least two distinct RNA strands. The dsRNA molecule(s) employed in the methods and compositions of the invention mediate the reduction of expression of a target sequence, for example, by mediating RNA interference “RNAi” or gene silencing in a sequence-specific manner. In the context of the present invention, the dsRNA is capable of reducing or eliminating the level or expression of a target polynucleotide or the polypeptide encoded thereby in a pest.

[0031] The dsRNA can reduce or eliminate the expression level of the target sequence by influencing the level of the target RNA transcript, by influencing translation and thereby affecting the level of the encoded polypeptide, or by influencing expression at the pre-transcriptional level (i.e., via the modulation of chromatin structure, methylation pattern, etc., to alter gene expression). See, for example, Verdel et al. (2004) *Science* 303:672-676; Pal-Bhadra et al. (2004) *Science* 303:669-672; Allshire (2002) *Science* 297:1818-1819; Volpe et al. (2002) *Science* 297:1833-1837; Jenuwein (2002) *Science* 297:2215-2218; and Hall et al. (2002) *Science* 297:2232-2237. Methods to assay for functional dsRNA that are capable of reducing or eliminating the level of a sequence of interest are disclosed elsewhere herein. Accordingly, as used herein, the term “dsRNA” is meant to encompass other terms used to describe nucleic acid molecules that are capable of mediating RNA interference or gene silencing, including, for example, short-interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA), hairpin RNA, short hairpin RNA (shRNA), post-transcriptional gene silencing RNA (ptgsRNA), and others.

[0032] In specific embodiments, at least one strand of the duplex or double-stranded region of the dsRNA shares sufficient sequence identity or sequence complementarity to the target polynucleotide to allow for the dsRNA to reduce the level of expression of the target sequence. As used herein, the strand that is complementary to the target polynucleotide is the “antisense strand” and the strand homologous to the target polynucleotide is the “sense strand.”

[0033] In another embodiment, the dsRNA comprises a hairpin RNA. A hairpin RNA comprises an RNA molecule that is capable of folding back onto itself to form a double stranded structure. Multiple structures can be employed as

hairpin elements. In specific embodiments, the dsRNA suppression element comprises a hairpin element which comprises in the following order, a first segment, a second segment, and a third segment, where the first and the third segment share sufficient complementarity to allow the transcribed RNA to form a double-stranded stem-loop structure.

[0034] The “second segment” of the hairpin comprises a “loop” or a “loop region.” These terms are used synonymously herein and are to be construed broadly to comprise any nucleotide sequence that confers enough flexibility to allow self-pairing to occur between complementary regions of a polynucleotide (i.e., segments 1 and 3 which form the stem of the hairpin). For example, in some embodiments, the loop region may be substantially single stranded and act as a spacer between the self-complementary regions of the hairpin stem-loop. In some embodiments, the loop region can comprise a random or nonsense nucleotide sequence and thus not share sequence identity to a target polynucleotide. In other embodiments, the loop region comprises a sense or an anti-sense RNA sequence or fragment thereof that shares identity to a target polynucleotide. See, for example, International Patent Publication No. WO 02/00904, herein incorporated by reference. In specific embodiments, the loop region can be optimized to be as short as possible while still providing enough intramolecular flexibility to allow the formation of the base-paired stem region. Accordingly, the loop sequence is generally less than 1000, 900, 800, 700, 600, 500, 400, 300, 200, 100, 50, 25, 20, 19, 18, 17, 16, 15, 10 nucleotides or less.

[0035] The “first” and the “third” segment of the hairpin RNA molecule comprise the base-paired stem of the hairpin structure. The first and the third segments are inverted repeats of one another and share sufficient complementarity to allow the formation of the base-paired stem region. In specific embodiments, the first and the third segments are fully complementary to one another. Alternatively, the first and the third segment may be partially complementary to each other so long as they are capable of hybridizing to one another to form a base-paired stem region. The amount of complementarity between the first and the third segment can be calculated as a percentage of the entire segment. Thus, the first and the third segment of the hairpin RNA generally share at least 50%, 60%, 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, up to and including 100% complementarity.

[0036] The first and the third segment are at least about 1000, 500, 475, 450, 425, 400, 375, 350, 325, 300, 250, 225, 200, 175, 150, 125, 100, 75, 60, 50, 40, 30, 25, 22, 20, 19, 18, 17, 16, 15 or 10 nucleotides in length. In specific embodiments, the length of the first and/or the third segment is about 10-100 nucleotides, about 10 to about 75 nucleotides, about 10 to about 50 nucleotides, about 10 to about 40 nucleotides, about 10 to about 35 nucleotides, about 10 to about 30 nucleotides, about 10 to about 25 nucleotides, about 10 to about 19 nucleotides, about 10 to about 20 nucleotides, about 19 to about 50 nucleotides, about 50 nucleotides to about 100 nucleotides, about 100 nucleotides to about 150 nucleotides, about 100 nucleotides to about 300 nucleotides, about 150 nucleotides to about 200 nucleotides, about 200 nucleotides to about 250 nucleotides, about 250 nucleotides to about 300 nucleotides, about 300 nucleotides to about 350 nucleotides, about 350 nucleotides to about 400 nucleotides, about 400 nucleotide to about 500 nucleotides, about 600 nt, about 700 nt, about 800 nt, about 900 nt, about 1000 nt, about 1100 nt, about 1200 nt, 1300 nt, 1400 nt, 1500 nt, 1600 nt, 1700 nt,

1800 nt, 1900 nt, 2000 nt or longer. In other embodiments, the length of the first and/or the third segment comprises at least 10-19 nucleotides, 10-20 nucleotides; 19-35 nucleotides, 20-35 nucleotides; 30-45 nucleotides; 40-50 nucleotides; 50-100 nucleotides; 100-300 nucleotides; about 500-700 nucleotides; about 700-900 nucleotides; about 900-1100 nucleotides; about 1300-1500 nucleotides; about 1500-1700 nucleotides; about 1700-1900 nucleotides; about 1900-2100 nucleotides; about 2100-2300 nucleotides; or about 2300-2500 nucleotides. See, for example, International Publication No. WO 0200904. In non-limiting examples the first stem of the hairpin comprises nucleotides 1-380 of SEQ ID NO: 45; nucleotides 1-266 of SEQ ID NO:50; nucleotides 1-675 of SEQ ID NO:37; or nucleotides 1-132 of SEQ ID NO: 40 or active variants and fragments thereof. In specific embodiments, the first and the third segment comprise at least 20 nucleotides having at least 85% complementary to the first segment. In still other embodiments, the first and the third segments which form the stem-loop structure of the hairpin comprises 3' or 5' overhang regions having unpaired nucleotide residues.

[0037] In specific embodiments, the sequences used in the first, the second, and/or the third segments comprise domains that are designed to have sufficient sequence identity to a target polynucleotide of interest and thereby have the ability to decrease the level of expression of the target polynucleotide. The specificity of the inhibitory RNA transcripts is therefore generally conferred by these domains of the silencing element. Thus, in some embodiments of the invention, the first, second and/or third segment of the silencing element comprise a domain having at least 10, at least 15, at least 19, at least 20, at least 21, at least 22, at least 23, at least 24, at least 25, at least 30, at least 40, at least 50, at least 100, at least 200, at least 300, at least 500, at least 1000, or more than 1000 nucleotides that share sufficient sequence identity to the target polynucleotide to allow for a decrease in expression levels of the target polynucleotide when expressed in an appropriate cell. In other embodiments, the domain is between about 15 to 50 nucleotides, about 19-35 nucleotides, about 20-35 nucleotides, about 25-50 nucleotides, about 19 to 75 nucleotides, about 20 to 75 nucleotides, about 40-90 nucleotides about 15-100 nucleotides 10-100 nucleotides, about 10 to about 75 nucleotides, about 10 to about 50 nucleotides, about 10 to about 40 nucleotides, about 10 to about 35 nucleotides, about 10 to about 30 nucleotides, about 10 to about 25 nucleotides, about 10 to about 20 nucleotides, about 10 to about 19 nucleotides, about 50 nucleotides to about 100 nucleotides, about 100 nucleotides to about 150 nucleotides, about 150 nucleotides to about 200 nucleotides, about 200 nucleotides to about 250 nucleotides, about 250 nucleotides to about 300 nucleotides, about 300 nucleotides to about 350 nucleotides, about 350 nucleotides to about 400 nucleotides, about 400 nucleotide to about 500 nucleotides or longer. In other embodiments, the length of the first and/or the third segment comprises at least 10-20 nucleotides, at least 10-19 nucleotides, 20-35 nucleotides, 30-45 nucleotides, 40-50 nucleotides, 50-100 nucleotides, or about 100-300 nucleotides.

[0038] In specific embodiments, the domain of the first, the second, and/or the third segment has 100% sequence identity to the target polynucleotide. In other embodiments, the domain of the first, the second and/or the third segment having homology to the target polypeptide have at least 50%, 60%, 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or greater sequence identity to a region

of the target polynucleotide. The sequence identity of the domains of the first, the second and/or the third segments to the target polynucleotide need only be sufficient to decrease expression of the target polynucleotide of interest. See, for example, Chuang and Meyerowitz (2000) *Proc. Natl. Acad. Sci. USA* 97:4985-4990; Stoutjesdijk et al. (2002) *Plant Physiol.* 129:1723-1731; Waterhouse and Helliwell (2003) *Nat. Rev. Genet.* 4:29-38; Pandolfini et al. *BMC Biotechnology* 3:7, and U.S. Patent Publication No. 20030175965; each of which is herein incorporated by reference. A transient assay for the efficiency of hpRNA constructs to silence gene expression in vivo has been described by Panstruga et al. (2003) *Mol. Biol. Rep.* 30:135-140, herein incorporated by reference.

[0039] The amount of complementarity shared between the first, second, and/or third segment and the target polynucleotide or the amount of complementarity shared between the first segment and the third segment (i.e., the stem of the hairpin structure) may vary depending on the organism in which gene expression is to be controlled. Some organisms or cell types may require exact pairing or 100% identity, while other organisms or cell types may tolerate some mismatching. In some cells, for example, a single nucleotide mismatch in the targeting sequence abrogates the ability to suppress gene expression. In these cells, the suppression cassettes of the invention can be used to target the suppression of mutant genes, for example, oncogenes whose transcripts comprise point mutations and therefore they can be specifically targeted using the methods and compositions of the invention without altering the expression of the remaining wild-type allele.

[0040] Any region of the target polynucleotide can be used to design the domain of the silencing element that shares sufficient sequence identity to allow expression of the hairpin transcript to decrease the level of the target polynucleotide. For instance, the domain can be designed to share sequence identity to the 5' untranslated region of the target polynucleotide(s), the 3' untranslated region of the target polynucleotide(s), exonic regions of the target polynucleotide(s), intronic regions of the target polynucleotide(s), and any combination thereof. In specific embodiments, a domain of the silencing element shares sufficient homology to at least about 15, 16, 17, 18, 19, 20, 22, 25 or 30 consecutive nucleotides from about nucleotides 1-50, 25-75, 75-125, 50-100, 125-175, 175-225, 100-150, 150-200, 200-250, 225-275, 275-325, 250-300, 325-375, 375-425, 300-350, 350-400, 425-475, 400-450, 475-525, 450-500, 525-575, 575-625, 550-600, 625-675, 675-725, 600-650, 625-675, 675-725, 650-700, 725-825, 825-875, 750-800, 875-925, 925-975, 850-900, 925-975, 975-1025, 950-1000, 1000-1050, 1025-1075, 1075-1125, 1050-1100, 1125-1175, 1100-1200, 1175-1225, 1225-1275, 1200-1300, 1325-1375, 1375-1425, 1300-1400, 1425-1475, 1475-1525, 1400-1500, 1525-1575, 1575-1625, 1625-1675, 1675-1725, 1725-1775, 1775-1825, 1825-1875, 1875-1925, 1925-1975, 1975-2025, 2025-2075, 2075-2125, 2125-2175, 2175-2225, 1500-1600, 1600-1700, 1700-1800, 1800-1900, 1900-2000 of the target sequence. In some instances to optimize the siRNA sequences employed in the hairpin, the synthetic oligodeoxyribonucleotide/RNase H method can be used to determine sites on the target mRNA that are in a conformation that is susceptible to RNA silencing. See, for example, Vickers et al. (2003) *J. Biol. Chem.* 278:7108-7118 and Yang et al. (2002) *Proc. Natl. Acad. Sci. USA* 99:9442-9447, herein incorporated by reference. These

studies indicate that there is a significant correlation between the RNase-H-sensitive sites and sites that promote efficient siRNA-directed mRNA degradation.

[0041] The hairpin silencing element may also be designed such that the sense sequence or the antisense sequence do not correspond to a target polynucleotide. In this embodiment, the sense and antisense sequence flank a loop sequence that comprises a nucleotide sequence corresponding to all or part of the target polynucleotide. Thus, it is the loop region that determines the specificity of the RNA interference. See, for example, WO 02/00904, herein incorporated by reference.

[0042] In addition, transcriptional gene silencing (TGS) may be accomplished through use of a hairpin suppression element where the inverted repeat of the hairpin shares sequence identity with the promoter region of a target polynucleotide to be silenced. See, for example, Aufsatz et al. (2002) *PNAS* 99 (Suppl. 4):16499-16506 and Mette et al. (2000) *EMBO J* 19(19):5194-5201. In other embodiments, the dsRNA can comprise a small RNA (sRNA). sRNAs can comprise both micro RNA (miRNA) and short-interfering RNA (siRNA) (Meister and Tuschl (2004) *Nature* 431:343-349 and Bonetta et al. (2004) *Nature Methods* 1:79-86). miRNAs are regulatory agents comprising about 19 ribonucleotides which are highly efficient at inhibiting the expression of target polynucleotides. See, for example Javier et al. (2003) *Nature* 425: 257-263, herein incorporated by reference. For miRNA interference, the silencing element can be designed to express a dsRNA molecule that forms a hairpin structure containing a 19-nucleotide sequence that is complementary to the target polynucleotide of interest. The miRNA can be synthetically made, or transcribed as a longer RNA which is subsequently cleaved to produce the active miRNA. Specifically, the miRNA can comprise 19 nucleotides of the sequence having homology to a target polynucleotide in sense orientation and 19 nucleotides of a corresponding antisense sequence that is complementary to the sense sequence.

[0043] When expressing an miRNA, it is recognized that various forms of an miRNA can be transcribed including, for example, the primary transcript (termed the "pri-miRNA") which is processed through various nucleolytic steps to a shorter precursor miRNA (termed the "pre-miRNA"); the pre-miRNA; or the final (mature) miRNA is present in a duplex, the two strands being referred to as the miRNA (the strand that will eventually basepair with the target) and miRNA*. The pre-miRNA is a substrate for a form of dicer that removes the miRNA/miRNA* duplex from the precursor, after which, similarly to siRNAs, the duplex can be taken into the RISC complex. It has been demonstrated that miRNAs can be transgenically expressed and be effective through expression of a precursor form, rather than the entire primary form (Parizotto et al. (2004) *Genes & Development* 18:2237-2242 and Guo et al. (2005) *Plant Cell* 17:1376-1386).

[0044] The methods and compositions of the invention employ silencing elements that when transcribed "form" a dsRNA molecule. Accordingly, the heterologous polynucleotide being expressed need not form the dsRNA by itself, but can interact with other sequences in the plant cell or in the pest gut after ingestion to allow the formation of the dsRNA. For example, a chimeric polynucleotide that can selectively silence the target polynucleotide can be generated by expressing a chimeric construct comprising the target sequence for a miRNA or siRNA to a sequence corresponding to all or part of the gene or genes to be silenced. In this embodiment, the dsRNA is "formed" when the target for the miRNA or siRNA

interacts with the miRNA present in the cell. The resulting dsRNA can then reduce the level of expression of the gene or genes to be silenced. See, for example, US Application Publication 2007-0130653, entitled "Methods and Compositions for Gene Silencing", herein incorporated by reference. The construct can be designed to have a target for an endogenous miRNA or alternatively, a target for a heterologous and/or synthetic miRNA can be employed in the construct. If a heterologous and/or synthetic miRNA is employed, it can be introduced into the cell on the same nucleotide construct as the chimeric polynucleotide or on a separate construct. As discussed elsewhere herein, any method can be used to introduce the construct comprising the heterologous miRNA.

IV. Variants and Fragments

[0045] By "fragment" is intended a portion of the polynucleotide or a portion of the amino acid sequence and hence protein encoded thereby. Fragments of a polynucleotide may encode protein fragments that retain the biological activity of the native protein. Alternatively, fragments of a polynucleotide that are useful as a silencing element do not need to encode fragment proteins that retain biological activity. Thus, fragments of a nucleotide sequence may range from at least about 10, about 15, about 19 nucleotides, about 20 nucleotides, about 22 nucleotides, about 50 nucleotides, about 75 nucleotides, about 100 nucleotides, 200 nucleotides, 300 nucleotides, 400 nucleotides, 500 nucleotides, 600 nucleotides, 700 nucleotides and up to the full-length polynucleotide employed in the invention. Alternatively, fragments of a nucleotide sequence may range from 1-50, 25-75, 75-125, 50-100, 125-175, 175-225, 100-150, 100-300, 150-200, 200-250, 225-275, 275-325, 250-300, 325-375, 375-425, 300-350, 350-400, 425-475, 400-450, 475-525, 450-500, 525-575, 575-625, 550-600, 625-675, 675-725, 600-650, 625-675, 675-725, 650-700, 725-825, 825-875, 750-800, 875-925, 925-975, 850-900, 925-975, 975-1025, 950-1000, 1000-1050, 1025-1075, 1075-1125, 1050-1100, 1125-1175, 1100-1200, 1175-1225, 1225-1275, 1200-1300, 1325-1375, 1375-1425, 1300-1400, 1425-1475, 1475-1525, 1400-1500, 1525-1575, 1575-1625, 1625-1675, 1675-1725, 1725-1775, 1775-1825, 1825-1875, 1875-1925, 1925-1975, 1975-2025, 2025-2075, 2075-2125, 2125-2175, 2175-2225, 1500-1600, 1600-1700, 1700-1800, 1800-1900, 1900-2000 of any one of SEQ ID NO: 1-236. Methods to assay for the activity of a desired silencing element are described elsewhere herein.

[0046] "Variants" is intended to mean substantially similar sequences. For polynucleotides, a variant comprises a deletion and/or addition of one or more nucleotides at one or more internal sites within the native polynucleotide and/or a substitution of one or more nucleotides at one or more sites in the native polynucleotide. A variant of a polynucleotide that is useful as a silencing element will retain the ability to reduce expression of the target polynucleotide and, in some embodiments, thereby control a pest of interest. As used herein, a "native" polynucleotide or polypeptide comprises a naturally occurring nucleotide sequence or amino acid sequence, respectively. For polynucleotides, conservative variants include those sequences that, because of the degeneracy of the genetic code, encode the amino acid sequence of one of the polypeptides employed in the invention. Variant polynucleotides also include synthetically derived polynucleotide, such as those generated, for example, by using site-directed mutagenesis, but continue to retain the desired activity. Generally, variants of a particular polynucleotide of

the invention (i.e., a silencing element) will have at least about 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity to that particular polynucleotide as determined by sequence alignment programs and parameters described elsewhere herein.

[0047] Variants of a particular polynucleotide of the invention (i.e., the reference polynucleotide) can also be evaluated by comparison of the percent sequence identity between the polypeptide encoded by a variant polynucleotide and the polypeptide encoded by the reference polynucleotide. Percent sequence identity between any two polypeptides can be calculated using sequence alignment programs and parameters described elsewhere herein. Where any given pair of polynucleotides employed in the invention is evaluated by comparison of the percent sequence identity shared by the two polypeptides they encode, the percent sequence identity between the two encoded polypeptides is at least about 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity.

[0048] The following terms are used to describe the sequence relationships between two or more polynucleotides or polypeptides: (a) "reference sequence", (b) "comparison window", (c) "sequence identity", and, (d) "percentage of sequence identity."

[0049] (a) As used herein, "reference sequence" is a defined sequence used as a basis for sequence comparison. A reference sequence may be a subset or the entirety of a specified sequence; for example, as a segment of a full-length cDNA or gene sequence, or the complete cDNA or gene sequence.

[0050] (b) As used herein, "comparison window" makes reference to a contiguous and specified segment of a polynucleotide sequence, wherein the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two polynucleotides. Generally, the comparison window is at least 20 contiguous nucleotides in length, and optionally can be 30, 40, 50, 100, or longer. Those of skill in the art understand that to avoid a high similarity to a reference sequence due to inclusion of gaps in the polynucleotide sequence a gap penalty is typically introduced and is subtracted from the number of matches.

[0051] Unless otherwise stated, sequence identity/similarity values provided herein refer to the value obtained using GAP Version 10 using the following parameters: % identity and % similarity for a nucleotide sequence using GAP Weight of 50 and Length Weight of 3, and the nws gapdna.cmp scoring matrix; % identity and % similarity for an amino acid sequence using GAP Weight of 8 and Length Weight of 2, and the BLOSUM62 scoring matrix; or any equivalent program thereof. By "equivalent program" is intended any sequence comparison program that, for any two sequences in question, generates an alignment having identical nucleotide or amino acid residue matches and an identical percent sequence identity when compared to the corresponding alignment generated by GAP Version 10.

[0052] (c) As used herein, "sequence identity" or "identity" in the context of two polynucleotides or polypeptide sequences makes reference to the residues in the two sequences that are the same when aligned for maximum correspondence over a specified comparison window. When percentage of sequence identity is used in reference to proteins it

is recognized that residue positions which are not identical often differ by conservative amino acid substitutions, where amino acid residues are substituted for other amino acid residues with similar chemical properties (e.g., charge or hydrophobicity) and therefore do not change the functional properties of the molecule. When sequences differ in conservative substitutions, the percent sequence identity may be adjusted upwards to correct for the conservative nature of the substitution. Sequences that differ by such conservative substitutions are said to have “sequence similarity” or “similarity”. Means for making this adjustment are well known to those of skill in the art. Typically this involves scoring a conservative substitution as a partial rather than a full mismatch, thereby increasing the percentage sequence identity. Thus, for example, where an identical amino acid is given a score of 1 and a non-conservative substitution is given a score of zero, a conservative substitution is given a score between zero and 1. The scoring of conservative substitutions is calculated, e.g., as implemented in the program PC/GENE (Intelligenetics, Mountain View, Calif.).

[0053] (d) As used herein, “percentage of sequence identity” means the value determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison, and multiplying the result by 100 to yield the percentage of sequence identity.

[0054] A method is further provided for identifying a silencing element from the target polynucleotides set forth in SEQ ID NO:1-236. Such methods comprise obtaining a candidate fragment of any one of SEQ ID NO:1-236 which is of sufficient length to act as a silencing element and thereby reduce the expression of the target polynucleotide and/or control a desired pest; expressing said candidate polynucleotide fragment in an appropriate expression cassette to produce a candidate silencing element and determining if said candidate polynucleotide fragment has the activity of a silencing element and thereby reduce the expression of the target polynucleotide and/or controls a desired pest. Methods of identifying such candidate fragments based on the desired pathway for suppression are known. For example, various bioinformatics programs can be employed to identify the region of the target polynucleotides that could be exploited to generate a silencing element. See, for example, Elbahir et al. (2001) *Genes and Development* 15:188-200, Schwartz et al. (2003) *Cell* 115:199-208, Khvorova et al. (2003) *Cell* 115:209-216. See also, siRNA at Whitehead (jura.wi.mit.edu/bioc/siRNAext/) which calculates the binding energies for both sense and antisense siRNAs. See, also genscript.com/ssl-bin/app/mai?op=known; Block-iT™ RNAi designer from Invitrogen and GenScript siRNA Construct Builder.

V. DNA Constructs

[0055] The use of the term “polynucleotide” is not intended to limit the present invention to polynucleotides comprising DNA. Those of ordinary skill in the art will recognize that polynucleotides can comprise ribonucleotides and combina-

tions of ribonucleotides and deoxyribonucleotides. Such deoxyribonucleotides and ribonucleotides include both naturally occurring molecules and synthetic analogues. The polynucleotides of the invention also encompass all forms of sequences including, but not limited to, single-stranded forms, double-stranded forms, hairpins, stem-and-loop structures, and the like.

[0056] The polynucleotide encoding the silencing element or in specific embodiments employed in the methods and compositions of the invention can be provided in expression cassettes for expression in a plant or organism of interest. It is recognized that multiple silencing elements including multiple identical silencing elements, multiple silencing elements targeting different regions of the target sequence, or multiple silencing elements from different target sequences can be used. In this embodiment, it is recognized that each silencing element can be contained in a single or separate cassette, DNA construct, or vector. As discussed, any means of providing the silencing element is contemplated. A plant or plant cell can be transformed with a single cassette comprising DNA encoding one or more silencing elements or separate cassettes comprising each silencing element can be used to transform a plant or plant cell or host cell. Likewise, a plant transformed with one component can be subsequently transformed with the second component. One or more silencing elements can also be brought together by sexual crossing. That is, a first plant comprising one component is crossed with a second plant comprising the second component. Progeny plants from the cross will comprise both components.

[0057] The expression cassette can include 5' and 3' regulatory sequences operably linked to the polynucleotide of the invention. “Operably linked” is intended to mean a functional linkage between two or more elements. For example, an operable linkage between a polynucleotide of the invention and a regulatory sequence (i.e., a promoter) is a functional link that allows for expression of the polynucleotide of the invention. Operably linked elements may be contiguous or non-contiguous. When used to refer to the joining of two protein coding regions, by operably linked is intended that the coding regions are in the same reading frame. The cassette may additionally contain at least one additional polynucleotide to be cotransformed into the organism. Alternatively, the additional polypeptide(s) can be provided on multiple expression cassettes. Expression cassettes can be provided with a plurality of restriction sites and/or recombination sites for insertion of the polynucleotide to be under the transcriptional regulation of the regulatory regions. The expression cassette may additionally contain selectable marker genes.

[0058] The expression cassette can include in the 5'-3' direction of transcription, a transcriptional and translational initiation region (i.e., a promoter), a polynucleotide comprising the silencing element employed in the methods and compositions of the invention, and a transcriptional and translational termination region (i.e., termination region) functional in plants. In other embodiment, the double stranded RNA is expressed from a suppression cassette. Such a cassette can comprise two convergent promoters that drive transcription of an operably linked silencing element. “Convergent promoters” refers to promoters that are oriented on either terminus of the operably linked silencing element such that each promoter drives transcription of the silencing element in opposite directions, yielding two transcripts. In such embodi-

ments, the convergent promoters allow for the transcription of the sense and anti-sense strand and thus allow for the formation of a dsRNA.

[0059] The regulatory regions (i.e., promoters, transcriptional regulatory regions, and translational termination regions) and/or the polynucleotides employed in the invention may be native/analogous to the host cell or to each other. Alternatively, the regulatory regions and/or the polynucleotide employed in the invention may be heterologous to the host cell or to each other. As used herein, "heterologous" in reference to a sequence is a sequence that originates from a foreign species, or, if from the same species, is substantially modified from its native form in composition and/or genomic locus by deliberate human intervention. For example, a promoter operably linked to a heterologous polynucleotide is from a species different from the species from which the polynucleotide was derived, or, if from the same/analogous species, one or both are substantially modified from their original form and/or genomic locus, or the promoter is not the native promoter for the operably linked polynucleotide. As used herein, a chimeric gene comprises a coding sequence operably linked to a transcription initiation region that is heterologous to the coding sequence.

[0060] The termination region may be native with the transcriptional initiation region, may be native with the operably linked polynucleotide encoding the silencing element, may be native with the plant host, or may be derived from another source (i.e., foreign or heterologous) to the promoter, the polynucleotide comprising silencing element, the plant host, or any combination thereof. Convenient termination regions are available from the Ti-plasmid of *A. tumefaciens*, such as the octopine synthase and nopaline synthase termination regions. See also Guerineau et al. (1991) *Mol. Gen. Genet.* 262:141-144; Proudfoot (1991) *Cell* 64:671-674; Sanfacon et al. (1991) *Genes Dev.* 5:141-149; Mogen et al. (1990) *Plant Cell* 2:1261-1272; Munroe et al. (1990) *Gene* 91:151-158; Ballas et al. (1989) *Nucleic Acids Res.* 17:7891-7903; and Joshi et al. (1987) *Nucleic Acids Res.* 15:9627-9639.

[0061] Additional sequence modifications are known to enhance gene expression in a cellular host. These include elimination of sequences encoding spurious polyadenylation signals, exon-intron splice site signals, transposon-like repeats, and other such well-characterized sequences that may be deleterious to gene expression. The G-C content of the sequence may be adjusted to levels average for a given cellular host, as calculated by reference to known genes expressed in the host cell. When possible, the sequence is modified to avoid predicted hairpin secondary mRNA structures.

[0062] In preparing the expression cassette, the various DNA fragments may be manipulated, so as to provide for the DNA sequences in the proper orientation and, as appropriate, in the proper reading frame. Toward this end, adapters or linkers may be employed to join the DNA fragments or other manipulations may be involved to provide for convenient restriction sites, removal of superfluous DNA, removal of restriction sites, or the like. For this purpose, in vitro mutagenesis, primer repair, restriction, annealing, resubstitutions, e.g., transitions and transversions, may be involved.

[0063] A number of promoters can be used in the practice of the invention. The polynucleotide encoding the silencing element can be combined with constitutive, tissue-preferred, or other promoters for expression in plants.

[0064] Such constitutive promoters include, for example, the core promoter of the Rsyn7 promoter and other constitutive

promoters disclosed in WO 99/43838 and U.S. Pat. No. 6,072,050; the core CaMV 35S promoter (Odell et al. (1985) *Nature* 313:810-812); rice actin (McElroy et al. (1990) *Plant Cell* 2:163-171); ubiquitin (Christensen et al. (1989) *Plant Mol. Biol.* 12:619-632 and Christensen et al. (1992) *Plant Mol. Biol.* 18:675-689); pEMU (Last et al. (1991) *Theor. Appl. Genet.* 81:581-588); MAS (Velten et al. (1984) *EMBO J.* 3:2723-2730); ALS promoter (U.S. Pat. No. 5,659,026), and the like. Other constitutive promoters include, for example, U.S. Pat. Nos. 5,608,149; 5,608,144; 5,604,121; 5,569,597; 5,466,785; 5,399,680; 5,268,463; 5,608,142; and 6,177,611.

[0065] An inducible promoter, for instance, a pathogen-inducible promoter could also be employed. Such promoters include those from pathogenesis-related proteins (PR proteins), which are induced following infection by a pathogen; e.g., PR proteins, SAR proteins, beta-1,3-glucanase, chitinase, etc. See, for example, Redolfi et al. (1983) *Neth. J. Plant Pathol.* 89:245-254; Uknes et al. (1992) *Plant Cell* 4:645-656; and Van Loon (1985) *Plant Mol. Virol.* 4:111-116. See also WO 99/43819, herein incorporated by reference.

[0066] Additionally, as pathogens find entry into plants through wounds or insect damage, a wound-inducible promoter may be used in the constructions of the invention. Such wound-inducible promoters include potato proteinase inhibitor (pin II) gene (Ryan (1990) *Ann. Rev. Phytopath.* 28:425-449; Duan et al. (1996) *Nature Biotechnology* 14:494-498); wun1 and wun2, U.S. Pat. No. 5,428,148; win1 and win2 (Stanford et al. (1989) *Mol. Gen. Genet.* 215:200-208); systemin (McGurl et al. (1992) *Science* 225:1570-1573); WIP1 (Rohmeier et al. (1993) *Plant Mol. Biol.* 22:783-792; Eckelkamp et al. (1993) *FEBS Letters* 323:73-76); MPI gene (Corderok et al. (1994) *Plant J.* 6(2):141-150); and the like, herein incorporated by reference.

[0067] Chemical-regulated promoters can be used to modulate the expression of a gene in a plant through the application of an exogenous chemical regulator. Depending upon the objective, the promoter may be a chemical-inducible promoter, where application of the chemical induces gene expression, or a chemical-repressible promoter, where application of the chemical represses gene expression. Chemical-inducible promoters are known in the art and include, but are not limited to, the maize In2-2 promoter, which is activated by benzenesulfonamide herbicide safeners, the maize GST promoter, which is activated by hydrophobic electrophilic compounds that are used as pre-emergent herbicides, and the tobacco PR-1a promoter, which is activated by salicylic acid. Other chemical-regulated promoters of interest include steroid-responsive promoters (see, for example, the glucocorticoid-inducible promoter in Schena et al. (1991) *Proc. Natl. Acad. Sci. USA* 88:10421-10425 and McNellis et al. (1998) *Plant J.* 14(2):247-257) and tetracycline-inducible and tetracycline-repressible promoters (see, for example, Gatz et al. (1991) *Mol. Gen. Genet.* 227:229-237, and U.S. Pat. Nos. 5,814,618 and 5,789,156), herein incorporated by reference.

[0068] Tissue-preferred promoters can be utilized to target enhanced expression within a particular plant tissue. Tissue-preferred promoters include Yamamoto et al. (1997) *Plant J.* 12(2):255-265; Kawamata et al. (1997) *Plant Cell Physiol.* 38(7):792-803; Hansen et al. (1997) *Mol. Gen. Genet.* 254(3):337-343; Russell et al. (1997) *Transgenic Res.* 6(2):157-168; Rinehart et al. (1996) *Plant Physiol.* 112(3):1331-1341; Van Camp et al. (1996) *Plant Physiol.* 112(2):525-535; Canevascini et al. (1996) *Plant Physiol.* 112(2):513-524; Yamamoto

et al. (1994) *Plant Cell Physiol.* 35(5):773-778; Lam (1994) *Results Probl. Cell Differ.* 20:181-196; Orozco et al. (1993) *Plant Mol. Biol.* 23(6):1129-1138; Matsuoka et al. (1993) *Proc Natl. Acad. Sci. USA* 90(20):9586-9590; and Guevara-Garcia et al. (1993) *Plant J.* 4(3):495-505. Such promoters can be modified, if necessary, for weak expression.

[0069] Leaf-preferred promoters are known in the art. See, for example, Yamamoto et al. (1997) *Plant J.* 12(2):255-265; Kwon et al. (1994) *Plant Physiol.* 105:357-67; Yamamoto et al. (1994) *Plant Cell Physiol.* 35(5):773-778; Gotor et al. (1993) *Plant J.* 3:509-18; Orozco et al. (1993) *Plant Mol. Biol.* 23(6):1129-1138; and Matsuoka et al. (1993) *Proc. Natl. Acad. Sci. USA* 90(20):9586-9590.

[0070] Root-preferred promoters are known and can be selected from the many available from the literature or isolated de novo from various compatible species. See, for example, Hire et al. (1992) *Plant Mol. Biol.* 20(2):207-218 (soybean root-specific glutamine synthetase gene); Keller and Baumgartner (1991) *Plant Cell* 3(10):1051-1061 (root-specific control element in the GRP 1.8 gene of French bean); Sanger et al. (1990) *Plant Mol. Biol.* 14(3):433-443 (root-specific promoter of the mannopine synthase (MAS) gene of *Agrobacterium tumefaciens*); and Miao et al. (1991) *Plant Cell* 3(1):11-22 (full-length cDNA clone encoding cytosolic glutamine synthetase (GS), which is expressed in roots and root nodules of soybean). See also Bogusz et al. (1990) *Plant Cell* 2(7):633-641, where two root-specific promoters isolated from hemoglobin genes from the nitrogen-fixing nonlegume *Parasponia andersonii* and the related non-nitrogen-fixing nonlegume *Trema tomentosa* are described. The promoters of these genes were linked to a β -glucuronidase reporter gene and introduced into both the nonlegume *Nicotiana tabacum* and the legume *Lotus corniculatus*, and in both instances root-specific promoter activity was preserved. Leach and Aoyagi (1991) describe their analysis of the promoters of the highly expressed rolC and rolD root-inducing genes of *Agrobacterium rhizogenes* (see *Plant Science* (Limerick) 79(1):69-76). They concluded that enhancer and tissue-preferred DNA determinants are dissociated in those promoters. Teeri et al. (1989) used gene fusion to lacZ to show that the *Agrobacterium* T-DNA gene encoding octopine synthase is especially active in the epidermis of the root tip and that the TR2' gene is root specific in the intact plant and stimulated by wounding in leaf tissue, an especially desirable combination of characteristics for use with an insecticidal or larvicidal gene (see *EMBO J.* 8(2):343-350). The TR1' gene, fused to nptII (neomycin phosphotransferase II) showed similar characteristics. Additional root-preferred promoters include the ViENOD-GRP3 gene promoter (Kuster et al. (1995) *Plant Mol. Biol.* 29(4):759-772); and rolB promoter (Capana et al. (1994) *Plant Mol. Biol.* 25(4):681-691. See also U.S. Pat. Nos. 5,837,876; 5,750,386; 5,633,363; 5,459,252; 5,401,836; 5,110,732; and 5,023,179.

[0071] In one embodiment of this invention the plant-expressed promoter is a vascular-specific promoter such as a phloem-specific promoter. A "vascular-specific" promoter, as used herein, is a promoter which is at least expressed in vascular cells, or a promoter which is preferentially expressed in vascular cells. Expression of a vascular-specific promoter need not be exclusively in vascular cells, expression in other cell types or tissues is possible. A "phloem-specific promoter" as used herein, is a plant-expressible promoter which is at least expressed in phloem cells, or a promoter which is preferentially expressed in phloem cells.

[0072] Expression of a phloem-specific promoter need not be exclusively in phloem cells, expression in other cell types or tissues, e.g., xylem tissue, is possible. In one embodiment of this invention, a phloem-specific promoter is a plant-expressible promoter at least expressed in phloem cells, wherein the expression in non-phloem cells is more limited (or absent) compared to the expression in phloem cells. Examples of suitable vascular-specific or phloem-specific promoters in accordance with this invention include but are not limited to the promoters selected from the group consisting of: the SCSV3, SCSV4, SCSV5, and SCSV7 promoters (Schunmann et al. (2003) *Plant Functional Biology* 30:453-60; the rolC gene promoter of *Agrobacterium rhizogenes* (Kiyokawa et al. (1994) *Plant Physiology* 104:801-02; Pandolfini et al. (2003) *BioMedCentral (BMC) Biotechnology* 3:7, (www.biomedcentral.com/1472-6750/3/7); Graham et al. (1997) *Plant Mol. Biol.* 33:729-35; Guivarc'h et al. (1996); Almon et al. (1997) *Plant Physiol.* 115:1599-607; the rolA gene promoter of *Agrobacterium rhizogenes* (Dehio et al. (1993) *Plant Mol. Biol.* 23:1199-210); the promoter of the *Agrobacterium tumefaciens* T-DNA gene 5 (Korber et al. (1991) *EMBO J.* 10:3983-91); the rice sucrose synthase RSs1 gene promoter (Shi et al. (1994) *J. Exp. Bot.* 45:623-31); the CoYMV or Commelina yellow mottle badnavirus promoter (Medberry et al. (1992) *Plant Cell* 4:185-92; Zhou et al. (1998) *Chin. J. Biotechnol.* 14:9-16); the CFDV or coconut foliar decay virus promoter (Rohde et al. (1994) *Plant Mol. Biol.* 27:623-28; Helm and Rhode (1998) *J. Gen. Virol.* 79:1495-99); the RTBV or rice tungro bacilliform virus promoter (Yin and Beachy (1995) *Plant J.* 7:969-80; Yin et al. (1997) *Plant J.* 12:1179-80); the pea glutamine synthase GS3A gene (Edwards et al. (1990) *Proc. Natl. Acad. Sci. USA* 87:3459-63; Brears et al. (1991) *Plant J.* 1:235-44); the inv CD111 and inv CD141 promoters of the potato invertase genes (Hedley et al. (2000) *J. Exp. Botany* 51:817-21); the promoter isolated from *Arabidopsis* shown to have phloem-specific expression in tobacco by Kertbundit et al. (1991) *Proc. Natl. Acad. Sci. USA* 88:5212-16); the VAHOX1 promoter region (Tornero et al. (1996) *Plant J.* 9:639-48); the pea cell wall invertase gene promoter (Zhang et al. (1996) *Plant Physiol.* 112:1111-17); the promoter of the endogenous cotton protein related to chitinase of US published patent application 20030106097, an acid invertase gene promoter from carrot (Ramloch-Lorenz et al. (1993) *The Plant J.* 4:545-54); the promoter of the sulfate transporter gene Sultr1;3 (Yoshimoto et al. (2003) *Plant Physiol.* 131:1511-17); a promoter of a sucrose synthase gene (Nolte and Koch (1993) *Plant Physiol.* 101:899-905); and the promoter of a tobacco sucrose transporter gene (Kuhn et al. (1997) *Science* 275:1298-1300).

[0073] Possible promoters also include the Black Cherry promoter for Prunasin Hydrolase (PH DL1.4 PRO) (U.S. Pat. No. 6,797,859), Thioredoxin H promoter from cucumber and rice (Fukuda A et al. (2005). *Plant Cell Physiol.* 46(11):1779-86), Rice (RSs1) (Shi, T. Wang et al. (1994). *J. Exp. Bot.* 45(274): 623-631) and maize sucrose synthase -1 promoters (Yang, N-S. et al. (1990) *PNAS* 87:4144-4148), PP2 promoter from pumpkin Guo, H. et al. (2004) *Transgenic Research* 13:559-566), At SUC2 promoter (Truernit, E. et al. (1995) *Planta* 196(3):564-70., At SAM-1 (S-adenosylmethionine synthetase) (Mijnsbrugge K V. et al. (1996) *Plant Cell Physiol.* 37(8): 1108-1115), and the Rice tungro bacilliform virus (RTBV) promoter (Bhattacharyya-Pakrasi et al. (1993) *Plant J.* 4(1):71-79).

[0074] The expression cassette can also comprise a selectable marker gene for the selection of transformed cells. Selectable marker genes are utilized for the selection of transformed cells or tissues. Marker genes include genes encoding antibiotic resistance, such as those encoding neomycin phosphotransferase II (NEO) and hygromycin phosphotransferase (HPT), as well as genes conferring resistance to herbicidal compounds, such as glufosinate ammonium, bromoxynil, imidazolinones, and 2,4-dichlorophenoxyacetate (2,4-D). Additional selectable markers include phenotypic markers such as β -galactosidase and fluorescent proteins such as green fluorescent protein (GFP) (Su et al. (2004) *Biotechnol Bioeng* 85:610-9 and Fetter et al. (2004) *Plant Cell* 16:215-28), cyan fluorescent protein (CYP) (Bolte et al. (2004) *J. Cell Science* 117:943-54 and Kato et al. (2002) *Plant Physiol* 129:913-42), and yellow fluorescent protein (PhiYFP™ from Evrogen, see, Bolte et al. (2004) *J. Cell Science* 117:943-54). For additional selectable markers, see generally, Yarranton (1992) *Curr. Opin. Biotech.* 3:506-511; Christopherson et al. (1992) *Proc. Natl. Acad. Sci. USA* 89:6314-6318; Yao et al. (1992) *Cell* 71:63-72; Reznikoff (1992) *Mol. Microbiol.* 6:2419-2422; Barkley et al. (1980) in *The Operon*, pp. 177-220; Hu et al. (1987) *Cell* 48:555-566; Brown et al. (1987) *Cell* 49:603-612; Figge et al. (1988) *Cell* 52:713-722; Deuschle et al. (1989) *Proc. Natl. Acad. Sci. USA* 86:5400-5404; Fuerst et al. (1989) *Proc. Natl. Acad. Sci. USA* 86:2549-2553; Deuschle et al. (1990) *Science* 248:480-483; Gossen (1993) Ph.D. Thesis, University of Heidelberg; Reines et al. (1993) *Proc. Natl. Acad. Sci. USA* 90:1917-1921; Labow et al. (1990) *Mol. Cell. Biol.* 10:3343-3356; Zambretti et al. (1992) *Proc. Natl. Acad. Sci. USA* 89:3952-3956; Baim et al. (1991) *Proc. Natl. Acad. Sci. USA* 88:5072-5076; Wyborski et al. (1991) *Nucleic Acids Res.* 19:4647-4653; Hillenand-Wissman (1989) *Topics Mol. Struc. Biol.* 10:143-162; Degenkolb et al. (1991) *Antimicrob. Agents Chemother.* 35:1591-1595; Kleinschmidt et al. (1988) *Biochemistry* 27:1094-1104; Bonin (1993) Ph.D. Thesis, University of Heidelberg; Gossen et al. (1992) *Proc. Natl. Acad. Sci. USA* 89:5547-5551; Oliva et al. (1992) *Antimicrob. Agents Chemother.* 36:913-919; Hlavka et al. (1985) *Handbook of Experimental Pharmacology*, Vol. 78 (Springer-Verlag, Berlin); Gill et al. (1988) *Nature* 334:721-724. Such disclosures are herein incorporated by reference. The above list of selectable marker genes is not meant to be limiting. Any selectable marker gene can be used in the present invention.

VI. Compositions Comprising Silencing Elements

[0075] One or more of the polynucleotides comprising the silencing element can be provided as an external composition such as a spray or powder to the plant, plant part, seed, a pest, or an area of cultivation. In another example, a plant is transformed with a DNA construct or expression cassette for expression of at least one silencing element. In either composition, the silencing element, when ingested by an insect, can reduce the level of a target pest sequence and thereby control the pest (i.e., a Coleopteran plant pest including a *Diabrotica* plant pest, such as, *D. virgifera virgifera*, *D. barberi*, or *D. undecimpunctata howardi*). It is recognized that the composition can comprise a cell (such as plant cell or a bacterial cell), in which a polynucleotide encoding the silencing element is stably incorporated into the genome and operably linked to promoters active in the cell. Compositions comprising a mixture of cells, some cells expressing at least one silencing element are also encompassed. In other

embodiments, compositions comprising the silencing elements are not contained in a cell. In such embodiments, the composition can be applied to an area inhabited by a pest. In one embodiment, the composition is applied externally to a plant (i.e., by spraying a field or area of cultivation) to protect the plant from the pest.

[0076] The composition of the invention can further be formulated as bait. In this embodiment, the compositions comprise a food substance or an attractant which enhances the attractiveness of the composition to the pest.

[0077] The composition comprising the silencing element can be formulated in an agriculturally suitable and/or environmentally acceptable carrier. Such carriers can be any material that the animal, plant or environment to be treated can tolerate. Furthermore, the carrier must be such that the composition remains effective at controlling a pest. Examples of such carriers include water, saline, Ringer's solution, dextrose or other sugar solutions, Hank's solution, and other aqueous physiologically balanced salt solutions, phosphate buffer, bicarbonate buffer and Tris buffer. In addition, the composition may include compounds that increase the half-life of a composition. Various insecticidal formulations can also be found in, for example, US Publications 2008/0275115, 2008/0242174, 2008/0027143, 2005/0042245, and 2004/0127520, each of which is herein incorporated by reference.

[0078] It is recognized that the polynucleotides comprising sequences encoding the silencing element can be used to transform organisms to provide for host organism production of these components, and subsequent application of the host organism to the environment of the target pest(s). Such host organisms include baculoviruses, bacteria, and the like. In this manner, the combination of polynucleotides encoding the silencing element may be introduced via a suitable vector into a microbial host, and said host applied to the environment, or to plants or animals.

[0079] The term "introduced" in the context of inserting a nucleic acid into a cell, means "transfection" or "transformation" or "transduction" and includes reference to the incorporation of a nucleic acid into a eukaryotic or prokaryotic cell where the nucleic acid may be stably incorporated into the genome of the cell (e.g., chromosome, plasmid, plastid, or mitochondrial DNA), converted into an autonomous replicon, or transiently expressed (e.g., transfected mRNA).

[0080] Microbial hosts that are known to occupy the "phytosphere" (phylloplane, phyllosphere, rhizosphere, and/or rhizoplane) of one or more crops of interest may be selected. These microorganisms are selected so as to be capable of successfully competing in the particular environment with the wild-type microorganisms, provide for stable maintenance and expression of the sequences encoding the silencing element, and desirably, provide for improved protection of the components from environmental degradation and inactivation.

[0081] Such microorganisms include bacteria, algae, and fungi. Of particular interest are microorganisms such as bacteria, e.g., *Pseudomonas*, *Erwinia*, *Serratia*, *Klebsiella*, *Xanthomonas*, *Streptomyces*, *Rhizobium*, *Rhodopseudomonas*, *Methylius*, *Agrobacterium*, *Acetobacter*, *Lactobacillus*, *Arthrobacter*, *Azotobacter*, *Leuconostoc*, and *Alcaligenes*, fungi, particularly yeast, e.g., *Saccharomyces*, *Cryptococcus*, *Kluyveromyces*, *Sporobolomyces*, *Rhodotorula*, and *Aureobasidium*. Of particular interest are such phytosphere bacterial species as *Pseudomonas syringae*, *Pseudomonas fluo-*

rescens, *Serratia marcescens*, *Acetobacter xylinum*, *Agrobacteria*, *Rhodopseudomonas spheroides*, *Xanthomonas campestris*, *Rhizobium melioli*, *Alcaligenes entrophus*, *Clavibacter xyli* and *Azotobacter vinlandir*, and phytosphere yeast species such as *Rhodotorula rubra*, *R. glutinis*, *R. marina*, *R. aurantiaca*, *Cryptococcus albidus*, *C. diffluens*, *C. laurentii*, *Saccharomyces rosei*, *S. pretoriensis*, *S. cerevisiae*, *Sporobolomyces rosues*, *S. odoratus*, *Kluyveromyces veronae*, and *Aureobasidium pollulans*.

[0082] A number of ways are available for introducing the polynucleotide comprising the silencing element into the microbial host under conditions that allow for stable maintenance and expression of such nucleotide encoding sequences. For example, expression cassettes can be constructed which include the nucleotide constructs of interest operably linked with the transcriptional and translational regulatory signals for expression of the nucleotide constructs, and a nucleotide sequence homologous with a sequence in the host organism, whereby integration will occur, and/or a replication system that is functional in the host, whereby integration or stable maintenance will occur.

[0083] Transcriptional and translational regulatory signals include, but are not limited to, promoters, transcriptional initiation start sites, operators, activators, enhancers, other regulatory elements, ribosomal binding sites, an initiation codon, termination signals, and the like. See, for example, U.S. Pat. Nos. 5,039,523 and 4,853,331; EPO 0480762A2; Sambrook et al. (2000); *Molecular Cloning: A Laboratory Manual* (3rd ed.; Cold Spring Harbor Laboratory Press, Plainview, N.Y.); Davis et al. (1980) *Advanced Bacterial Genetics* (Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y.); and the references cited therein.

[0084] Suitable host cells include the prokaryotes and the lower eukaryotes, such as fungi. Illustrative prokaryotes, both Gram-negative and Gram-positive, include Enterobacteriaceae, such as *Escherichia*, *Erwinia*, *Shigella*, *Salmonella*, and *Proteus*; Bacillaceae; Rhizobiaceae, such as *Rhizobium*; Spirillaceae, such as photobacterium, *Zymomonas*, *Serratia*, *Aeromonas*, *Vibrio*, *Desulfovibrio*, *Spirillum*; Lactobacillaceae; Pseudomonadaceae, such as *Pseudomonas* and *Acetobacter*; Azotobacteraceae and Nitrobacteraceae. Among eukaryotes are fungi, such as Phycomycetes and Ascomycetes, which includes yeast, such as *Saccharomyces* and *Schizosaccharomyces*; and Basidiomycetes yeast, such as *Rhodotorula*, *Aureobasidium*, *Sporobolomyces*, and the like.

[0085] Characteristics of particular interest in selecting a host cell for purposes of the invention include ease of introducing the coding sequence into the host, availability of expression systems, efficiency of expression, stability in the host, and the presence of auxiliary genetic capabilities. Characteristics of interest for use as a pesticide microcapsule include protective qualities, such as thick cell walls, pigmentation, and intracellular packaging or formation of inclusion bodies; leaf affinity; lack of mammalian toxicity; attractiveness to pests for ingestion; and the like. Other considerations include ease of formulation and handling, economics, storage stability, and the like.

[0086] Host organisms of particular interest include yeast, such as *Rhodotorula* spp., *Aureobasidium* spp., *Saccharomyces* spp., and *Sporobolomyces* spp., phylloplane organisms such as *Pseudomonas* spp., *Erwinia* spp., and *Flavobacterium* spp., and other such organisms, including *Pseudomonas*

aeruginosa, *Pseudomonas fluorescens*, *Saccharomyces cerevisiae*, *Bacillus thuringiensis*, *Escherichia coli*, *Bacillus subtilis*, and the like.

[0087] The sequences encoding the silencing elements encompassed by the invention can be introduced into microorganisms that multiply on plants (epiphytes) to deliver these components to potential target pests. Epiphytes, for example, can be gram-positive or gram-negative bacteria.

[0088] The silencing element can be fermented in a bacterial host and the resulting bacteria processed and used as a microbial spray in the same manner that *Bacillus thuringiensis* strains have been used as insecticidal sprays. Any suitable microorganism can be used for this purpose. *Pseudomonas* has been used to express *Bacillus thuringiensis* endotoxins as encapsulated proteins and the resulting cells processed and sprayed as an insecticide Gaertner et al. (1993), in *Advanced Engineered Pesticides*, ed. L. Kim (Marcel Dekker, Inc.).

[0089] Alternatively, the components of the invention are produced by introducing heterologous genes into a cellular host. Expression of the heterologous sequences results, directly or indirectly, in the intracellular production of the silencing element. These compositions may then be formulated in accordance with conventional techniques for application to the environment hosting a target pest, e.g., soil, water, and foliage of plants. See, for example, EPA 0192319, and the references cited therein.

[0090] In the present invention, a transformed microorganism can be formulated with an acceptable carrier into separate or combined compositions that are, for example, a suspension, a solution, an emulsion, a dusting powder, a dispersible granule, a wettable powder, and an emulsifiable concentrate, an aerosol, an impregnated granule, an adjuvant, a coatable paste, and also encapsulations in, for example, polymer substances.

[0091] Such compositions disclosed above may be obtained by the addition of a surface-active agent, an inert carrier, a preservative, a humectant, a feeding stimulant, an attractant, an encapsulating agent, a binder, an emulsifier, a dye, a UV protectant, a buffer, a flow agent or fertilizers, micronutrient donors, or other preparations that influence plant growth. One or more agrochemicals including, but not limited to, herbicides, insecticides, fungicides, bactericides, nematocides, molluscicides, acaricides, plant growth regulators, harvest aids, and fertilizers, can be combined with carriers, surfactants or adjuvants customarily employed in the art of formulation or other components to facilitate product handling and application for particular target pests. Suitable carriers and adjuvants can be solid or liquid and correspond to the substances ordinarily employed in formulation technology, e.g., natural or regenerated mineral substances, solvents, dispersants, wetting agents, tackifiers, binders, or fertilizers. The active ingredients of the present invention (i.e., at least one silencing element) are normally applied in the form of compositions and can be applied to the crop area, plant, or seed to be treated. For example, the compositions may be applied to grain in preparation for or during storage in a grain bin or silo, etc. The compositions may be applied simultaneously or in succession with other compounds. Methods of applying an active ingredient or a composition that contains at least one silencing element include, but are not limited to, foliar application, seed coating, and soil application. The number of applications and the rate of application depend on the intensity of infestation by the corresponding pest.

[0092] Suitable surface-active agents include, but are not limited to, anionic compounds such as a carboxylate of, for example, a metal; carboxylate of a long chain fatty acid; an N-acylsarcosinate; mono- or di-esters of phosphoric acid with fatty alcohol ethoxylates or salts of such esters; fatty alcohol sulfates such as sodium dodecyl sulfate, sodium octadecyl sulfate, or sodium cetyl sulfate; ethoxylated fatty alcohol sulfates; ethoxylated alkylphenol sulfates; lignin sulfonates; petroleum sulfonates; alkyl aryl sulfonates such as alkyl-benzene sulfonates or lower alkyl-naphthalene sulfonates, e.g., butyl-naphthalene sulfonate; salts of sulfonated naphthalene-formaldehyde condensates; salts of sulfonated phenol-formaldehyde condensates; more complex sulfonates such as the amide sulfonates, e.g., the sulfonated condensation product of oleic acid and N-methyl taurine; or the dialkyl sulfosuccinates, e.g., the sodium sulfonate or dioctyl succinate. Non-ionic agents include condensation products of fatty acid esters, fatty alcohols, fatty acid amides or fatty-alkyl- or alkenyl-substituted phenols with ethylene oxide, fatty esters of polyhydric alcohol ethers, e.g., sorbitan fatty acid esters, condensation products of such esters with ethylene oxide, e.g., polyoxyethylene sorbitan fatty acid esters, block copolymers of ethylene oxide and propylene oxide, acetylenic glycols such as 2,4,7,9-tetraethyl-5-decyn-4,7-diol, or ethoxylated acetylenic glycols. Examples of a cationic surface-active agent include, for instance, an aliphatic mono-, di-, or polyamine such as an acetate, naphthenate or oleate; or oxygen-containing amine such as an amine oxide of polyoxyethylene alkylamine; an amide-linked amine prepared by the condensation of a carboxylic acid with a di- or polyamine; or a quaternary ammonium salt.

[0093] Examples of inert materials include, but are not limited to, inorganic minerals such as kaolin, phyllosilicates, carbonates, sulfates, phosphates, or botanical materials such as cork, powdered corncobs, peanut hulls, rice hulls, and walnut shells.

[0094] The compositions comprising the silencing element can be in a suitable form for direct application or as a concentrate of primary composition that requires dilution with a suitable quantity of water or other dilutant before application.

[0095] The compositions (including the transformed microorganisms) can be applied to the environment of an insect pest (such as a Coleoptera plant pest or a *Diabrotica* plant pest) by, for example, spraying, atomizing, dusting, scattering, coating or pouring, introducing into or on the soil, introducing into irrigation water, by seed treatment or general application or dusting at the time when the pest has begun to appear or before the appearance of pests as a protective measure. For example, the composition(s) and/or transformed microorganism(s) may be mixed with grain to protect the grain during storage. It is generally important to obtain good control of pests in the early stages of plant growth, as this is the time when the plant can be most severely damaged. The compositions can conveniently contain another insecticide if this is thought necessary. In an embodiment of the invention, the composition(s) is applied directly to the soil, at a time of planting, in granular form of a composition of a carrier and dead cells of a *Bacillus* strain or transformed microorganism of the invention. Another embodiment is a granular form of a composition comprising an agrochemical such as, for example, a herbicide, an insecticide, a fertilizer, in an inert carrier, and dead cells of a *Bacillus* strain or transformed microorganism of the invention.

VII. Plants, Plant Parts, and Methods of Introducing Sequences into Plants

[0096] In one embodiment, the methods of the invention involve introducing a polynucleotide into a plant. "Introducing" is intended to mean presenting to the plant the polynucleotide in such a manner that the sequence gains access to the interior of a cell of the plant. The methods of the invention do not depend on a particular method for introducing a sequence into a plant, only that the polynucleotide or polypeptides gains access to the interior of at least one cell of the plant. Methods for introducing polynucleotides into plants are known in the art including, but not limited to, stable transformation methods, transient transformation methods, and virus-mediated methods.

[0097] "Stable transformation" is intended to mean that the nucleotide construct introduced into a plant integrates into the genome of the plant and is capable of being inherited by the progeny thereof. "Transient transformation" is intended to mean that a polynucleotide is introduced into the plant and does not integrate into the genome of the plant or a polypeptide is introduced into a plant.

[0098] Transformation protocols as well as protocols for introducing polypeptides or polynucleotide sequences into plants may vary depending on the type of plant or plant cell, i.e., monocot or dicot, targeted for transformation. Suitable methods of introducing polypeptides and polynucleotides into plant cells include microinjection (Crossway et al. (1986) *Biotechniques* 4:320-334), electroporation (Riggs et al. (1986) *Proc. Natl. Acad. Sci. USA* 83:5602-5606, *Agrobacterium*-mediated transformation (U.S. Pat. No. 5,563,055 and U.S. Pat. No. 5,981,840), direct gene transfer (Paszowski et al. (1984) *EMBO J.* 3:2717-2722), and ballistic particle acceleration (see, for example, U.S. Pat. No. 4,945,050; U.S. Pat. No. 5,879,918; U.S. Pat. No. 5,886,244; and, U.S. Pat. No. 5,932,782; Tomes et al. (1995) in *Plant Cell, Tissue, and Organ Culture: Fundamental Methods*, ed. Gamborg and Phillips (Springer-Verlag, Berlin); McCabe et al. (1988) *Biotechnology* 6:923-926; and Lec1 transformation (WO 00/28058). Also see Weissinger et al. (1988) *Ann. Rev. Genet.* 22:421-477; Sanford et al. (1987) *Particulate Science and Technology* 5:27-37 (onion); Christou et al. (1988) *Plant Physiol.* 87:671-674 (soybean); McCabe et al. (1988) *Bio/Technology* 6:923-926 (soybean); Finer and McMullen (1991) *In Vitro Cell Dev. Biol.* 27P:175-182 (soybean); Singh et al. (1998) *Theor. Appl. Genet.* 96:319-324 (soybean); Datta et al. (1990) *Biotechnology* 8:736-740 (rice); Klein et al. (1988) *Proc. Natl. Acad. Sci. USA* 85:4305-4309 (maize); Klein et al. (1988) *Biotechnology* 6:559-563 (maize); U.S. Pat. Nos. 5,240,855; 5,322,783; and, 5,324,646; Klein et al. (1988) *Plant Physiol.* 91:440-444 (maize); Fromm et al. (1990) *Biotechnology* 8:833-839 (maize); Hooykaas-Van Slooter et al. (1984) *Nature* (London) 311:763-764; U.S. Pat. No. 5,736,369 (cereals); Bytebier et al. (1987) *Proc. Natl. Acad. Sci. USA* 84:5345-5349 (Liliaceae); De Wet et al. (1985) in *The Experimental Manipulation of Ovule Tissues*, ed. Chapman et al. (Longman, New York), pp. 197-209 (pollen); Kaeppler et al. (1990) *Plant Cell Reports* 9:415-418 and Kaeppler et al. (1992) *Theor. Appl. Genet.* 84:560-566 (whisker-mediated transformation); D'Halluin et al. (1992) *Plant Cell* 4:1495-1505 (electroporation); Li et al. (1993) *Plant Cell Reports* 12:250-255 and Christou and Ford (1995) *Annals of Botany* 75:407-413 (rice); Osjoda et al. (1996)

Nature Biotechnology 14:745-750 (maize via *Agrobacterium tumefaciens*); all of which are herein incorporated by reference.

[0099] In other embodiments, the polynucleotide of the invention may be introduced into plants by contacting plants with a virus or viral nucleic acids. Generally, such methods involve incorporating a nucleotide construct of the invention within a viral DNA or RNA molecule. Further, it is recognized that promoters of the invention also encompass promoters utilized for transcription by viral RNA polymerases. Methods for introducing polynucleotides into plants and expressing a protein encoded therein, involving viral DNA or RNA molecules, are known in the art. See, for example, U.S. Pat. Nos. 5,889,191, 5,889,190, 5,866,785, 5,589,367, 5,316,931, and Porta et al. (1996) *Molecular Biotechnology* 5:209-221; herein incorporated by reference.

[0100] Methods are known in the art for the targeted insertion of a polynucleotide at a specific location in the plant genome. In one embodiment, the insertion of the polynucleotide at a desired genomic location is achieved using a site-specific recombination system. See, for example, WO99/25821, WO99/25854, WO99/25840, WO99/25855, and WO99/25853, all of which are herein incorporated by reference. Briefly, the polynucleotide of the invention can be contained in transfer cassette flanked by two non-recombinogenic recombination sites. The transfer cassette is introduced into a plant having stably incorporated into its genome a target site which is flanked by two non-recombinogenic recombination sites that correspond to the sites of the transfer cassette. An appropriate recombinase is provided and the transfer cassette is integrated at the target site. The polynucleotide of interest is thereby integrated at a specific chromosomal position in the plant genome.

[0101] The cells that have been transformed may be grown into plants in accordance with conventional ways. See, for example, McCormick et al. (1986) *Plant Cell Reports* 5:81-84. These plants may then be grown, and either pollinated with the same transformed strain or different strains, and the resulting progeny having constitutive expression of the desired phenotypic characteristic identified. Two or more generations may be grown to ensure that expression of the desired phenotypic characteristic is stably maintained and inherited and then seeds harvested to ensure expression of the desired phenotypic characteristic has been achieved. In this manner, the present invention provides transformed seed (also referred to as "transgenic seed") having a polynucleotide of the invention, for example, an expression cassette of the invention, stably incorporated into their genome.

[0102] As used herein, the term plant includes plant cells, plant protoplasts, plant cell tissue cultures from which plants can be regenerated, plant calli, plant clumps, and plant cells that are intact in plants or parts of plants such as embryos, pollen, ovules, seeds, leaves, flowers, branches, fruit, kernels, ears, cobs, husks, stalks, roots, root tips, anthers, and the like. Grain is intended to mean the mature seed produced by commercial growers for purposes other than growing or reproducing the species. Progeny, variants, and mutants of the regenerated plants are also included within the scope of the invention, provided that these parts comprise the introduced polynucleotides.

[0103] The present invention may be used for transformation of any plant species, including, but not limited to, monocots and dicots. Examples of plant species of interest include, but are not limited to, corn (*Zea mays*), *Brassica* sp. (e.g., *B.*

napus, *B. rapa*, *B. juncea*), particularly those *Brassica* species useful as sources of seed oil, alfalfa (*Medicago sativa*), rice (*Oryza sativa*), rye (*Secale cereale*), sorghum (*Sorghum bicolor*, *Sorghum vulgare*), millet (e.g., pearl millet (*Pennisetum glaucum*), proso millet (*Panicum miliaceum*), foxtail millet (*Setaria italica*), finger millet (*Eleusine coracana*)), sunflower (*Helianthus annuus*), safflower (*Carthamus tinctorius*), wheat (*Triticum aestivum*), soybean (*Glycine max*), tobacco (*Nicotiana tabacum*), potato (*Solanum tuberosum*), peanuts (*Arachis hypogaea*), cotton (*Gossypium barbadense*, *Gossypium hirsutum*), sweet potato (*Ipomoea batatas*), cassava (*Manihot esculenta*), coffee (*Coffea* spp.), coconut (*Cocos nucifera*), pineapple (*Ananas comosus*), citrus trees (*Citrus* spp.), cocoa (*Theobroma cacao*), tea (*Camellia sinensis*), banana (*Musa* spp.), avocado (*Persea americana*), fig (*Ficus casica*), guava (*Psidium guajava*), mango (*Mangifera indica*), olive (*Olea europaea*), papaya (*Carica papaya*), cashew (*Anacardium occidentale*), macadamia (*Macadamia integrifolia*), almond (*Prunus amygdalus*), sugar beets (*Beta vulgaris*), sugarcane (*Saccharum* spp.), oats, barley, vegetables, ornamentals, and conifers.

[0104] Vegetables include tomatoes (*Lycopersicon esculentum*), lettuce (e.g., *Lactuca sativa*), green beans (*Phaseolus vulgaris*), lima beans (*Phaseolus limensis*), peas (*Lathyrus* spp.), and members of the genus *Cucumis* such as cucumber (*C. sativus*), cantaloupe (*C. cantalupensis*), and musk melon (*C. melo*). Ornamentals include azalea (*Rhododendron* spp.), hydrangea (*Macrophylla hydrangea*), hibiscus (*Hibiscus rosasanensis*), roses (*Rosa* spp.), tulips (*Tulipa* spp.), daffodils (*Narcissus* spp.), petunias (*Petunia hybrida*), carnation (*Dianthus caryophyllus*), poinsettia (*Euphorbia pulcherrima*), and chrysanthemum.

[0105] Conifers that may be employed in practicing the present invention include, for example, pines such as loblolly pine (*Pinus taeda*), slash pine (*Pinus elliotii*), ponderosa pine (*Pinus ponderosa*), lodgepole pine (*Pinus contorta*), and Monterey pine (*Pinus radiata*); Douglas-fir (*Pseudotsuga menziesii*); Western hemlock (*Tsuga canadensis*); Sitka spruce (*Picea glauca*); redwood (*Sequoia sempervirens*); true firs such as silver fir (*Abies amabilis*) and balsam fir (*Abies balsamea*); and cedars such as Western red cedar (*Thuja plicata*) and Alaska yellow-cedar (*Chamaecyparis nootkatensis*). In specific embodiments, plants of the present invention are crop plants (for example, corn, alfalfa, sunflower, *Brassica*, soybean, cotton, safflower, peanut, sorghum, wheat, millet, tobacco, etc.). In other embodiments, corn and soybean plants are optimal, and in yet other embodiments corn plants are optimal.

[0106] Other plants of interest include grain plants that provide seeds of interest, oil-seed plants, and leguminous plants. Seeds of interest include grain seeds, such as corn, wheat, barley, rice, sorghum, rye, etc. Oil-seed plants include cotton, soybean, safflower, sunflower, *Brassica*, maize, alfalfa, palm, coconut, etc. Leguminous plants include beans and peas. Beans include guar, locust bean, fenugreek, soybean, garden beans, cowpea, mungbean, lima bean, fava bean, lentils, chickpea, etc.

VIII. Methods of Use

[0107] The methods of the invention comprise methods for controlling a pest (i.e., a Coleopteran plant pest, including a *Diabrotica* plant pest, such as, *D. virgifera virgifera*, *D. barberi*, or *D. undecimpunctata howardi*). The method comprises feeding to a pest a composition comprising a silencing

element of the invention, wherein said silencing element, when ingested by a pest (i.e., a Coleopteran plant pest including a *Diabrotica* plant pest, such as, *D. virgifera virgifera*, *D. barberi*, or *D. undecimpunctata howardi*), reduces the level of a target polynucleotide of the pest and thereby controls the pest. The pest can be fed the silencing element in a variety of ways. For example, in one embodiment, the polynucleotide comprising the silencing element is introduced into a plant. As the Coleopteran plant pest or *Diabrotica* plant pest feeds on the plant or part thereof expressing these sequences, the silencing element is delivered to the pest. When the silencing element is delivered to the plant in this manner, it is recognized that the silencing element can be expressed constitutively or alternatively, it may be produced in a stage-specific manner by employing the various inducible or tissue-preferred or developmentally regulated promoters that are discussed elsewhere herein. In specific embodiments, the silencing element is expressed in the roots, stalk or stem, leaf including pedicel, xylem and phloem, fruit or reproductive tissue, silk, flowers and all parts therein or any combination thereof.

[0108] In another method, a composition comprising at least one silencing element of the invention is applied to a plant. In such embodiments, the silencing element can be formulated in an agronomically suitable and/or environmentally acceptable carrier, which is preferably, suitable for dispersal in fields. In addition, the carrier can also include compounds that increase the half life of the composition. In specific embodiments, the composition comprising the silencing element is formulated in such a manner such that it persists in the environment for a length of time sufficient to allow it to be delivered to a pest. In such embodiments, the composition can be applied to an area inhabited by a pest. In one embodiment, the composition is applied externally to a plant (i.e., by spraying a field) to protect the plant from pests.

[0109] In certain embodiments, the constructs of the present invention can be stacked with any combination of polynucleotide sequences of interest in order to create plants with a desired trait. A trait, as used herein, refers to the phenotype derived from a particular sequence or groups of sequences. For example, the polynucleotides of the present invention may be stacked with any other polynucleotides encoding polypeptides having pesticidal and/or insecticidal activity, such as other *Bacillus thuringiensis* toxic proteins (described in U.S. Pat. Nos. 5,366,892; 5,747,450; 5,737,514; 5,723,756; 5,593,881; and Geiser et al. (1986) *Gene* 48:109), lectins (Van Damme et al. (1994) *Plant Mol. Biol.* 24:825, pentin (described in U.S. Pat. No. 5,981,722), and the like. The combinations generated can also include multiple copies of any one of the polynucleotides of interest. The polynucleotides of the present invention can also be stacked with any other gene or combination of genes to produce plants with a variety of desired trait combinations including, but not limited to, traits desirable for animal feed such as high oil genes (e.g., U.S. Pat. No. 6,232,529); balanced amino acids (e.g., hordothionins (U.S. Pat. Nos. 5,990,389; 5,885,801; 5,885,802; and 5,703,409); barley high lysine (Williamson et al. (1987) *Eur. J. Biochem.* 165:99-106; and WO 98/20122) and high methionine proteins (Pedersen et al. (1986) *J. Biol. Chem.* 261:6279; Kirihara et al. (1988) *Gene* 71:359; and Musumura et al. (1989) *Plant Mol. Biol.* 12:123)); increased digestibility (e.g., modified storage proteins (U.S. application Ser. No. 10/053,410, filed Nov. 7, 2001); and thioredoxins

(U.S. application Ser. No. 10/005,429, filed Dec. 3, 2001)); the disclosures of which are herein incorporated by reference.

[0110] The polynucleotides of the present invention can also be stacked with traits desirable for disease or herbicide resistance (e.g., fumonisin detoxification genes (U.S. Pat. No. 5,792,931); avirulence and disease resistance genes (Jones et al. (1994) *Science* 266:789; Martin et al. (1993) *Science* 262:1432; Mindrinos et al. (1994) *Cell* 78:1089); acetolactate synthase (ALS) mutants that lead to herbicide resistance such as the S4 and/or Hra mutations; inhibitors of glutamine synthase such as phosphinothricin or basta (e.g., bar gene); and glyphosate resistance (EPSPS gene)); and traits desirable for processing or process products such as high oil (e.g., U.S. Pat. No. 6,232,529); modified oils (e.g., fatty acid desaturase genes (U.S. Pat. No. 5,952,544; WO 94/11516)); modified starches (e.g., ADPG pyrophosphorylases (AGPase), starch synthases (SS), starch branching enzymes (SBE), and starch debranching enzymes (SDBE)); and polymers or bioplastics (e.g., U.S. Pat. No. 5,602,321; beta-ketothiolase, polyhydroxybutyrate synthase, and acetoacetyl-CoA reductase (Schubert et al. (1988) *J. Bacteriol.* 170:5837-5847) facilitate expression of polyhydroxyalkanoates (PHAs)); the disclosures of which are herein incorporated by reference. One could also combine the polynucleotides of the present invention with polynucleotides providing agronomic traits such as male sterility (e.g., see U.S. Pat. No. 5,583,210), stalk strength, flowering time, or transformation technology traits such as cell cycle regulation or gene targeting (e.g., WO 99/61619, WO 00/17364, and WO 99/25821); the disclosures of which are herein incorporated by reference.

[0111] These stacked combinations can be created by any method including, but not limited to, cross-breeding plants by any conventional or TopCross methodology, or genetic transformation. If the sequences are stacked by genetically transforming the plants, the polynucleotide sequences of interest can be combined at any time and in any order. For example, a transgenic plant comprising one or more desired traits can be used as the target to introduce further traits by subsequent transformation. The traits can be introduced simultaneously in a co-transformation protocol with the polynucleotides of interest provided by any combination of transformation cassettes. For example, if two sequences will be introduced, the two sequences can be contained in separate transformation cassettes (trans) or contained on the same transformation cassette (cis). Expression of the sequences can be driven by the same promoter or by different promoters. In certain cases, it may be desirable to introduce a transformation cassette that will suppress the expression of the polynucleotide of interest. This may be combined with any combination of other suppression cassettes or overexpression cassettes to generate the desired combination of traits in the plant. It is further recognized that polynucleotide sequences can be stacked at a desired genomic location using a site-specific recombination system. See, for example, WO99/25821, WO99/25854, WO99/25840, WO99/25855, and WO99/25853, all of which are herein incorporated by reference.

[0112] Methods and compositions are further provided which allow for an increase in RNAi produced from the silencing element. In such embodiments, the methods and compositions employ a first polynucleotide comprising a silencing element for a target pest sequence operably linked to a promoter active in the plant cell; and, a second polynucleotide comprising a suppressor enhancer element comprising the target pest sequence or an active variant or fragment

thereof operably linked to a promoter active in the plant cell. The combined expression of the silencing element with suppressor enhancer element leads to an increased amplification of the inhibitory RNA produced from the silencing element over that achievable with only the expression of the silencing element alone. In addition to the increased amplification of the specific RNAi species itself, the methods and compositions further allow for the production of a diverse population of RNAi species that can enhance the effectiveness of disrupting target gene expression. As such, when the suppressor enhancer element is expressed in a plant cell in combination with the silencing element, the methods and composition can allow for the systemic production of RNAi throughout the plant; the production of greater amounts of RNAi than would be observed with just the silencing element construct alone; and, the improved loading of RNAi into the phloem of the plant, thus providing better control of phloem feeding insects by an RNAi approach. Thus, the various methods and compositions provide improved methods for the delivery of inhibitory RNA to the target organism. See, for example, U.S. application Ser. No. 12/351,093, entitled “*Compositions and Methods for the Suppression of Target Polynucleotides*”, filed Jan. 9, 2009 and herein incorporated by reference in its entirety.

[0113] As used herein, a “suppressor enhancer element” comprises a polynucleotide comprising the target sequence to be suppressed or an active fragment or variant thereof. It is recognized that the suppressor enhancer element need not be identical to the target sequence, but rather, the suppressor enhancer element can comprise a variant of the target sequence, so long as the suppressor enhancer element has sufficient sequence identity to the target sequence to allow for an increased level of the RNAi produced by the silencing element over that achievable with only the expression of the silencing element. Similarly, the suppressor enhancer element can comprise a fragment of the target sequence, wherein the fragment is of sufficient length to allow for an increased level of the RNAi produced by the silencing element over that achievable with only the expression of the silencing element. Thus, in specific embodiments, the suppressor enhancer element comprises a polynucleotide set forth in SEQ ID NO: 1-236 or an active variant or fragment thereof.

[0114] It is recognized that multiple suppressor enhancer elements from the same target sequence or from different target sequences, or from different regions of the same target sequence can be employed. For example, the suppressor enhancer elements employed can comprise fragments of the target sequence derived from different region of the target sequence (i.e., from the 3'UTR, coding sequence, intron, and/or 5'UTR). Further, the suppressor enhancer element can be contained in an expression cassette, as described elsewhere herein, and in specific embodiments, the suppressor enhancer element is on the same or on a different DNA vector or construct as the silencing element. The suppressor enhancer element can be operably linked to a promoter as disclosed herein. It is recognized that the suppressor enhancer element can be expressed constitutively or alternatively, it may be produced in a stage-specific manner employing the various inducible or tissue-preferred or developmentally regulated promoters that are discussed elsewhere herein.

[0115] In specific embodiments, employing both a silencing element and the suppressor enhancer element the systemic production of RNAi occurs throughout the entire plant. In further embodiments, the plant or plant parts of the inven-

tion have an improved loading of RNAi into the phloem of the plant than would be observed with the expression of the silencing element construct alone and, thus provide better control of phloem feeding insects by an RNAi approach. In specific embodiments, the plants, plant parts, and plant cells of the invention can further be characterized as allowing for the production of a diversity of RNAi species that can enhance the effectiveness of disrupting target gene expression.

[0116] In specific embodiments, the combined expression of the silencing element and the suppressor enhancer element increases the concentration of the inhibitory RNA in the plant cell, plant, plant part, plant tissue or phloem over the level that is achieved when the silencing element is expressed alone.

[0117] As used herein, an “increased level of inhibitory RNA” comprises any statistically significant increase in the level of RNAi produced in a plant having the combined expression when compared to an appropriate control plant. For example, an increase in the level of RNAi in the plant, plant part or the plant cell can comprise at least about a 1%, about a 1%-5%, about a 5%-10%, about a 10%-20%, about a 20%-30%, about a 30%-40%, about a 40%-50%, about a 50%-60%, about 60-70%, about 70%-80%, about a 80%-90%, about a 90%-100% or greater increase in the level of RNAi in the plant, plant part, plant cell, or phloem when compared to an appropriate control. In other embodiments, the increase in the level of RNAi in the plant, plant part, plant cell, or phloem can comprise at least about a 1 fold, about a 1 fold-5 fold, about a 5 fold-10 fold, about a 10 fold-20 fold, about a 20 fold-30 fold, about a 30 fold-40 fold, about a 40 fold-50 fold, about a 50 fold-60 fold, about 60 fold-70 fold, about 70 fold-80 fold, about a 80 fold-90 fold, about a 90 fold-100 fold or greater increase in the level of RNAi in the plant, plant part, plant cell or phloem when compared to an appropriate control. Methods to assay for an increase in the level of RNAi are discussed elsewhere herein.

[0118] The following examples are offered by way of illustration and not by way of limitation.

EXPERIMENTAL

Example 1

In Vitro Transcript dsRNA Screening Method

[0119] A cDNA library was produced from neonate western corn rootworm larvae by standard methods. A selected cDNA clone containing an expressed sequence tag is amplified in a PCR using universal primers to the plasmid backbone and flanking the EST insert. The universal primers also contain T7 RNA polymerase sites. 1 ul of the PCR reaction is used as the template for an in vitro transcription (IVT) reaction to produce long double stranded RNAs. Following enzymatic digestion and removal of the DNA template and single stranded RNA, the IVT reaction products are incorporated into artificial insect diet as described below.

Insect Bioassays

[0120] 2.5 ul of the IVT reaction are added to a given well of a 96 well microtiter plate. 25 ul of molten lowmelt Western corn rootworm diet are added to the sample and shaken on an orbital shaker to mix the sample and diet. Once the diet has solidified, neonate rootworms are added to the well. An average of 5 neonates is added to each well. After the plate is infested, the plate is sealed with mylar and a single hole in

punched in the mylar over each well to allow air exchange. 4 replicate wells are produced for each sample. The assay is scored for activity 7 days post infestation. The possible scores are dead, severely stunted (little or now growth but alive), stunted (growth to second instar but not equivalent to controls), or no activity. Samples demonstrating mortality or severe stunting were advanced to confirmation. Primary assays and confirmation assays were performed with the southern corn rootworm.

[0121] Following confirmation, a simple dose response assay was performed with both southern and western corn rootworms. Samples for dose response assays were produced in the same manner with the following modification; samples were further purified using column purification prior to enzymatic treatment. Samples were also normalized to 0.5 ug/ul and all samples were evaluated by gel electrophoresis. Dose response assays were performed with the following rates; 50, 25, 12, 6, 3, and 1.5 ppm

Example 2

Sequences Having Insecticidal Activity

[0122] DNA sequences which encode double stranded RNAs which were shown to have insecticidal activity against corn rootworms using the assay described in Example 1 are set forth below. Non-limiting examples of target polynucleotides are set forth below in Table 1.

TABLE 1

SEQ ID NO: 1
>iwm2c.pk005.e1.fis1
SEQ ID NO: 2
>iwm2c.pk004.b13.fis1
SEQ ID NO: 3
>iwm2s.pk003.o11.fis1
SEQ ID NO: 4
>iwm2c.pk002.e24.fis1
SEQ ID NO: 5
>iwm2c.pk002.e24.fis1
SEQ ID NO: 6
>iwm2c.pk011.n17.fis1
SEQ ID NO: 7
>idv1c.pk001.d14.f.fis1
SEQ ID NO: 8
>idv1c.pk001.e9.f.fis1
SEQ ID NO: 9
>idv1c.pk001.m5.f.fis1
SEQ ID NO: 10
>idv1c.pk001.n1.f.fis1
SEQ ID NO: 11
>idv1c.pk002.e5.f.fis1
SEQ ID NO: 12
>idv1c.pk002.f20.f.fis1
SEQ ID NO: 13
>idv1c.pk002.j17.f.fis1
SEQ ID NO: 14
>idv1c.pk002.n13.f.fis1
SEQ ID NO: 15
>idv1c.pk003.d6.f.fis1
SEQ ID NO: 16
>idv1c.pk003.f8.f.fis1
SEQ ID NO: 17
>idv1c.pk003.f9.f.fis1
SEQ ID NO: 18
>idv1c.pk003.j4.f.fis1
SEQ ID NO: 19
>idv1c.pk003.j6.f.fis1
SEQ ID NO: 20
>idv1c.pk003.j20.f.fis1
SEQ ID NO: 21
>idv1c.pk003.l1.f.fis1

TABLE 1-continued

SEQ ID NO: 22
>idv1c.pk003.m1.f.fis1
SEQ ID NO: 23
>idv1c.pk003.m10.f.fis1
SEQ ID NO: 24
>idv1c.pk003.o13.f.fis1
SEQ ID NO: 25
>idv1c.pk003.o22.f.fis1
SEQ ID NO: 26
>idv1c.pk003.p13.f.fis1
SEQ ID NO: 27
>idv1c.pk004.b12.f.fis1
SEQ ID NO: 28
>idv1c.pk004.d17.f.fis1
SEQ ID NO: 29
>idv1c.pk004.f20.f.fis1
SEQ ID NO: 30
>idv1c.pk004.k5.f.fis1
SEQ ID NO: 31
>idv1c.pk004.l15.f.fis1
SEQ ID NO: 32
>idv1c.pk004.m6.f.fis1
SEQ ID NO: 33
>idv1c.pk004.o4.f.fis1
SEQ ID NO: 34
>idv1c.pk004.o9.f.fis1
SEQ ID NO: 35
>idv1c.pk004.p1.f.fis1
SEQ ID NO: 36
>idv1c.pk013.a15.f.fis1
SEQ ID NO: 37
>idv1c.pk013.b11.f.fis1
SEQ ID NO: 38
>idv1c.pk013.c21.f.fis1
SEQ ID NO: 39
>idv1c.pk013.d22.f.fis1
SEQ ID NO: 40
>idv1c.pk013.h1.f.fis1
SEQ ID NO: 41
>idv1c.pk013.h14.f.fis1
SEQ ID NO: 42
>idv1c.pk013.k1.f.fis1
SEQ ID NO: 43
>idv1c.pk014.a19.f.fis1
SEQ ID NO: 44
>idv1c.pk014.b9.f.fis1
SEQ ID NO: 45
>idv1c.pk014.b17.f.fis1
SEQ ID NO: 46
>idv1c.pk014.c14.f.fis1
SEQ ID NO: 47
>idv1c.pk014.d11.f.fis1
SEQ ID NO: 48
>idv1c.pk014.f3.f.fis1
SEQ ID NO: 49
>idv1c.pk014.j2.f.fis1
SEQ ID NO: 50
>idv1c.pk014.k23.f.fis1
SEQ ID NO: 51
>idv1c.pk014.m5.f.fis1
SEQ ID NO: 52
>idv1c.pk014.m13.f.fis1
SEQ ID NO: 53
>idv1c.pk014.n16.f.fis1
SEQ ID NO: 54
>idv1c.pk014.n23.f.fis1
SEQ ID NO: 55
>idv1c.pk014.o1.f.fis1
SEQ ID NO: 56
>idv1c.pk015.a16.f.fis1
SEQ ID NO: 57
>idv1c.pk015.b8.f.fis1
SEQ ID NO: 58
>idv1c.pk015.g10.f.fis1
SEQ ID NO: 59
>idv1c.pk015.l13.f.fis1

TABLE 1-continued

SEQ ID NO: 60
 >idv1c.pk015.n19.f.fis1
 SEQ ID NO: 61
 >idv1c.pk015.p2.f.fis1
 SEQ ID NO: 62
 >idv1c.pk016.a9.f.fis1
 SEQ ID NO: 63
 >idv1c.pk016.f12.f.fis1
 SEQ ID NO: 64
 >idv1c.pk016.f21.f.fis1
 SEQ ID NO: 65
 >idv1c.pk016.h15.f.fis1
 SEQ ID NO: 66
 >idv1c.pk016.h19.f.fis1
 SEQ ID NO: 67
 >idv1c.pk016.j12.f.fis1
 SEQ ID NO: 68
 >idv1c.pk016.j15.f.fis1
 SEQ ID NO: 69
 >idv1c.pk016.k9.f.fis1
 SEQ ID NO: 70
 >idv1c.pk016.p18.f.fis1
 SEQ ID NO: 71
 >idv1c.pk017.c3.f.fis1
 SEQ ID NO: 72
 >idv1c.pk017.d14.f.fis1
 SEQ ID NO: 73
 >idv1c.pk017.e22.f.fis1
 SEQ ID NO: 74
 >idv1c.pk017.f1.f.fis1
 SEQ ID NO: 75
 >idv1c.pk017.h14.f.fis1
 SEQ ID NO: 76
 >idv1c.pk017.n19.f.fis1
 SEQ ID NO: 77
 >idv1c.pk017.p2.f.fis1
 SEQ ID NO: 78
 >idv1c.pk018.a5.f.fis1
 SEQ ID NO: 79
 >idv1c.pk018.c11.f.fis1
 SEQ ID NO: 80
 >idv1c.pk018.d5.f.fis1
 SEQ ID NO: 81
 >idv1c.pk018.d14.f.fis1
 SEQ ID NO: 82
 >idv1c.pk018.e10.f.fis1
 A
 SEQ ID NO: 83
 >idv1c.pk018.e20.f.fis1
 SEQ ID NO: 84
 >idv1c.pk018.f19.f.fis1
 SEQ ID NO: 85
 >idv1c.pk018.f22.f.fis1
 SEQ ID NO: 86
 >idv1c.pk018.g20.f.fis1
 SEQ ID NO: 87
 >idv1c.pk018.h21.f.fis1
 SEQ ID NO: 88
 >idv1c.pk018.m5.f.fis1
 SEQ ID NO: 89
 >idv1c.pk019.c4.f.fis1
 SEQ ID NO: 90
 >idv1c.pk019.i5.f.fis1
 SEQ ID NO: 91
 >idv1c.pk019.k3.f.fis1
 SEQ ID NO: 92
 >idv1c.pk019.l7.f.fis1
 SEQ ID NO: 93
 >idv1c.pk020.a8.f.fis1
 SEQ ID NO: 94
 >idv1c.pk020.b11.f.fis1
 SEQ ID NO: 95
 >idv1c.pk020.g17.f.fis1
 SEQ ID NO: 96
 >idv1c.pk020.i7.f.fis1
 SEQ ID NO: 97

TABLE 1-continued

>idv1c.pk020.i24.f.fis1
 SEQ ID NO: 98
 >idv1c.pk020.k19.f.fis1
 SEQ ID NO: 99
 >idv1c.pk020.l3.f.fis1
 SEQ ID NO: 100
 >idv1c.pk020.p23.f.fis1
 SEQ ID NO: 101
 >idv1c.pk021.c21.f.fis1
 SEQ ID NO: 102
 >idv1c.pk021.d22.f.fis1
 SEQ ID NO: 103
 >idv1c.pk021.g16.f.fis1
 SEQ ID NO: 104
 >idv1c.pk021.h12.f.fis1
 SEQ ID NO: 105
 >idv1c.pk021.m20.f.fis1
 SEQ ID NO: 106
 >idv1c.pk004.j11.f.fis1
 SEQ ID NO: 107
 >idv1c.pk001.o20.f
 SEQ ID NO: 108
 >idv1c.pk002.a20.f
 SEQ ID NO: 109
 >idv1c.pk002.c15.f
 SEQ ID NO: 110
 >idv1c.pk002.i21.f
 SEQ ID NO: 111
 >idv1c.pk024.b23.f
 SEQ ID NO: 112
 >idv1c.pk024.e1.f
 SEQ ID NO: 113
 >idv1c.pk024.e24.f
 SEQ ID NO: 114
 >idv1c.pk024.k17.f
 SEQ ID NO: 115
 >idv1c.pk024.m13.f
 SEQ ID NO: 116
 >idv1c.pk024.n1.f
 SEQ ID NO: 117
 >idv1c.pk024.o3.f
 SEQ ID NO: 118
 >idv1c.pk025.a4.f
 SEQ ID NO: 119
 >idv1c.pk025.c5.f
 SEQ ID NO: 120
 >idv1c.pk025.c23.f
 SEQ ID NO: 121
 >idv1c.pk025.d18.f
 SEQ ID NO: 122
 >idv1c.pk025.d20.f
 SEQ ID NO: 123
 >idv1c.pk025.f24.f
 SEQ ID NO: 124
 >idv1c.pk025.j20.f
 SEQ ID NO: 125
 >idv1c.pk025.l10.f
 SEQ ID NO: 126
 >idv1c.pk026.a16.f
 SEQ ID NO: 127
 >idv1c.pk026.b23.f
 SEQ ID NO: 128
 >idv1c.pk026.d22.f
 SEQ ID NO: 129
 >idv1c.pk026.e6.f
 SEQ ID NO: 130
 >idv1c.pk026.g12.f
 SEQ ID NO: 131
 >idv1c.pk026.h15.f
 SEQ ID NO: 132
 >idv1c.pk026.i12.f
 SEQ ID NO: 133
 >idv1c.pk026.j18.f
 SEQ ID NO: 134
 >idv1c.pk026.k13.f
 SEQ ID NO: 135

TABLE 1-continued

>idv1c.pk027.b21.f
 SEQ ID NO: 136
 >idv1c.pk027.c7.f
 SEQ ID NO: 137
 >idv1c.pk027.k4.f
 SEQ ID NO: 138
 >idv1c.pk027.p21.f
 SEQ ID NO: 139
 >idv1c.pk028.b7.f
 SEQ ID NO: 140
 >idv1c.pk028.c22.f
 SEQ ID NO: 141
 >idv1c.pk028.h6.f
 SEQ ID NO: 142
 >idv1c.pk028.i16.f
 SEQ ID NO: 143
 >idv1c.pk028.m11.f
 SEQ ID NO: 144
 >idv1c.pk028.o18.f
 SEQ ID NO: 145
 >idv1c.pk029.a17.f
 SEQ ID NO: 146
 >idv1c.pk029.d16.f
 SEQ ID NO: 147
 >idv1c.pk029.i22.f
 SEQ ID NO: 148
 >idv1c.pk029.j20.f
 SEQ ID NO: 149
 >idv1c.pk029.k11.f
 SEQ ID NO: 150
 >idv1c.pk029.l22.f
 SEQ ID NO: 151
 >idv1c.pk030.e10.f
 SEQ ID NO: 152
 >idv1c.pk030.e21.f
 C
 SEQ ID NO: 153
 >idv1c.pk030.h13.f
 SEQ ID NO: 154
 >idv1c.pk030.h23.f
 SEQ ID NO: 155
 >idv1c.pk030.i19.f
 SEQ ID NO: 156
 >idv1c.pk030.m22.f
 SEQ ID NO: 157
 >idv1c.pk030.o7.f
 SEQ ID NO: 158
 >idv1c.pk031.a11.f
 SEQ ID NO: 159
 >idv1c.pk031.e16.f
 SEQ ID NO: 160
 >idv1c.pk031.g2.f
 SEQ ID NO: 161
 >idv1c.pk031.g22.f
 SEQ ID NO: 162
 >idv1c.pk031.i13.f
 SEQ ID NO: 163
 >idv1c.pk031.m3.f
 SEQ ID NO: 164
 >idv1c.pk032.b4.f
 SEQ ID NO: 165
 >idv1c.pk032.e16.f
 SEQ ID NO: 166
 >idv1c.pk032.f14.f
 SEQ ID NO: 167
 >idv1c.pk032.m9.f
 SEQ ID NO: 168
 >idv1c.pk033.a15.f
 SEQ ID NO: 169
 >idv1c.pk033.b14.f
 SEQ ID NO: 170
 >idv1c.pk033.m3.f
 SEQ ID NO: 171
 >idv1c.pk033.n10.f
 SEQ ID NO: 172
 >idv1c.pk033.n18.f

TABLE 1-continued

SEQ ID NO: 173
 >idv1c.pk034.e8.f
 SEQ ID NO: 174
 >idv1c.pk034.p24.f
 SEQ ID NO: 175
 >idv1c.pk035.f21.f
 SEQ ID NO: 176
 >idv1c.pk035.g1.f
 SEQ ID NO: 177
 >idv1c.pk035.h19.f
 SEQ ID NO: 178
 >idv1c.pk035.j4.f
 SEQ ID NO: 179
 >idv1c.pk035.m1.f
 SEQ ID NO: 180
 >idv1c.pk035.o13.f
 SEQ ID NO: 181
 >idv1c.pk036.a14.f
 SEQ ID NO: 182
 >idv1c.pk036.e18.f
 SEQ ID NO: 183
 >idv1c.pk036.f4.f
 SEQ ID NO: 184
 >idv1c.pk036.f9.f
 SEQ ID NO: 185
 >idv1c.pk036.i17.f
 SEQ ID NO: 186
 >idv1c.pk036.i20.f
 SEQ ID NO: 187
 >idv1c.pk036.k23.f
 SEQ ID NO: 188
 >idv1c.pk034.k22.f
 SEQ ID NO: 189
 >idv1c.pk002.c7.f
 SEQ ID NO: 190
 >idv1c.pk002.f18.f
 SEQ ID NO: 191
 >idv1c.pk002.i23.f
 SEQ ID NO: 192
 >idv1c.pk002.j24.f
 SEQ ID NO: 193
 >idv1c.pk002.m16.f
 SEQ ID NO: 194
 >idv1c.pk002.n13.f
 SEQ ID NO: 195
 >idv1c.pk024.c7.f
 SEQ ID NO: 196
 >idv1c.pk024.j15.f
 SEQ ID NO: 197
 >idv1c.pk025.b17.f
 SEQ ID NO: 198
 >idv1c.pk025.f3.f
 SEQ ID NO: 199
 >idv1c.pk025.i8.f
 SEQ ID NO: 200
 >idv1c.pk025.l17.f
 SEQ ID NO: 201
 >idv1c.pk025.o24.f
 SEQ ID NO: 202
 >idv1c.pk025.p9.f
 SEQ ID NO: 203
 >idv1c.pk026.f20.f
 SEQ ID NO: 204
 >idv1c.pk026.p8.f
 SEQ ID NO: 205
 >idv1c.pk026.p22.f
 SEQ ID NO: 206
 >idv1c.pk027.a14.f
 SEQ ID NO: 207
 >idv1c.pk027.g7.f
 SEQ ID NO: 208
 >idv1c.pk027.k23.f
 SEQ ID NO: 209
 >idv1c.pk028.b17.f
 SEQ ID NO: 210
 >idv1c.pk028.f11.f

TABLE 1-continued

SEQ ID NO: 211
>idv1c.pk029.c3.f
SEQ ID NO: 212
>idv1c.pk029.f5.f
SEQ ID NO: 213
>idv1c.pk029.j4.f
SEQ ID NO: 214
>idv1c.pk030.b23.f
SEQ ID NO: 215
>idv1c.pk030.f9.f
SEQ ID NO: 216
>idv1c.pk030.g11.f
SEQ ID NO: 217
>idv1c.pk031.c20.f
SEQ ID NO: 218
>idv1c.pk031.d1.f
SEQ ID NO: 219
>idv1c.pk031.j1.f
SEQ ID NO: 220
>idv1c.pk031.j6.f
SEQ ID NO: 221
>idv1c.pk031.p16.f
SEQ ID NO: 222
>idv1c.pk032.a16.f
SEQ ID NO: 223
>idv1c.pk032.f11.f
SEQ ID NO: 224
>idv1c.pk032.i21.f
SEQ ID NO: 225
>idv1c.pk032.n18.f
SEQ ID NO: 226
>idv1c.pk032.p5.f
SEQ ID NO: 227
>idv1c.pk033.d24.f
SEQ ID NO: 228
>idv1c.pk033.j21.f
SEQ ID NO: 229
>idv1c.pk033.o9.f
SEQ ID NO: 230
>idv1c.pk033.p15.f
SEQ ID NO: 231
>idv1c.pk033.p16.f
SEQ ID NO: 232
>idv1c.pk034.i2.f
SEQ ID NO: 233
>idv1c.pk034.j6.f
SEQ ID NO: 234
>idv1c.pk035.i17.f
SEQ ID NO: 235
>idv1c.pk035.k18.f
SEQ ID NO: 236
>idv1c.pk036.i19.f
SEQ ID NO: 237
Construct expressing SEQ ID NO: 8 as a hairpin RNA. The construct comprises: UBI1ZM promoter 5'UTR and 1 st intron operably linked to SEQ ID NO: 8 operably linked to the ADH1 intron operably linked to the complement of SEQ ID NO: 8.
SEQ ID NO: 238
Construct expressing SEQ ID NO: 26 as a hairpin RNA. The construct comprises: UBI1ZM promoter 5'UTR and 1 st intron operably linked to SEQ ID NO: 26 operably linked to the ADH1 intron operably linked to the complement of SEQ ID NO: 26.
SEQ ID NO: 239
Construct expressing SEQ ID NO: 17 as a hairpin RNA. The construct comprises: UBI1ZM promoter 5'UTR and 1 st intron operably linked to SEQ ID NO: 17 operably linked to the ADH1 intron operably linked to the complement of SEQ ID NO: 17.
SEQ ID NO: 240
Construct expressing SEQ ID NO: 28 as a hairpin RNA. The construct comprises: UBI1ZM promoter 5'UTR and 1 st intron operably linked to SEQ ID NO: 28 operably linked to the ADH1 intron operably linked to the complement of SEQ ID NO: 28.
SEQ ID NO: 241
Construct expressing SEQ ID NO: 28 as a hairpin RNA. The construct comprises: UBI1ZM promoter 5'UTR and 1 st intron operably linked to

TABLE 1-continued

SEQ ID NO: 28 operably linked to the ADH1 intron operably linked to the complement of SEQ ID NO: 28.
SEQ ID NO: 242
Construct expressing SEQ ID NO: 13 as a hairpin RNA. The construct comprises: UBI1ZM promoter 5'UTR and 1 st intron operably linked to SEQ ID NO: 13 operably linked to the ADH1 intron operably linked to the complement of SEQ ID NO: 13.
SEQ ID NO: 243
Construct expressing SEQ ID NO: 40 as a hairpin RNA. The construct comprises: UBI1ZM promoter 5'UTR and 1 st intron operably linked to SEQ ID NO: 40 operably linked to the ADH1 intron operably linked to the complement of SEQ ID NO: 40.
SEQ ID NO: 244
Construct expressing SEQ ID NO: 72 as a hairpin RNA. The construct comprises: UBI1ZM promoter 5'UTR and 1 st intron operably linked to SEQ ID NO: 72 operably linked to the ADH1 intron operably linked to the complement of SEQ ID NO: 72.
SEQ ID NO: 245
Construct expressing SEQ ID NO: 73 as a hairpin RNA. The construct comprises: UBI1ZM promoter 5'UTR and 1 st intron operably linked to SEQ ID NO: 73 operably linked to the ADH1 intron operably linked to the complement of SEQ ID NO: 73
SEQ ID NO: 246
Construct expressing SEQ ID NO: 15 as a hairpin RNA. The construct comprises: UBI1ZM promoter 5'UTR and 1 st intron operably linked to SEQ ID NO: 15 operably linked to the ADH1 intron operably linked to the complement of SEQ ID NO: 15.
SEQ ID NO: 247
Construct expressing SEQ ID NO: 18 as a hairpin RNA. The construct comprises: UBI1ZM promoter 5'UTR and 1 st intron operably linked to SEQ ID NO: 18 operably linked to the ADH1 intron operably linked to the complement of SEQ ID NO: 18.
SEQ ID NO: 248
Construct expressing nt 1-380 of SEQ ID NO: 45 as a hairpin RNA. The construct comprises: UBI1ZM promoter 5'UTR and 1 st intron operably linked to nt 1-380 of SEQ ID NO: 45 operably linked to the ADH1 intron operably linked to the complement of nt 1-380 of SEQ ID NO: 45.
SEQ ID NO: 249
Construct expressing nt 1-675 of SEQ ID NO: 37 as a hairpin RNA. The construct comprises: UBI1ZM promoter 5'UTR and 1 st intron operably linked to nt 1-675 of SEQ ID NO: 37 operably linked to the ADH1 intron operably linked to the complement of nt 1-675 of SEQ ID NO: 37.
SEQ ID NO: 250
Construct expressing SEQ ID NO: 29 as a hairpin RNA. The construct comprises: UBI1ZM promoter 5'UTR and 1 st intron operably linked to SEQ ID NO: 29 operably linked to the ADH1 intron operably linked to the complement of SEQ ID NO: 29.
SEQ ID NO: 251
Construct expressing nt 1-266 of SEQ ID NO: 50 as a hairpin RNA. The construct comprises: UBI1ZM promoter 5'UTR and 1 st intron operably linked to nt 1-266 of SEQ ID NO: 50 operably linked to the ADH1 intron operably linked to the complement of 1-266 of SEQ ID NO: 50.
SEQ ID NO: 252
Construct expressing nt 16-585 of SEQ ID NO: 47 as a hairpin RNA. The construct comprises: UBI1ZM promoter 5'UTR and 1 st intron operably linked to nt 16-585 of SEQ ID NO: 47 operably linked to the ADH1 intron operably linked to the complement of nt 16-585 of SEQ ID NO: 47.

Example 3

Transformation of Maize

[0123] Immature maize embryos from greenhouse donor plants are bombarded with a plasmid containing the silencing element of the invention operably linked to either a tissue specific, tissue selective, or constitutive promoter and the selectable marker gene PAT (Wohlleben et al. (1988) *Gene* 70:25-37), which confers resistance to the herbicide Bialaphos. In one embodiment, the constructs will express a long double stranded RNA of the target sequence set forth in table 1. Such a construct can be linked to the dMMB promoter. Alternatively, the selectable marker gene is provided on a separate plasmid. Transformation is performed as follows. Media recipes follow below.

Preparation of Target Tissue

[0124] The ears are husked and surface sterilized in 30% Clorox bleach plus 0.5% Micro detergent for 20 minutes, and rinsed two times with sterile water. The immature embryos are excised and placed embryo axis side down (scutellum side up), 25 embryos per plate, on 560Y medium for 4 hours and then aligned within the 2.5 cm target zone in preparation for bombardment.

[0125] A plasmid vector comprising the silencing element of interest operably linked to either the tissue specific, tissue selective, or constitutive promoter is made. This plasmid DNA plus plasmid DNA containing a PAT selectable marker is precipitated onto 1.1 μm (average diameter) tungsten pellets using a CaCl_2 precipitation procedure as follows: 100 μl prepared tungsten particles in water; 10 μl (1 μg) DNA in Tris EDTA buffer (1 μg total DNA); 100 μl 2.5 M CaCl_2 ; and, 10 μl 0.1 M spermidine.

[0126] Each reagent is added sequentially to the tungsten particle suspension, while maintained on the multitube vortexer. The final mixture is sonicated briefly and allowed to incubate under constant vortexing for 10 minutes. After the precipitation period, the tubes are centrifuged briefly, liquid removed, washed with 500 ml 100% ethanol, and centrifuged for 30 seconds. Again the liquid is removed, and 105 μl 100% ethanol is added to the final tungsten particle pellet. For particle gun bombardment, the tungsten/DNA particles are briefly sonicated and 10 μl spotted onto the center of each macrocarrier and allowed to dry about 2 minutes before bombardment.

[0127] The sample plates are bombarded at level #4 in a particle gun. All samples receive a single shot at 650 PSI, with a total of ten aliquots taken from each tube of prepared particles/DNA.

[0128] Following bombardment, the embryos are kept on 560Y medium for 2 days, then transferred to 560R selection medium containing 3 mg/liter Bialaphos, and subcultured every 2 weeks. After approximately 10 weeks of selection, selection-resistant callus clones are transferred to 288J medium to initiate plant regeneration. Following somatic embryo maturation (2-4 weeks), well-developed somatic embryos are transferred to medium for germination and transferred to the lighted culture room. Approximately 7-10 days later, developing plantlets are transferred to 272V hormone-free medium in tubes for 7-10 days until plantlets are well established. Plants are then transferred to inserts in flats (equivalent to 2.5" pot) containing potting soil and grown for 1 week in a growth chamber, subsequently grown an additional 1-2 weeks in the greenhouse, then transferred to classic 600 pots (1.6 gallon) and grown to maturity.

[0129] Plants are monitored and scored for the appropriate marker, such as the control of a Coleoptera plant pest, such as a *Diabrotica* plant pest and have insecticidal activity. For example, R_0 plant roots are fed to western corn rootworm larvae (WCR, *Diabrotica virgifera*). Transgenic corn roots are handed-off in Petri dishes with MSOD medium containing antibiotics and glyphosate for in vitro selection. Two WCR larvae are infested per root in each dish with a fine tip paintbrush. The dishes are sealed with Parafilm to prevent the larvae from escaping. The assays are placed into a 27° C., 60% RH Percival incubator in complete darkness. Contamination and larval quality are monitored. After six days of feeding on root tissue, the larvae are transferred to WCR diet in a 96 well plate. The larvae are allowed to feed on the diet for eight days making the full assay fourteen days long. Larval

mass and survivorship are recorded for analysis. A one-way ANOVA analysis and a Dunnett's test is performed on the larval mass data to look for statistical significance compared to an untransformed negative control. WCR larvae stunting is measured after feeding on two events and compared to growth of larvae fed on negative control plants.

[0130] In other assays, transgenic corn plants (R_0) generated are planted into 10-inch pots containing Metromix soil after reaching an appropriate size. When plants reach the V4 growth stage, approximately 1000 Western corn rootworm (WCR, *Diabrotica virgifera*) eggs are infested into the root zone. Non-transgenic corn of the same genotype is infested at a similar growth stage to serve as a negative control. Eggs are pre-incubated so hatch occurs within 24 hours of infestation. Larvae are allowed to feed on the root systems for 3 weeks. Plants are removed from the soil and washed so that the roots can be evaluated for larval feeding. Root damage is rated using a Node Injury Scale (NIS) to score the level of damage where a 0 indicates no damage, a 1 indicates that one node of roots is pruned to within 1.5 inches, a 2 indicates that 2 nodes are pruned, while a 3 indicates that 3 nodes are pruned. Because the plants being used for evaluation are directly out of tissue culture after transformation and because transformation events are unique, only a single plant is evaluated per event at this time. The plants in the assay that present signs or symptoms of larval feeding indicate that a successful infestation is obtained. Negative control plant roots are moderately to severely damaged averaging whereas roots of the transgenic plants provide substantial control of larval feeding, with about 0.2 or less on the Node Injury Scale.

[0131] Bombardment medium (560Y) comprises 4.0 g/l N6 basal salts (SIGMA C-1416), 1.0 ml/l Eriksson's Vitamin Mix (1000 $\times$ SIGMA-1511), 0.5 mg/l thiamine HCl, 120.0 g/l sucrose, 1.0 mg/l 2,4-D, and 2.88 g/l L-proline (brought to volume with D-I H_2O following adjustment to pH 5.8 with KOH); 2.0 g/l Gelrite (added after bringing to volume with D-I H_2O); and 8.5 mg/l silver nitrate (added after sterilizing the medium and cooling to room temperature). Selection medium (560R) comprises 4.0 g/l N6 basal salts (SIGMA C-1416), 1.0 ml/l Eriksson's Vitamin Mix (1000 $\times$ SIGMA-1511), 0.5 mg/l thiamine HCl, 30.0 g/l sucrose, and 2.0 mg/l 2,4-D (brought to volume with D-I H_2O following adjustment to pH 5.8 with KOH); 3.0 g/l Gelrite (added after bringing to volume with D-I H_2O); and 0.85 mg/l silver nitrate and 3.0 mg/l bialaphos (both added after sterilizing the medium and cooling to room temperature).

[0132] Plant regeneration medium (288J) comprises 43 g/l MS salts (GIBCO 11117-074), 5.0 ml/l MS vitamins stock solution (0.100 g nicotinic acid, 0.02 g/l thiamine HCl, 0.10 g/l pyridoxine HCl, and 0.40 g/l glycine brought to volume with polished D-I H_2O) (Murashige and Skoog (1962) *Physiol. Plant.* 15:473), 100 mg/l myo-inositol, 0.5 mg/l zeatin, 60 g/l sucrose, and 1.0 ml/l of 0.1 mM abscisic acid (brought to volume with polished D-I H_2O after adjusting to pH 5.6); 3.0 g/l Gelrite (added after bringing to volume with D-I H_2O); and 1.0 mg/l indoleacetic acid and 3.0 mg/l bialaphos (added after sterilizing the medium and cooling to 60° C.). Hormone-free medium (272V) comprises 4.3 g/l MS salts (GIBCO 11117-074), 5.0 ml/l MS vitamins stock solution (0.100 g/l nicotinic acid, 0.02 g/l thiamine HCl, 0.10 g/l pyridoxine HCl, and 0.40 g/l glycine brought to volume with polished D-I H_2O), 0.1 g/l myo-inositol, and 40.0 g/l sucrose (brought to volume with polished D-I H_2O after adjusting pH

to 5.6); and 6 g/l bacto-agar (added after bringing to volume with polished D-I H₂O), sterilized and cooled to 60° C.

Example 4

Agrobacterium-Mediated Transformation of Maize

[0133] For *Agrobacterium*-mediated transformation of maize with a silencing element of the invention, the method of Zhao is employed (U.S. Pat. No. 5,981,840, and PCT patent publication WO98/32326; the contents of which are hereby incorporated by reference). Such as a construct can, for example, express a long double stranded RNA of the target sequence set forth in table 1. Such a construct can be linked to the dMMB promoter. Briefly, immature embryos are isolated from maize and the embryos contacted with a suspension of *Agrobacterium*, where the bacteria are capable of transferring the polynucleotide comprising the silencing element to at least one cell of at least one of the immature embryos (step 1: the infection step). In this step the immature embryos are immersed in an *Agrobacterium* suspension for the initiation of inoculation. The embryos are co-cultured for a time with the *Agrobacterium* (step 2: the co-cultivation step). The immature embryos are cultured on solid medium following the infection step. Following this co-cultivation period an optional "resting" step is contemplated. In this resting step, the embryos are incubated in the presence of at least one antibiotic known to inhibit the growth of *Agrobacterium* without the addition of a selective agent for plant transformants (step 3: resting step). The immature embryos are cultured on solid medium with antibiotic, but without a selecting agent, for elimination of *Agrobacterium* and for a resting phase for the infected cells. Next, inoculated embryos are cultured on medium containing a selective agent and growing transformed callus is recovered (step 4: the selection step). The immature embryos are cultured on solid medium with a selective agent resulting in the selective growth of transformed cells. The callus is then regenerated into plants (step 5: the regeneration step), and calli grown on selective medium are cultured on solid medium to regenerate the plants. Assays for insecticidal activity can be performed as described above in Example, 5.

Example 5

Soybean Embryo Transformation

Culture Conditions

[0134] Soybean embryogenic suspension cultures (cv. Jack) are maintained in 35 ml liquid medium SB196 (see recipes below) on rotary shaker, 150 rpm, 26° C. with cool white fluorescent lights on 16:8 hr day/night photoperiod at light intensity of 60-85 µE/m²/s. Cultures are subcultured every 7 days to two weeks by inoculating approximately 35 mg of tissue into 35 ml of fresh liquid SB196 (the preferred subculture interval is every 7 days).

[0135] Soybean embryogenic suspension cultures are transformed with the plasmids and DNA fragments described in the examples above by the method of particle gun bombardment (Klein et al. (1987) *Nature*, 327:70).

Soybean Embryogenic Suspension Culture Initiation

[0136] Soybean cultures are initiated twice each month with 5-7 days between each initiation.

[0137] Pods with immature seeds from available soybean plants 45-55 days after planting are picked, removed from their shells and placed into a sterilized magenta box. The soybean seeds are sterilized by shaking them for 15 minutes in a 5% Clorox solution with 1 drop of ivory soap (95 ml of autoclaved distilled water plus 5 ml Clorox and 1 drop of soap). Mix well. Seeds are rinsed using 2 1-liter bottles of sterile distilled water and those less than 4 mm are placed on individual microscope slides. The small end of the seed are cut and the cotyledons pressed out of the seed coat. Cotyledons are transferred to plates containing SB1 medium (25-30 cotyledons per plate). Plates are wrapped with fiber tape and stored for 8 weeks. After this time secondary embryos are cut and placed into SB196 liquid media for 7 days.

Preparation of DNA for Bombardment

[0138] Either an intact plasmid or a DNA plasmid fragment containing the genes of interest and the selectable marker gene are used for bombardment. Plasmid DNA for bombardment are routinely prepared and purified using the method described in the Promega™ Protocols and Applications Guide, Second Edition (page 106). Fragments of the plasmids carrying the silencing element of interest are obtained by gel isolation of double digested plasmids. In each case, 100 µg of plasmid DNA is digested in 0.5 ml of the specific enzyme mix that is appropriate for the plasmid of interest. The resulting DNA fragments are separated by gel electrophoresis on 1% SeaPlaque GTG agarose (BioWhittaker Molecular Applications) and the DNA fragments containing silencing element of interest are cut from the agarose gel. DNA is purified from the agarose using the GELase digesting enzyme following the manufacturer's protocol.

[0139] A 50 µl aliquot of sterile distilled water containing 3 mg of gold particles (3 mg gold) is added to 5 µl of a 1 µg/µl DNA solution (either intact plasmid or DNA fragment prepared as described above), 50 µl 2.5M CaCl₂ and 20 µl of 0.1 M spermidine. The mixture is shaken 3 min on level 3 of a vortex shaker and spun for 10 sec in a bench microfuge. After a wash with 400 µl 100% ethanol the pellet is suspended by sonication in 40 µl of 100% ethanol. Five µl of DNA suspension is dispensed to each flying disk of the Biolistic PDS1000/HE instrument disk. Each 5 µl aliquot contains approximately 0.375 mg gold per bombardment (i.e. per disk).

Tissue Preparation and Bombardment with DNA

[0140] Approximately 150-200 mg of 7 day old embryonic suspension cultures are placed in an empty, sterile 60×15 mm petri dish and the dish covered with plastic mesh. Tissue is bombarded 1 or 2 shots per plate with membrane rupture pressure set at 1100 PSI and the chamber evacuated to a vacuum of 27-28 inches of mercury. Tissue is placed approximately 3.5 inches from the retaining/stopping screen.

Selection of Transformed Embryos

[0141] Transformed embryos were selected either using hygromycin (when the hygromycin phosphotransferase, HPT, gene was used as the selectable marker) or chlorsulfuron (when the acetolactate synthase, ALS, gene was used as the selectable marker).

Hygromycin (HPT) Selection

[0142] Following bombardment, the tissue is placed into fresh SB196 media and cultured as described above. Six days post-bombardment, the SB196 is exchanged with fresh

SB196 containing a selection agent of 30 mg/L hygromycin. The selection media is refreshed weekly. Four to six weeks post selection, green, transformed tissue may be observed growing from untransformed, necrotic embryogenic clusters. Isolated, green tissue is removed and inoculated into multiwell plates to generate new, clonally propagated, transformed embryogenic suspension cultures.

Chlorsulfuron (ALS) Selection

[0143] Following bombardment, the tissue is divided between 2 flasks with fresh SB196 media and cultured as described above. Six to seven days post-bombardment, the SB196 is exchanged with fresh SB196 containing selection agent of 100 ng/ml Chlorsulfuron. The selection media is refreshed weekly. Four to six weeks post selection, green, transformed tissue may be observed growing from untransformed, necrotic embryogenic clusters. Isolated, green tissue is removed and inoculated into multiwell plates containing SB196 to generate new, clonally propagated, transformed embryogenic suspension cultures.

Regeneration of Soybean Somatic Embryos into Plants

[0144] In order to obtain whole plants from embryogenic suspension cultures, the tissue must be regenerated.

Embryo Maturation

[0145] Embryos are cultured for 4-6 weeks at 26° C. in SB196 under cool white fluorescent (Phillips cool white Econowatt F40/CW/RS/EW) and Agro (Phillips F40 Agro) bulbs (40 watt) on a 16:8 hr photoperiod with light intensity of 90-120 uE/m²s. After this time embryo clusters are removed to a solid agar media, SB166, for 1-2 weeks. Clusters are then subcultured to medium SB103 for 3 weeks. During this period, individual embryos can be removed from the clusters and screened for the appropriate marker or the ability of the plant, when injected with the silencing elements, to control the Coleopteran plant pest or the *Diabrotica* plant pest.

Embryo Desiccation and Germination

[0146] Matured individual embryos are desiccated by placing them into an empty, small petri dish (35×10 mm) for approximately 4-7 days. The plates are sealed with fiber tape (creating a small humidity chamber). Desiccated embryos are planted into SB71-4 medium where they were left to germinate under the same culture conditions described above. Germinated plantlets are removed from germination medium and rinsed thoroughly with water and then planted in Redi-Earth in 24-cell pack tray, covered with clear plastic dome. After 2 weeks the dome is removed and plants hardened off for a further week. If plantlets looked hardy they are transplanted to 10" pot of Redi-Earth with up to 3 plantlets per pot.

Media Recipes

[0147]

SB 196 - FN Lite liquid proliferation medium (per liter) -	
MS FeEDTA - 100x Stock 1	10 ml
MS Sulfate - 100x Stock 2	10 ml
FN Lite Halides - 100x Stock 3	10 ml
FN Lite P, B, Mo - 100x Stock 4	10 ml
B5 vitamins (1 ml/L)	1.0 ml

-continued

2,4-D (10 mg/L final concentration)	1.0 ml
KNO ₃	2.83 gm
(NH ₄) ₂ SO ₄	0.463 gm
Asparagine	1.0 gm
Sucrose (1%)	10 gm
pH 5.8	

FN Lite Stock Solutions

Stock #		1000 ml	500 ml
1	MS Fe EDTA 100x Stock		
	Na ₂ EDTA*	3.724 g	1.862 g
	FeSO ₄ —7H ₂ O	2.784 g	1.392 g
2	MS Sulfate 100x stock		
	MgSO ₄ —7H ₂ O	37.0 g	18.5 g
	MnSO ₄ —H ₂ O	1.69 g	0.845 g
	ZnSO ₄ —7H ₂ O	0.86 g	0.43 g
	CuSO ₄ —5H ₂ O	0.0025 g	0.00125 g
3	FN Lite Halides 100x Stock		
	CaCl ₂ —2H ₂ O	30.0 g	15.0 g
	KI	0.083 g	0.0715 g
	CoCl ₂ —6H ₂ O	0.0025 g	0.00125 g
4	FN Lite P, B, Mo 100x Stock		
	KH ₂ PO ₄	18.5 g	9.25 g
	H ₃ BO ₃	0.62 g	0.31 g
	Na ₂ MoO ₄ —2H ₂ O	0.025 g	0.0125 g

*Add first, dissolve in dark bottle while stirring

[0148] SB1 solid medium (per liter) comprises: 1 pkg. MS salts (Gibco/BRL-Cat# 11117-066); 1 ml B5 vitamins 1000x stock; 31.5 g sucrose; 2 ml 2,4-D (20 mg/L final concentration); pH 5.7; and, 8 g TC agar.

[0149] SB 166 solid medium (per liter) comprises: 1 pkg. MS salts (Gibco/BRL-Cat# 11117-066); 1 ml B5 vitamins 1000x stock; 60 g maltose; 750 mg MgCl₂ hexahydrate; 5 g activated charcoal; pH 5.7; and, 2 g gelrite.

[0150] SB 103 solid medium (per liter) comprises: 1 pkg. MS salts (Gibco/BRL-Cat# 11117-066); 1 ml B5 vitamins 1000x stock; 60 g maltose; 750 mg MgCl₂ hexahydrate; pH 5.7; and, 2 g gelrite.

[0151] SB 71-4 solid medium (per liter) comprises: 1 bottle Gamborg's B5 salts w/sucrose (Gibco/BRL-Cat# 21153-036); pH 5.7; and, 5 g TC agar.

[0152] 2,4-D stock is obtained premade from Phytotech cat# D 295-concentration is 1 mg/ml.

[0153] B5 Vitamins Stock (per 100 ml) which is stored in aliquots at -20 C comprises: 10 g myo-inositol; 100 mg nicotinic acid; 100 mg pyridoxine HCl; and, 1 g thiamine. If the solution does not dissolve quickly enough, apply a low level of heat via the hot stir plate. Chlorsulfuron Stock comprises 1 mg/ml in 0.01 N Ammonium Hydroxide

Example 6

Expression of Silencing Elements in Maize

[0154] The silencing elements set forth in SEQ ID NO: 8, 26, 17, 28 and 10 were expressed in a maize plant as hairpins and the plant was tested for insecticidal activity against corn root worms. The sequences set forth in SEQ ID NO: 8, 26, 17, 28 and 10 were engineered to be expressed as a hairpin. The constructs comprised the following components: the maize ubiquitin promoter/5'UTR/1st intron operably linked SEQ ID NO:8, 26, 17, 28 or 10::ADH1 intron::complement of SEQ ID NO:8, 26, 17, 28 and 10. Plasmids PHP41121, PHP41134, PHP41127, PHP41130, PHP41118 were generated as summarized below in Table 2.

TABLE 2

SEQ ID NO of silencing element	SEQ ID NO of construct w/promoter and silencing element	Clone name of silencing element	Sequence homology of the silencing element	Plasmid name
8	237	idv1c.pk001.e9.f	Ribosomal protein s10E	PHP41121
26	238	idv1c.ph003.p13.f	Ribosomal protein 27 kD	PHP41134
17	239	idv1c.pk003.f9.f	proteinase	PHP41127
28	240	idv1c.pk004.d17.f	Tribolium	PHP41130
10	241	idv1c.pk001.n1.f	No hits	PHP41118

[0155] Maize plants were transformed with Plasmids PHP41121, PHP41134, PHP41127, PHP41130, PHP41118 and plants expressing the silencing elements denoted in Table 2 were transplanted from 722V plates into greenhouse flats containing Fafard Superfine potting mix. Approximately 10 to 14 days after transplant, plants (now at growth stage V2-V3) were transplanted into treepots containing Fafard Superfine potting mix. At 14 days post greenhouse send date, plants were infested with 100 eggs of western corn root worms (WCRW)/plant. For later sets, a second infestation of 100 eggs WCRW/plant was done 14 days after the first infestation and scoring was at 14 days after the second infestation. 21 days post infestation, plants were scored using CRWNIS. Those plants with a score of ≤ 0.5 are transplanted into large pots containing SB300 for seed. As shown in FIG. 1, each of SEQ ID NO: 8, 26, 17, 28 and 10 had insecticidal activity.

Example 7

Insect Bioassays

[0156] 2.5 ul of an in-vitro transcription reaction which synthesized one of the sequences set forth in SEQ ID NO: 107-236 were added to a given well of a 96 well microtiter plate. 25 ul of molten lowmelt western corn rootworm diet were added to the sample and shaken on an orbital shaker to mix the sample and diet. Once the diet had solidified, neonate rootworms were added to the well. An average of 5 neonates were added to each well. After the plate was infested, the plate was sealed with mylar and a single hole was punched in the mylar over each well to allow air exchange. 4 replicate wells were produced for each sample. The assay was scored for activity 7 days post infestation. Table 3 provides insecticidal bioassay data employing the southern corn rootworm. The possible scores are dead (D), severely stunted (SS; little or no growth but alive), stunted (S; growth to second instar but not equivalent to controls), contaminated (c), or no activity.

[0157] Following confirmation, a simple dose response assay was performed with both southern and western corn rootworms. See, Tables 4 and 5 below. Samples for dose response assays were produced in the same manner described above with the following modification: samples were further purified using column purification prior to enzymatic treatment. Samples were also normalized to 0.5 ug/ul and all samples were evaluated by gel electrophoresis. Dose response assays were performed with the following rates: crude, 0.5, 0.25, 0.0125 ppm, and 0.125 dilutions (equivalent to 51, 25, 12.5 and 6 ppm).

TABLE 3

Insecticidal Bioassay Data Against Southern Corn Root Worm					
Clone name					
idv1c.pk001.o20.f	S	S	S	S	S
idv1c.pk002.a20.f	S	S	S	S	S
idv1c.pk002.c7.f	SS	SS	SS	SS	SS
idv1c.pk002.c15.f	S	S	S	S	S
idv1c.pk002.f18.f	SS	SS	S	SS	SS
idv1c.pk002.i21.f	S	S	S	S	S
idv1c.pk002.i23.f	SS	SS	SS	SS	SS
idv1c.pk002.j24.f	SS	SS	SS	SS	SS
idv1c.pk002.m16.f	SS	SS	SS	SS	SS
idv1c.pk002.n13.f	SS	SS	SS	SS	SS
idv1c.pk024.b23.f	S	S	S	S	S
idv1c.pk024.c7.f	SS	SS	D	SS	SS
idv1c.pk024.e1.f	S	S	S	S	S
idv1c.pk024.e24.f	S	S	S	S	S
idv1c.pk024.j15.f	SS	SS	SS	SS	SS
idv1c.pk024.k17.f	S	S	S	S	S
idv1c.pk024.m13.f	S	S	S	S	S
idv1c.pk024.n1.f	S	S	S	S	S
idv1c.pk024.o3.f	S	S	S	S	S
idv1c.pk025.a4.f	S	S	S	S	S
idv1c.pk025.b17.f	SS	SS	SS	SS	SS
idv1c.pk025.c5.f	S	S	S	S	S
idv1c.pk025.c23.f	S	SS	S	S	S
idv1c.pk025.d18.f	S	S	S	S	S
idv1c.pk025.d20.f	S	S	S	S	S
idv1c.pk025.f3.f	SS	SS	SS	SS	SS
idv1c.pk025.f24.f	S	S	S	S	S
idv1c.pk025.i8.f	SS	SS	SS	S	SS
idv1c.pk025.j20.f	S	S	S	S	S
idv1c.pk025.i10.f	S	S	S	S	S
idv1c.pk025.i17.f	SS	S	SS	SS	SS
idv1c.pk025.o24.f	SS	SS	SS	SS	SS
idv1c.pk025.p9.f	SS	SS	S	SS	SS
idv1c.pk026.a16.f	S	S	S	S	S
idv1c.pk026.b23.f	S	S	S	S	S
idv1c.pk026.d22.f	S	S	S	S	S
idv1c.pk026.e6.f	S	S	S	S	S
idv1c.pk026.f20.f	SS	SS	SS	SS	SS
idv1c.pk026.g12.f	S	S	S	S	S
idv1c.pk026.h15.f	S	S	S	S	S
idv1c.pk026.i12.f	S	S	S	S	S
idv1c.pk026.j18.f	S	S	S	S	S
idv1c.pk026.k13.f	S	S	S	S	S
idv1c.pk026.p8.f	SS	SS	S	S	SS
idv1c.pk026.p22.f	SS	SS	SS	SS	SS
idv1c.pk027.a14.f	SS	SS	SS	SS	SS
idv1c.pk027.b21.f	S	S	S	S	S
idv1c.pk027.c7.f	S	S	S	S	S
idv1c.pk027.g7.f	SS	SS	SS	SS	SS
idv1c.pk027.k4.f	S	S	S	S	S
idv1c.pk027.k23.f	SS	SS	SS	SS	SS
idv1c.pk027.p21.f	S	S	S	S	S
idv1c.pk028.b7.f	S	S	S	S	S
idv1c.pk028.b17.f	S	SS	SS	S	SS
idv1c.pk028.c22.f	S	S	S	S	S
idv1c.pk028.f11.f	SS	SS	SS	SS	SS
idv1c.pk028.h6.f	S	S	S	S	S
idv1c.pk028.i16.f	S	S	S	S	S
idv1c.pk028.m11.f	S	S	S	S	S
idv1c.pk028.o18.f	S	S	S	S	S
idv1c.pk029.a17.f	S	S	S	S	S
idv1c.pk029.c3.f	SS	SS	SS	SS	SS
idv1c.pk029.d16.f	S	S	S	S	S
idv1c.pk029.f5.f	SS	SS	SS	S	SS
idv1c.pk029.i22.f	S	S	S	S	S
idv1c.pk029.j4.f	SS	SS	SS	SS	SS
idv1c.pk029.j20.f	S	S	S	S	S
idv1c.pk029.k11.f	S	S	S	S	S
idv1c.pk029.l22.f	S	S	S	S	S
idv1c.pk030.b23.f	SS	SS	SS	SS	SS
idv1c.pk030.e10.f	S	S	S	S	S
idv1c.pk030.e21.f	S	S	S	S	S

TABLE 3-continued

Insecticidal Bioassay Data Against Southern Corn Root Worm					
Clone name					
idv1c.pk030.f9.f	SS	SS	SS	SS	SS
idv1c.pk030.g11.f	SS	SS	SS	SS	SS
idv1c.pk030.h13.f	S	S	S	S	S
idv1c.pk030.h23.f	S	S	S	S	S
idv1c.pk030.i9.f	S	S	S	S	S
idv1c.pk030.m22.f	S	S	S	S	S
idv1c.pk030.o7.f	S	S	S	S	S
idv1c.pk031.a11.f	S	S	S	S	S
idv1c.pk031.c20.f	SS	SS	SS	SS	SS
idv1c.pk031.d1.f	SS	SS	SS	SS	SS
idv1c.pk031.e16.f	S	S	S	S	S
idv1c.pk031.g2.f	S	S	S	S	S
idv1c.pk031.g22.f	S	S	S	S	S
idv1c.pk031.i13.f	S	S	S	S	S
idv1c.pk031.j1.f	SS	SS	SS	SS	SS
idv1c.pk031.j6.f	SS	SS	SS	SS	SS
idv1c.pk031.m3.f	S	S	S	S	S
idv1c.pk031.p16.f	SS	SS	SS	SS	SS
idv1c.pk032.a16.f	SS	SS	SS	SS	SS
idv1c.pk032.b4.f	S	S	S	S	S
idv1c.pk032.e16.f	S	S	S	S	S
idv1c.pk032.f11.f	SS	SS	SS	SS	SS
idv1c.pk032.f14.f	S	S	S	S	S
idv1c.pk032.i21.f	SS	SS	SS	SS	SS
idv1c.pk032.m9.f	S	S	S	S	S
idv1c.pk032.n18.f	SS	SS	SS	SS	SS
idv1c.pk032.p5.f	SS	SS	SS	SS	SS
idv1c.pk033.a15.f	S	S	S	S	S
idv1c.pk033.b14.f	S	S	S	S	S
idv1c.pk033.d24.f	SS	SS	SS	SS	SS

TABLE 3-continued

Insecticidal Bioassay Data Against Southern Corn Root Worm					
Clone name					
idv1c.pk033.j21.f	SS	SS	SS	SS	SS
idv1c.pk033.m3.f	S	S	S	S	S
idv1c.pk033.n10.f	S	S	S	S	S
idv1c.pk033.n18.f	S	S	S	S	S
idv1c.pk033.o9.f	SS	SS	SS	SS	SS
idv1c.pk033.p15.f	SS	SS	SS	SS	SS
idv1c.pk033.p16.f	SS	SS	SS	SS	SS
idv1c.pk034.e8.f	S	S	S	S	S
idv1c.pk034.i2.f	SS	SS	SS	SS	SS
idv1c.pk034.j6.f	SS	SS	SS	SS	SS
idv1c.pk034.p24.f	S	S	S	S	S
idv1c.pk035.f21.f	S	S	S	S	S
idv1c.pk035.g1.f	S	S	S	S	S
idv1c.pk035.h19.f	S	S	S	S	S
idv1c.pk035.i17.f	SS	SS	SS	SS	SS
idv1c.pk035.j4.f	S	S	S	S	S
idv1c.pk035.k18.f	SS	SS	SS	SS	SS
idv1c.pk035.m1.f	S	S	S	S	S
idv1c.pk035.o13.f	S	S	S	S	S
idv1c.pk036.a14.f	S	S	S	S	S
idv1c.pk036.e18.f	S	S	S	S	S
idv1c.pk036.f4.f	S	S	S	S	S
idv1c.pk036.f9.f	S	S	S	S	S
idv1c.pk036.i17.f	S	S	S	S	S
idv1c.pk036.i19.f	SS	SS	SS	SS	SS
idv1c.pk036.i20.f	S	S	S	S	S
idv1c.pk036.k23.f	S	S	S	S	S

*columns in Table 3 represent replicate wells 1, 2, 3, and 4 and the average.

TABLE 4

Insect Bioassays Against Southern and Western Corn Root Worm.													
Clone name	Seq id	SCRW				WCRW				SCRW 2			
		Crude	0.5	0.25	0.125	Crude	0.5	0.25	0.125	Crude	0.5	0.25	0.125
idv1c.pk034.k22.f	DNA directed polymerase	SS	S	S	S	D	D	S	S	SS	S	S	S
idv1c.pk002.c7.f	regulatory; prolactin; binding element	SS	S	N	N	S	S	N	N	SS	N	N	N
idv1c.pk002.f18.f	cadherin like	S	N	N	N	S	N	N	N	S	N	N	N
idv1c.pk002.i23.f	mitochondrial NADH dehydrogenase Fe—S protein	S	N	N	N	S	S	S	S	S	S	N	N
idv1c.pk002.j24.f	Human DNA sequence from clone RP5-858M22	S	S	N	N	N	N	N	N	S	S	N	N
idv1c.pk002.m16.f	conserved hypothetical protein	SS	N	N	N	SS	N	N	N	SS	S	N	N
idv1c.pk002.n13.f	16s ribosomal RNA gene	S	N	N	N	SS	SS	N	N	S	S	N	N
idv1c.pk024.c7.f	conserved hypothetical protein	SS	S	N	N	SS	SS	N	N	SS	S	N	N
idv1c.pk024.j15.f		SS	N	N	N	N	N	N	N	SS	N	N	N
idv1c.pk025.b17.f	cadherin like	SS	S	N	N	SS	SS	S	N	SS	S	N	N
idv1c.pk025.f3.f	alpha tubulin	SS	SS	S	S	SS	SS	N	N	SS	SS	S	S
idv1c.pk025.i8.f	chromaffin granule amine transporter	SS	S	S	S	SS	SS	SS	S	SS	S	N	S
idv1c.pk025.i17.f	Cytochrome b561 domain-containing protein 2	S	S	N	N	S	S	N	N	S	S	N	N
idv1c.pk025.o24.f	ATP-dependent RNA helicase	N	N	N	N	SS	S	N	N	S	N	N	N
idv1c.pk025.p9.f	conserved insect hypothetical protein	S	N	N	N	N	N	N	N	S	N	N	N

TABLE 4-continued

Insect Bioassays Against Southern and Western Corn Root Worm.													
Clone name	Seq id	SCRW				WCRW				SCRW 2			
		Crude	0.5	0.25	0.125	Crude	0.5	0.25	0.125	Crude	0.5	0.25	0.125
idv1c.pk026.f20.f	NADH-ubiquinone oxidoreductase 24 kDa subunit	S	S	N	N	SS	N	N	N	S	S	N	N
idv1c.pk026.p8.f	Sec61 gamma subunit alpha	SS	N	N	N	SS	SS	S	S	SS	S	S	N
idv1c.pk026.p22.f	no hits	S	N	N	N	SS	S	N	N	S	N	N	N
idv1c.pk027.a14.f	conserved insect sequence	S	N	N	N	N	N	N	N	S	N	N	N
idv1c.pk027.g7.f	conserved hypothetical protein	SS	SS	S	S	S	S	S	S	SS	SS	S	S
idv1c.pk027.k23.f	low homology to zebrafish sequence	SS	N	N	N	SS	S	S	S	SS	N	N	N
idv1c.pk028.b17.f	highly similar to conserved <i>drosophila</i> sequence	SS	S	N	N	SS	SS	SS	SS	SS	S	N	N
idv1c.pk028.f11.f	dynein heavy chain of insects	S	S	N	N	S	N	N	N	S	S	N	N
idv1c.pk029.c3.f	COP9 complex homolog subunit 6	SS	N	N	N	S	S	S	S	SS	N	N	N
idv1c.pk029.f5.f	acyl-coa dehydrogenase	SS	S	N	N	SS	SS	SS	SS	SS	S	N	N
idv1c.pk029.j4.f	Lanc11 protein [<i>Tribolium castaneum</i>]	S	S	S	S	SS	SS	S	S	S	S	S	S
idv1c.pk030.b23.f	no hits	SS	S	N	N	SS	SS	SS	SS	SS	S	S	N
idv1c.pk030.f9.f	aspartate aminotransferase	S	N	N	N	S	N	N	N	S	S	S	N
idv1c.pk030.g11.f	low-density lipoprotein receptor, chaperonin	SS	SS	S	S	SS	N	N	N	SS	SS	S	S
idv1c.pk031.c20.f	1,4-dihydroxy-2-naphthoate octaprenyltransferase	SS	S	N	N	SS	SS	N	N	SS	S	N	N
idv1c.pk031.d1.f	no hits	SS	S	S	N	SS	SS	SS	S	SS	S	S	N
idv1c.pk031.j1.f	ribosomal protein S12	S	N	N	N	N	N	N	N	S	N	N	N
idv1c.pk031.j6.f	DEAD box ATP-dependent RNA helicase	S	N	N	N	SS	SS	SS	N	S	N	N	N
idv1c.pk031.p16.f	ribosomal protein L4e	S	S	S	S	SS	SS	SS	SS	S	S	S	S
idv1c.pk032.a16.f	conserved hypothetical protein	S	S	S	S	SS	SS	N	N	S	S	S	S
idv1c.pk032.f11.f	similar to pol-like protein	SS	SS	SS	S	SS	SS	SS	N	SS	SS	SS	S
idv1c.pk032.i21.f	no hits	SS	S	S	S	SS	SS	S	N	SS	S	S	S
idv1c.pk032.n18.f	sodium pump alpha subunit;	S	S	S	S	SS	SS	S	N	S	S	S	S
idv1c.pk032.p5.f	proteasome subunit alpha type 6	SS	S	N	N	N	N	N	N	SS	SS	S	N
idv1c.pk033.d24.f	similar to Uncharacterized protein ZK1236.4 [<i>Acyrtosiphon pisum</i>]	SS	S	S	N	SS	SS	SS	S	SS	S	S	N
idv1c.pk033.j21.f	ribosomal protein L35Ae	S	S	S	N	S	S	N	N	S	S	S	N
idv1c.pk033.o9.f	similar to ribosomal protein L10Ae	S	S	S	N	S	S	N	N	S	S	S	N
idv1c.pk033.p15.f	cadherin-like gene	SS	S	N	N	S	S	S	N	SS	S	S	N
idv1c.pk033.p16.f	conserved hypothetical protein	SS	S	N	N	SS	S	S	N	SS	S	S	N
idv1c.pk034.i2.f	ryanodine receptor-like protein	N	N	N	N	SS	SS	N	N	S	N	N	N
idv1c.pk034.j6.f	[<i>Tribolium castaneum</i>]	N	N	N	N	SS	SS	N	N	S	N	N	N
idv1c.pk035.i17.f	conserved hypothetical protein	S	N	N	N	SS	S	N	N	S	N	N	N
idv1c.pk035.k18.f	predicted protein	SS	S	N	N	SS	S	S	N	SS	SS	SS	S

TABLE 5

Insect Bioassays Against Southern and Western Corn Root Worm.											
Clone name	1° assay	1st	2nd	SCRW dose response #1				SCRW dose response #2			
	result	Confirmation	Confirmation	Crude	0.5	0.25	0.125	Crude	0.5	0.25	0.125
idv1c.pk001.o20.f	S	SS	SS	S	N	N	N	S	N	N	N
idv1c.pk002.a20.f	S	SS	SS	S	N	N	N	N	N	N	N
idv1c.pk002.c15.f	S	S	N	SS	S	N	N	SS	SS	S	N
idv1c.pk002.i21.f	S	SS	SS	SS	S	N	N	SS	S	S	S
idv1c.pk024.b23.f	S	SS	SS	SS	N	N	N	S	S	N	N
idv1c.pk024.e1.f	S	S	S	S	S	N	N	S	S	N	N
idv1c.pk024.e24.f	S	S	S	S	S	N	N	S	N	N	N
idv1c.pk024.k17.f	S	S	S	SS	N	N	N	SS	SS	N	N
idv1c.pk024.m13.f	S	S	S	S	N	N	N	S	S	N	N
idv1c.pk024.n1.f	S	S	S	S	S	S	S	S	S	N	N
idv1c.pk024.o3.f	S	SS	SS	S	S	S	S	N	N	N	N
idv1c.pk025.a4.f	S	SS	S	S	S	N	N	S	N	N	N
idv1c.pk025.c5.f	S	N	N	N	N	N	N	S	N	N	N
idv1c.pk025.c23.f	S	N	N	S	N	N	N	S	N	N	N
idv1c.pk025.d18.f	S	S	N	SS	SS	N	N	SS	SS	S	N
idv1c.pk025.d20.f	S	S	S	S	S	S	S	S	S	N	N
idv1c.pk025.f24.f	S	SS	SS	S	S	S	S	S	S	S	N
idv1c.pk025.j20.f	S	SS	SS	S	N	N	N	S	S	N	N
idv1c.pk025.l10.f	S	S	S	S	N	N	N	S	N	N	N
idv1c.pk026.a16.f	S	SS	SS	S	N	N	N	S	N	N	N
idv1c.pk026.b23.f	S	S	S	S	N	N	N	S	N	N	N
idv1c.pk026.d22.f	S	S	S	N	N	N	N	N	N	N	N
idv1c.pk026.e6.f	S	S	S	S	S	N	N	S	S	N	N
idv1c.pk026.g12.f	S	S	S	SS	S	N	N	SS	SS	N	N
idv1c.pk026.h15.f	S	N	N	S	N	N	N	N	N	N	N
idv1c.pk026.i12.f	S	N	N	N	N	N	N	N	N	N	N
idv1c.pk026.j18.f	S	S	N	S	S	N	N	SS	N	N	N
idv1c.pk026.k13.f	S	SS	SS	S	S	S	S	S	S	S	N
idv1c.pk027.b21.f	S	N	N	S	N	N	N	N	N	N	N
idv1c.pk027.c7.f	S	N	N	N	N	N	N	N	N	N	N
idv1c.pk027.k4.f	S	SS	SS	SS	N	N	N	SS	S	N	N
idv1c.pk027.p21.f	S	SS	SS	SS	S	N	N	SS	S	N	N
idv1c.pk028.b7.f	S	SS	SS	S	N	N	N	N	N	N	N
idv1c.pk028.c22.f	S	SS	SS	SS	N	N	N	SS	S	N	N
idv1c.pk028.h6.f	S	SS	SS	SS	N	N	N	SS	N	N	N
idv1c.pk028.i16.f	S	N	N	S	N	N	N	S	N	N	N
idv1c.pk028.m11.f	S	N	N	S	N	N	N	S	N	N	N
idv1c.pk028.o18.f	S	S	SS	S	S	S	S	S	S	S	N
idv1c.pk029.a17.f	S	S	S	S	S	S	S	S	N	N	N
idv1c.pk029.d16.f	S	S	S	S	S	S	S	S	S	S	S
idv1c.pk029.i22.f	S	S	S	SS	SS	S	S	SS	SS	S	N
idv1c.pk029.j20.f	S	S	S	SS	SS	S	S	SS	S	S	S
idv1c.pk029.k11.f	S	N	N	SS	S	S	N	SS	S	S	S
idv1c.pk029.l22.f	S	S	SS	S	S	N	N	S	N	N	N
idv1c.pk030.e10.f	S	S	S	SS	S	S	S	SS	S	S	S
idv1c.pk030.e21.f	S	S	S	SS	S	S	S	SS	SS	S	S
idv1c.pk030.h13.f	S	S	S	S	S	S	S	SS	S	S	S
idv1c.pk030.h23.f	S	SS	S	SS	SS	S	S	SS	S	S	N
idv1c.pk030.l9.f	S	N	N	S	N	N	N	S	S	N	N
idv1c.pk030.m22.f	S	N	N	S	N	N	N	S	N	N	N
idv1c.pk030.o7.f	S	S	SS	SS	S	N	N	SS	S	N	N
idv1c.pk031.a11.f	S	S	S	SS	S	S	S	SS	S	S	S
idv1c.pk031.e16.f	S	S	S	S	N	N	N	N	N	N	N
idv1c.pk031.g2.f	S	SS	SS	SS	S	S	N	SS	S	S	N
idv1c.pk031.g22.f	S	S	S	SS	N	N	N	SS	S	N	N
idv1c.pk031.i13.f	S	SS	SS	SS	S	S	S	SS	N	N	N
idv1c.pk031.m3.f	S	S	S	SS	S	S	N	SS	S	S	N
idv1c.pk032.b4.f	S	S	S	SS	S	N	N	SS	S	N	N
idv1c.pk032.e16.f	S	S	S	S	S	S	S	S	S	N	N
idv1c.pk032.f14.f	S	N	N	S	N	N	N	S	N	N	N
idv1c.pk032.m9.f	S	SS	SS	SS	N	N	N	SS	S	N	N
idv1c.pk033.a15.f	S	N	N	N	N	N	N	S	N	N	N
idv1c.pk033.b14.f	S	N	N	S	N	N	N	S	N	N	N
idv1c.pk033.m3.f	S	S	S	SS	N	N	N	SS	N	N	N
idv1c.pk033.n10.f	S	SS	SS	S	S	S	S	S	S	N	N
idv1c.pk033.n18.f	S	SS	SS	S	N	N	N	S	N	N	N
idv1c.pk034.e8.f	S	S	S	S	N	N	N	S	N	N	N
idv1c.pk034.p24.f	S	S	N	S	S	S	N	S	N	N	N
idv1c.pk035.f21.f	S	S	S	S	S	S	S	S	S	S	N
idv1c.pk035.g1.f	S	S	N	S	N	N	N	S	N	N	N

TABLE 5-continued

Insect Bioassays Against Southern and Western Corn Root Worm.											
Clone name	1° assay	1st	2nd	SCRW dose response #1				SCRW dose response #2			
	result	Confirmation	Confirmation	Crude	0.5	0.25	0.125	Crude	0.5	0.25	0.125
idv1c.pk035.h19.f	S	SS	SS	S	N	N	N	N	N	N	N
idv1c.pk035.j4.f	S	SS	SS	SS	S	S	S	SS	SS	S	S
idv1c.pk035.m1.f	S	S	S	S	S	S	S	S	S	S	N
idv1c.pk035.o13.f	S	S	S	S	N	N	S	S	N	N	N
idv1c.pk036.a14.f	S	S	N	SS	S	S	N	SS	S	S	N
idv1c.pk036.e18.f	S	S	S	S	S	S	N	S	S	S	N
idv1c.pk036.f4.f	S	S	S	S	S	S	S	S	S	N	N
idv1c.pk036.f9.f	S	S	S	SS	S	S	S	SS	S	S	N
idv1c.pk036.i17.f	S	S	S	S	S	S	S	S	S	S	N
idv1c.pk036.i20.f	S	S	S	SS	SS	N	N	SS	SS	S	N
idv1c.pk036.k23.f	S	S	S	S	S	N	N	S	S	S	N

Example 8

Expression of Silencing Elements in Maize

[0158] The silencing elements set forth in SEQ ID NO: 13, 40, 72 and 73 were expressed in a maize plant as hairpins and the plants were tested for insecticidal activity against corn root worms. The sequences set forth in SEQ ID NO: 13, 40, 72 and 73 were engineered to be expressed as a hairpin. The constructs comprised the following components: the maize ubiquitin promoter/5'UTR/1st intron operably linked to one of SEQ ID NO: 13, 40, 72 and 73::the ADH1 intron::complement of the corresponding SEQ ID NO. Plasmids PHP41136, PHP41567, PHP41992, PHP42000 were generated as summarized below in Table 6. PHP19288 was a control plasmid which lacked a silencing element.

TABLE 6

SEQ ID NO of silencing element	SEQ ID NO of construct w/ promoter and silencing element	Clone name of silencing element	Plasmid name
13	242	idv1c.pk002.j17.f	PHP41136
40	243	idv1c.pk013.h1.f	PHP41567
72	244	idv1c.pk017.d14.f	PHP41992
73	245	idv1c.pk017.e22.f	PHP42000

[0159] Maize plants were transformed with plasmids PHP41136, PHP41567, PHP41992, PHP42000, and PHP19288 (control lacking silencing element) and plants expressing the silencing elements denoted in Table 6 were transplanted from 272V plates into greenhouse flats containing Fafard Superfine potting mix. Plants were infected (100 eggs per plant) 14 days post green house send date and a second infestation (150 eggs per plant) was performed 14 days later. The scoring for insecticidal activity was done 14 days later (28 days post first infection). Each of SEQ ID NO: 13, 40, 72 and 73 had insecticidal activity in this assay.

[0160] As shown in FIG. 2, significant efficacy was shown with the PHP41136, PHP41567, PHP41992, and PHP42000 constructs. No significant difference between PHP41136 and the PHP positive control was seen. Table 7 provides a summary of the data shown in FIG. 2.

TABLE 7

Oneway Anova Summary of Fit					
Rsquare					0.440885
Adj Rsquare					0.412145
Root Mean Square Error					0.654125
Mean of Response					1.270885
Observations (or Sum Wgts)					226
Analysis of Variance					
Source	DF	Sum of Squares	Mean Square	F Ratio	Prob >F
Construct	11	72.20360	6.56396	15.3407	<.0001*
Error	214	91.56622	0.42788		
C. Total	225	163.76982			
Means for Oneway Anova					
Level	Number	Mean	Std Error	Lower 95%	Upper 95%
PHP Control	20	1.96000	0.14627	1.672	2.2483
PHP19288	22	1.59545	0.13946	1.321	1.8703
PHP41136	16	0.52813	0.16353	0.206	0.8505
PHP41567	17	0.82941	0.15865	0.517	1.1421
PHP41992	23	0.91304	0.13639	0.644	1.1819
PHP42000	21	0.78810	0.14274	0.507	1.0695

Std Error uses a pooled estimate of error variance

Example 9

Insect Bioassays

[0161] 2.5 ul of an in-vitro transcription reaction which synthesized one of the sequences set forth in SEQ ID NO: 13, 40, 72 and 73 was added to a given well of a 96 well microtiter plate. 25 ul of molten lowmelt western corn rootworm diet were added to the sample and shaken on an orbital shaker to mix the sample and diet. Once the diet solidified, neonate rootworms were added to the well. An average of 5 neonates was added to each well. After the plate was infested, the plate was sealed with mylar and a single hole was punched in the mylar over each well to allow air exchange. 4 replicate wells were produced for each sample. The assay was scored for activity 7 days post infestation. Dose response assays were performed with the following rates: 50, 25, 12.5, 6.5, 3.2, and 1.5 ppm. Table 8 provides insecticidal bioassay data employing the southern corn rootworm. The possible scores are dead (D), severely stunted (SS; little or no growth but alive), stunted (S; growth to second instar but not equivalent to controls), contaminated (c), or no activity.

TABLE 8

Comparison of T0 activity and dsRNA assay results														
	Gene id												T ₀ Gene	
	WCRW													
	SCRW						equivalent to 5 ng/cm2							
	50 ppm	25 ppm	12.5 ppm	6.5 ppm	3.2 ppm	1.5 ppm	50 ppm	25 ppm	12.5 ppm	6.5 ppm	3.2 ppm	1.5 ppm		PHP#
														testing results
Proteasome subunit alpha type 3	SS	SS	SS				SS	SS	SS	SS	SS	SS	41136	good
Low homology to sea urchin reverse transcriptase	N	N	N	N	N	N	SS	SS	SS	SS	SS	SS	41129	poor
Mosquito conserved hypo. Prot.	SS	SS	SS	SS	SS	SS	SS	SS	SS	SS	SS	SS	41124	poor
Syntaxin	ss	ss	ss	N	N	N	N	N	N	N	N	N	41558	poor
Ribosomal protein L27E	SS	SS	SS	SS	SS	SS	S	S	N	N	N	N	41567	good
No hits	SS	SS	S	N	N	N	S	N	N	N	N	N	41549	poor
Proteasome beta subunit	SS	SS	SS	SS	SS	SS	S	S	S	S	N	N	41999	poor
Cadherin like	S	S	S	S	S	S	SS	SS	SS	SS	S	S	41992	good
Ribosome biogenesis regulatory homolog	S	S	N	N	N	N	SS	SS	SS	SS	S	S	42000	good

Example 10

Expression of Silencing Elements in Maize

[0162] The silencing elements set forth in the various SEQ ID NOs denoted in Table 9 were expressed in a maize plant (via the FASTcorn highthroughput screening methods) as hairpins and the various plants were tested for insecticidal

activity against corn root worms. The sequences set forth in the SEQ ID NOs denoted in Table 9 were engineered to be expressed as a hairpin. The constructs comprised the following components: the maize ubiquitin promoter/5'UTR/1st intron operably linked SEQ ID NO set forth in Table 9::ADH1 intron::complement of the SEQ ID NO: set forth in Table 9. The various plasmids having these silencing expression constructs were generated as summarized below in Table 9.

TABLE 9

Row Labels	SEQ ID NO making up one stem of the hairpin	Clone name of silencing element	SEQ ID NO of full length expression vector	Pass	Weak pass	# tested	% rtPCR (+)	% actives of rtPCR+	Diet assay activity
PHP44742	nt 1-380 of SEQ ID NO: 45	idv1c.pk014.b17.f	248	100.0%	0.0%	19	90	100	s
PHP44107	8	idv1c.pk001.e9.f	237	94.7%	0.0%	19	95	100	ss
PHP44118	15	idv1c.pk003.d6.f	246	55.0%	10.0%	20	70	100	s
PHP44747	nt 1-266 of SEQ ID NO: 50	idv1c.pk014.k23.f	251	40.0%	13.3%	15	67	50	ss
PHP44116	18	idv1c.pk003.j4.f	247	31.6%	10.5%	19	25	100	ss
PHP44109	29	idv1c.pk004.f20.f	250	30.0%	10.0%	20	58	63	SS
PHP44750	nt 1-675 of SEQ ID NO: 37	idv1c.pk013.b11.f	249	30.0%	0.0%	10	50	33	s
PHP44119	9	idv1c.pk001.m5.f		26.3%	0.0%	19	No data	No data	ss
PHP44117	14	idv1c.pk002.n13.f		26.3%	5.3%	19	0	0	s
PHP44744	nt 1-132 of SEQ ID NO: 40	idv1c.pk013.h1.f	243	21.1%	5.3%	19	68	38	s
PHP44748	nt 16-585 of SEQ ID NO: 47	idv1c.pk014.d11.f	252	17.6%	5.9%	17	83	25	s
PHP44211	54	idv1c.pk014.n23.f		15.0%	0.0%	20	No data	No data	s
PHP44208	32	idv1c.pk004.n6.f		12.5%	25.0%	8	No data	No data	s
PHP45641	92	idv1c.pk019.l7.f		12.5%	0.0%	8	50	12	s
PHP44115	12	idv1c.pk002.f20.f		10.0%	10.0%	20	No data	No data	ss
PHP44122	27	idv1c.pk004.b12.f		10.0%	0.0%	20	No data	No data	ss
PHP44120	25	idv1c.pk003.o22.f		10.0%	15.0%	20	No data	No data	s
PHP44121	21	idv1c.pk003.l1.f		10.0%	5.0%	20	No data	No data	s
PHP44746	46	idv1c.pk014.c14.f		9.1%	18.2%	11	40	25	s
PHP44976	66	idv1c.pk016.h19.f		7.7%	0.0%	13	92	8	ss
PHP44213	23	idv1c.pk003.m10.f		5.6%	0.0%	18	No data	No data	s
PHP44113	26	idv1c.pk003.p13.f		5.3%	5.3%	19	No data	No data	ss

TABLE 9-continued

Row Labels	SEQ ID NO making up one stem of the hairpin	Clone name of silencing element	SEQ ID NO of full length expression vector	Pass	Weak pass	# tested	% rtPCR (+)	% actives of rtPCR+	Diet assay activity
PHP44114	24	idv1c.pk003.o13.f		5.3%	5.3%	19	No data	No data	s
PHP44745	33	idv1c.pk004.o4.f		5.3%	0.0%	19	76	0	s
PHP44210	11	idv1c.pk002.c5.f		5.0%	0.0%	20	No data	No data	ss
PHP44106	10	idv1c.pk001.n1.f		5.0%	15.0%	20	No data	No data	s
PHP44112	28	idv1c.pk004.d17.f		0.0%	0.0%	17	No data	No data	ss
PHP44216	20	idv1c.pk003.j20.f		0.0%	0.0%	12	No data	No data	ss
PHP44220	13	idv1c.pk002.j17.f		0.0%	0.0%	20	No data	No data	ss
PHP44209	56	idv1c.pk015.a16.f		0.0%	0.0%	14	No data	No data	s*
PHP44212	38	idv1c.pk013.c21.f		0.0%	0.0%	20	No data	No data	s*
PHP44215	39	idv1c.pk013.d22.f		0.0%	0.0%	18	No data	No data	s*
PHP44217	53	idv1c.pk014.n16.f		0.0%	0.0%	13	No data	No data	s*
PHP44221	48	idv1c.pk014.f3.f		0.0%	0.0%	10	No data	No data	s*
PHP44743	48	idv1c.pk013.k1.f		0.0%	0.0%	20	37	0	s*
PHP44756	49	idv1c.pk014.j2.f		0.0%	0.0%	20	0	0	s*
PHP44757	61	idv1c.pk015.p2.f		0.0%	0.0%	20	80	0	s*
PHP44975	65	idv1c.pk016.h15.f		0.0%	0.0%	5	31	0	s*
PHP44977	68	idv1c.pk016.j15.f		0.0%	0.0%	6	30	0	s*
PHP44982	75	idv1c.pk017.h14.f		0.0%	0.0%	11	55	0	s*
PHP44989	84	idv1c.pk018.f19.f		0.0%	0.0%	9	45	0	s*
PHP44991	87	idv1c.pk018.h21.f		0.0%	0.0%	12	60	0	s*
PHP44992	91	idv1c.pk019.k3.f		0.0%	0.0%	5	25	0	s*
PHP45629	99	idv1c.pk020.l3.f		0.0%	0.0%	13	80	0	s*
PHP45635	104	idv1c.pk021.h12.f		0.0%	0.0%	6	30	0	s*
PHP45636	98	idv1c.pk020.k19.f		0.0%	0.0%	14	70	0	s*
PHP45638	97	idv1c.pk020.i24.f		0.0%	0.0%	7	35	0	s*
PHP45640	95	idv1c.pk020.g17.f		0.0%	0.0%	15	75	0	s*
PHP44111	17	idv1c.pk003.f9.f		0.0%	0.0%	19	No data	No data	s
PHP44204	16	idv1c.pk003.f8.f		0.0%	0.0%	20	No data	No data	s
PHP44205	34	idv1c.pk004.o9.f		0.0%	0.0%	13	No data	No data	s
PHP44206	43	idv1c.pk014.a19.f		0.0%	0.0%	17	No data	No data	s
PHP44207	22	idv1c.pk003.m1.f		0.0%	0.0%	20	No data	No data	s
PHP44214	41	idv1c.pk013.h14.f		0.0%	0.0%	18	No data	No data	s
PHP44218	19	idv1c.pk003.j6.f		0.0%	0.0%	20	No data	No data	s
PHP44219	52	idv1c.pk014.m13.f		0.0%	0.0%	20	No data	No data	s
PHP44222	31	idv1c.pk004.l15.f		0.0%	5.6%	18	No data	No data	s
PHP44223	36	idv1c.pk013.a15.f		0.0%	5.3%	19	No data	No data	s
PHP44739	44	idv1c.pk014.b9.f		0.0%	0.0%	4	0	No data	s
PHP44741	51	idv1c.pk014.m5.f		0.0%	0.0%	3	0	0	s
PHP44749	57	idv1c.pk015.b8.f		0.0%	0.0%	3	0	0	s
PHP44752	60	idv1c.pk015.n19.f		0.0%	0.0%	10	70	0	s
PHP44753	71	idv1c.pk017.c3.f		0.0%	0.0%	19	85	0	s
PHP44973	59	idv1c.pk015.l13.f		no data	no data	0	24	No data	s*
PHP44978	69	idv1c.pk016.k9.f		no data	no data	0	10	No data	s*
PHP45630	102	idv1c.pk021.d22.f		no data	no data	0	5	No data	s*
PHP45631	105	idv1c.pk021.m20.f		no data	no data	0	30	No data	s*
PHP45637	96	idv1c.pk020.i7.f		no data	no data	0	15	No data	s*
PHP45639	94	idv1c.pk020.b11.f		no data	no data	0	15	No data	s*

[0163] Maize plants were transformed with PHP plasmids and plants expressing the silencing elements denoted in Table 9 were transplanted from 272V plates into greenhouse flats containing Fafard Superfine potting mix. Approximately 10 to 14 days after transplant, plants (now at growth stage V2-V3) were transplanted into tree pots containing Fafard Superfine potting mix. At 14 days post greenhouse send date, plants were infested with 100 eggs of western corn root worms (WCRW)/plant. For later sets, a second infestation of 100 eggs WCRW/plant was done 14 days after the first infestation and scoring was at 14 days after the second infestation. 21 days post infestation, plants were scored using CRWNIS. Those plants with a score of ≤ 0.5 are transplanted into large pots containing SB300 for seed. "Pass" as denoted in Table 9 is a Nodal injury score of 0.2 to 0. "Weak pass" as denoted in Table 9 is a score from >0.2 to 0.75 which was the cut off for advancing an event. "% rtPCR" as denoted in Table 9 is the percent of the 20 events with demonstrated expression of the hairpin as determined by rtPCR. "% actives of rtPCR" as denoted in Table 9 is the percent of rtPCR positives that also passed the CRWNIS test. So this last number could be 100%

even if only 10 of 20 events were rtPCR positive if all 10 also passed the CRWNIS test. The "diet assay activity" summarizes the data previously presented herein denoting either stunted (s) or severely stunted (ss) activity when the hairpins mixed with the CRW diet and fed directly to the bugs.

[0164] The article "a" and "an" are used herein to refer to one or more than one (i.e., to at least one) of the grammatical object of the article. By way of example, "an element" means one or more element.

[0165] All publications and patent applications mentioned in the specification are indicative of the level of those skilled in the art to which this invention pertains. All publications and patent applications are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

[0166] Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be obvious that certain changes and modifications may be practiced within the scope of the appended claims.

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 252

<210> SEQ ID NO 1

<211> LENGTH: 1442

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199,
200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212,
213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224,
225, 226, 227, 228

<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 1

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caggacagcg tgtacttgat gctcttttcc catgtgtaca ggggtgtact actgccattc    120
ccggagcttt cggttggtga aaaactgtaa tttcacaatc tctttccaaa tattccaact    180
ctgatgtcnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnct gaagtattga    240
gagatttccc tgaattgact gttgaaattg acgggcacac tgaatctatt atgaaacgta    300
ccgcattggt cgccaacaca tctaactatc ctgtagctgc tcgtgaagct tctatctata    360
ctggtattac tctttctgaa tacttccgtg atatgggtta caacgtatct atgatggctg    420
actcgacatc acgttggggc gaagctttga gagaaatttc aggtcgtttg gctgaaatgc    480
ctgccgattc cggttatccg gcttacttag gtgcccgttt ggcttccttc tacgaacgtg    540
ctggtcgcgt taaatgttta ggtaatccag acagagaagg atccgtttca attgtaggag    600
ccgtatcacc tcctggtggt gatttctcag atcctgttac cactgctact cttggtattg    660
tacagggtgt ctgggggttg gacaagaaac ttgcccacg taagcacttc ccttcagtag    720
actggcttgg atcatattcc aaatatatta gagcattgga cgacttttat gacaaaaact    780
tccaagagtt tattctctct agaaccaaa ttaaggaaat tcttcaggaa gaagatgac    840
tagccgaaat tgtgcagctg gtaggttaaag catctctggc agaaacggac aaaatcacct    900
tggaattgc caggcttctt aaagaagatt tcttgcaaca aaactcatac tcttcttatg    960
acagattctg tccattctat aaaactgtcg gtatgttgag aaacatgac ggtttgtacg   1020
acatggcgag acacgtgtga gaatcaaccg cacaatcaga aaataagatc acttgaacg   1080
taataagaga ttcaatgagt ggaattttat atcaacttag cagtatgaaa ttaaggatc   1140
ccgtaaaaga tgggtgaagct aaaatcaagg cagattttga tcaattatat gaagatatc   1200
agcaggcctt cagaaactta gaagattaaa tctttttaag gaaattttcc tattttgttc   1260
atcagtgtaa gtttaaaaa atagcgatat ttatcaaaaa gaataataag gcctctatcc   1320
ctcattctg tgaatattaa tatggcgtga ctaaagatag taactaaaga taggttttct   1380
cttttttgat attatcctgt acaaaaataa ttatgtaaat tgttaaaaaa aaaaaaaaaa   1440
aa                                                                                   1442
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<210> SEQ ID NO 2

<211> LENGTH: 1098

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 2

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gcattggacg acttttatga caaaaacttc caagagttta ttctctcttag aaccaaagtt    120
aaggaaattc ttcaggaaga agatgatcta gccgaaattg tgcagctggg aggtaaagca    180
tctctggcag aaacggacaa aatcaccttg gaaattgccca ggcttcttaa agaagatttc    240
ttgcaacaaa actcatactc ttcttatgac agattctgtc cattctataa aactgtcggg    300
atgttgagaa acatgatcgg tttgtacgac atggcgagac acgctgtaga atcaaccgca    360
caatcagaaa ataagatcac ttggaacgta ataagagatt caatgagtgg aattttatat    420
caacttagca gtatgaaatt taaggatccc gtaaaagatg gtgaagctaa aatcaaggca    480
gattttgatc aatttatatga agatattcag caggccttca gaaacttaga agattaaatc    540
tttttaagga aattttccta ttttgttcat cagtgttaagt ttaaaaatat agcgatatatt    600
atcaaaaaga ataataaggc ctctatccct cacttctgtg aatattaata tggccgtact    660
aatgatagta actaaagata ggttttctct tttttgatat tatcctgtac aaaataaatt    720
atgtaaatgt ttgaatatgt gtatagtttt tttgggtgag ggtacagtgc ttattaaata    780
ctttttaaac atttttcccg ccattccaat tactattaag tttttctggt ttaatacttt    840
tttaaatata cagggtgctta atacgttta tattttcagt attacttggg tttcttcattg    900
taaatgtttt taaatttttc ttttaccctt ttaatcttgt atattacatt acccaattaa    960
agttaattgt acagattaag ataaacgagt atcttataac atctattaga ttgttagaat   1020
caataaatgt agtgtaattg ttctgttttg aacaaataaa tgcatcatta ttgttgttta   1080
aaaaaaaaa aaaaaaaaaa                                     1098

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<210> SEQ ID NO 3

<211> LENGTH: 1766

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 3

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aagggtgctg ttttcaacat cgacaacggt tatttggaag gcctgtgtcg tggctttaa    120
tgtgggatcc tgaacaacat cgattatttg aatttggtcc agtgtgaaac tctgaagat    180
ttaaaactgc acttgcaagg cactgactat ggaacttttt tggccaatga accttcacct    240
ttgtcagtat ccgtcatcga ttcaagactt cgagaaaaac tcgtgattga gttccagcac    300
atgcgtaacc aagcagtaga gcctctctcg acatttatgg acttcattac ctacagttac    360
atgatcgaca acataatttt gcttattaca ggaactcttc accagagacc aatcagtgaa    420
ttaatcccta aatgtcacc ctaggtagc ttcgagcaaa tggagccat ccacgtagct    480
gctactccag ctgagtata caacgtgta ttggtggaca caccacttgc tccattcttc    540
gttgattgca tcagtgaaca agatttggat gaaatgaaca ttgaaattat cagaaacacc    600
ttatacaaa cttacttgga agcattttat accttctgca aggaaattgg aggtactact    660
gccgatagca tgttgtaaatt tttggctttt gaggcagata gacgtgctat tattattact    720
atcaactcgt ttggcactga attaagcaaa gatgaccgtg ctaagttgta ccctcgctgt    780
ggaagactca accccgatgg tttggctgct ctagtggagag ccgaggacta cgaccaagtt    840
aaagcagttg ctgaatacta cgctgaatat tccaaactgt ttgaaggagc tggcaacaac    900

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ccgggagaca aaacattgga agacaaatc tttgaatacg aagtacgtct taacatcaat    960
gctttcatgc aacagtttca ctttggggtg ttctactctt acttgaaatt gaaggaacag    1020
gaatgcagaa atattgtatg gattgctgaa tgtgtagctc aaaaacacag ggctaaaatc    1080
gataactaca tcccaatatt cttaaaggaa ttcttgtttg cactattggt tgcattccat    1140
ttggctcatt tagttcttag tgtcagtaag tggaattatc aaaagtatca gtttttatga    1200
ttcagatgta ctattcagac cttcagacaa atccagttag tacaatgttt tcgtttcaca    1260
ttttattatc actacatctt tcagtcgtcc aagattgtta tgaaattaaa tatacattaa    1320
atgtgttgat gttttaacaa tacatagcaa atcctcaaaa agaacaataa aaagactcgc    1380
agtttathtt gaaggaaaat ccattgagta ttaatgtatc ctaaaatag taatcataaa    1440
attacatggt catatcagtt ttatcgctt tcagaaatth gctgttacct atccttattg    1500
tttattatat tttttaatga tcggtatggt ttgatatta ttttagtttt ctggaaataa    1560
tattgcacaa attcttagtt atctgattca acatgtatca atgctttggt gagtcatatc    1620
ataaatatta ttatgttttc tgtgtataaa gcgtagctag gccaaaatgt tatttctggt    1680
gtatatgtaa gaataaataa aattatatgt atctgaaaaa aaaaaaaaaa aaaaaaaaaa    1740
aaaaaaaaa aaaaaaaaaa aaaaaa                                     1766

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<210> SEQ ID NO 4
<211> LENGTH: 1016
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 4

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gtgacatttg cttcagaact ttgaaactca caacacccac atatggagac ttaaacatt    60
tggtatccct cacaatgtcc ggtgtaacca cctgtcttag gttccagggt cagttgaatg    120
ctgatcttag aaaattggct gtcaacatgg ttcccttccc cgtctccac ttcttcatgc    180
ccggattcgc tccactcacc tcaagaggca gccacaata cagagcgttg acagttccag    240
agctcacaca gaaaatgttt gatgccaaga acatgatggc ggcttgtgat ccagacacg    300
gaaggtaacct tacagtagct gcagtatcca gaggtaggat gtcaatgaaa gaagttgacg    360
aacagatgct caacatccag aacaagaaca gcagctactt cgtcgaatgg atcccaaca    420
acgttaaaac agccgtttgt gatatccac caagaggtct caagatgtct gccactttca    480
tcggcaactc aaccgccatc caagaattgt tcaaacgtat ctccgaacag ttacagcta    540
tgttcaggag gaaagctttc ttgcattggt acaccggaga aggtatggat gaaatggaat    600
tcacggaagc agaatccaac atgaacgact tggatcaga ataccaacag taccaagaag    660
ccacagctga cgaagatgcc gaattcgacg aagaccagga agccgaagtc gacgagaact    720
aaatttcata cgtaattttt ggatctgaaa tcaaagcttt ataactttta tatttgtctc    780
ctctcctttt attttttatt taagcatggt tttgtacag tctctacatt cccgtttgta    840
aatttcgaat acactactta aattattcca agactgactt tttgttgctt gtgtttctgg    900
aatttcagga agtgtttaga tatttaacat gttttgcgaa ctgttttttt atgaataggc    960
attaaaactg ctgccattac ttataaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa    1016

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<210> SEQ ID NO 5
<211> LENGTH: 1016

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<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 5

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ctgatcttag aaaattggct gtcaacatgg ttccttccc cgtctccac ttcttcatgc    180
ccggattcgc tccactcacc tcaagaggca gccaacaata cagagcgttg acagttccag    240
agctcacaca gcaaatgttt gatgccaaga acatgatggc ggcttgtgat cccagacacg    300
gaaggtacct tacagtagct gcagtattca gaggtaggat gtcaatgaaa gaagttgacg    360
aacagatgct caacatccag aacaagaaca gcagctactt cgtcgaatgg atccccaaca    420
acgttaaaac agccgtttgt gatatccac caagaggtct caagatgtct gccactttca    480
tcggcaactc aaccgccatc caagaattgt tcaaacgtat ctccgaacag ttacagcta    540
tgttcaggag gaaagctttc ttgcatgggt acaccggaga aggtatggat gaaatggaat    600
tcacggaagc agaatccaac atgaacgact tggtatcaga ataccaacag taccaagaag    660
ccacagctga cgaagatgcc gaattcgacg aagaccagga agccgaagtc gacgagaact    720
aaatttcata cgtaattttt ggatctgaaa tcaaacgttt ataactttta tatttgtctc    780
ctctcctttt attttttatt taagcatggt tttgtacag tctctacatt cccgtttgta    840
aatttcgaat aactacttta aattattcca agactgactt tttgttgcct gtgtttctgg    900
aatttcagga agtgtttaga tatttaacat gttttgcgaa ctgttttttt atgaataggc    960
attaaaactg ctgccattac ttataaaaaa aaaaaaaaaa aaaaaaaa aaaaaa    1016

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<210> SEQ ID NO 6

<211> LENGTH: 1374

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 6

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ggacaacttc gtgtttggac agtctggagc tggaaacaac tgggccaagg gacattacac    60
agaaggtgct gaattagttg attcagtatt agatgttgta aggaaagaag ctgaatcatg    120
tgattgttta caaggattcc aactcacaca ctacttggga ggtggtagtg gatcaggtat    180
gggtaccctc ctatctcaa aaatccgtga agaataccca gacagaatta tgaacacata    240
ctcagtagtc ccctcaccca aagtatcaga taccgtagta gaaccatata acgccacact    300
ttcagtagat caattgtagt aaaacacaga tgaacatac tgtattgata atgaagctct    360
ctatgacatt tgettcagaa ctttgaaact cacaacaccc acatatggag acttaaacca    420
tttggtatcc ctcaaatgt cgggtgtaac cacctgtctt aggttcccag gtcagttgaa    480
tgctgatctt agaaaattgg ctgtcaacat ggttcccttc cccgctctcc acttcttcat    540
gcccggattc gctccactca cctcaagagg cagccaacaa tacagagcgt tgacagttcc    600
agagctcaca cagcaaatgt ttgatgcaa gaacatgatg gcggcttggt atcccagaca    660
cggaaggtag cttacagtag ctgcagtatt cagaggtagg atgtcaatga aagaagttga    720
cgaacagatg ctcaacatcc agaacaagaa cagcagctac ttcgtcgaat ggatcccaaa    780
caacgttaaa acagccgttt gtgatatccc accaagaggt ctcaagatgt ctgccacttt    840
catcggaac tcaaccgcca tccaagaatt gttcaaacgt atctctgaac agttttacagc    900

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tattgttcagg aggaaagctt tcttgcatg gtacaccgga gaaggatg atgaaatgga 960
attcacggaa gcagaatcca acatgaacga cttggatca gaataccaac agtaccaaga 1020
agccacagct gacgaagatg ccgaattcga cgaagaccag gaagccgaag tcgacgagaa 1080
ctaaatttca tacgttaatt ttggatctga aatcaaagct ttataacttt tatatttgc 1140
tcctctcctt ttatttttta tttaagcatg tttttgtac agtctctaca tccccgttg 1200
taaatttca atacactact taaattatc caagactgac ttttgttgc ttgtgttct 1260
ggaatttcag gaagtgttta gatatttaac atgttttgcg aactgtttt ttatgaatag 1320
gcattaaaa tgctgccatt acttataaaa aaaaaaaaa aaaaaaaaa aaaa 1374

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<210> SEQ ID NO 7
<211> LENGTH: 1128
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

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<400> SEQUENCE: 7

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ctattactac ctgttgtatt aagttacaaa gctaacttaa atcctcttc aaatgagttt 120
ataaactata tcaatagcaa gcaaacaca tgggttgctg gaaagaactt tgatgagaaa 180
ctttcaatcc aagaaataaa aaatttatta ggagcgagaa aaaggagttt aggagatgta 240
aaaggattta tgcacagtga agatattcaa gttccagatt ctttcgatgc aagggaaaac 300
tggaagact gttcagatgt tatcagcact attgtagacc aatctgcttg tggatcttgc 360
tgggcaatgt ctgcagcatc tgcaatgagt gacagacgat gcatagtcac ccagggaaaag 420
cttaaagtgc ctgtttctgc tgaaaattta ttgtcttgtt gcgatgactg tggatttga 480
tgcgccggag gatatataga tgatgcattg tcgttttggc aagagaatgg aattactaca 540
ggaggtcttt acggcagcaa ccagggttgt caatcatatt cgcttcaacc ttgtgaacat 600
catacaaatg gtactaaagt gcaatgcagt actttgaact acggcacacc ttcttcaga 660
agcgatcaat gtgacgatac cgcactaaat tataagtcag agttaactta tgcctcaggt 720
ccagtgaatt actatactac agttccaat atgcaaaaagg aaatattgac aaatgggccg 780
atacaaaact gttttgatgt gtacagcgat ttcttcagtt acaaaagtgg tgtttatcaa 840
catgtcgctg gagattatgt aggaggacat gccgtcagag ttttaggttg gggagtagag 900
aatggagtcg cttattggtt ggctgctaata tcatggaatg aagattgggg agacaaggga 960
ttgtttaaaa taattcgcgg aacaaatgaa tgcagtttcg agaatggtat ggttgcgtca 1020
actccaagag tctaattcta aacaaaatat tggaaatagg cttaattctg gtttatttta 1080
aataaaacac ttgatcccaa aaaaaaaaa aaaaaaaaa aaaaaaaa 1128

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<210> SEQ ID NO 8
<211> LENGTH: 600
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

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<400> SEQUENCE: 8

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gaatagagta tgtatttacg aatacctctt caaagaggga gtcattgtag ctaaaaaaga 120
ttaccatgcc ccaaaacacc tcgaactaga aactatccct aaccttcaag taattaaggc 180

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tttacaatca cttaaatcaa aagggttacgt aaaggaacaa ttcgcctgga ggcattatta	240
ttgggtatttg actaactctg gcatcgaata cctccgcaca ttcttacct tacctggaga	300
aattgtccca tctaccttga aacgcccagc aaggacagaa accacccgtc ctagaccagc	360
tgctctcaga tctgagacat ctaaaccttc agaagaccgt gcaggatata gaaggactcc	420
tggaggccct ggagctgaca agaaagctga tgttggtcca ggaactggag atgttgagtt	480
caggcaagga ttcggacgtg gacgggcacc acaataaatt tattgataag ttaattttta	540
taaattgatc agccaataaa aagtttggtt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	600

<210> SEQ ID NO 9

<211> LENGTH: 1874

<212> TYPE: DNA

<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 9

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caataaatgc aatgcaagta ataagtcaat tagttattaa aaatacattg atactccaat	120
attagtatat aaaagaaaca aaacatatca aaattattta agtagtggag tccaaataga	180
ctattttctt ttttgggctt tttctgcagc ttttgtagct tttccggcgc tgggatcttt	240
gaaggcaacg ctcttgatga ctccactgc aacggtttgc ctcatgtcac ggacagcaaa	300
acgtccaagg ggtgggaatt cttggaatga ttctacacac atgggcttgg tgggtacca	360
gttgacaatg gcggcatcac cagatttgat ggctttggga tttctctcag tggctctacc	420
agaacgacgg tcaacctttt ctttgccaaa aggatcgata ggccgtgctt tcgcagtccc	480
tatgcatact gaacatcagg atcaagccag cttttgccct tttgctctac gcgaggtttc	540
tgctctcgct gagctggcct taggacacct gcgttattct ttgacagacg tacgccecca	600
gtcaaaactcc ccgcctggca gtgtcctcga atcgaaatcag gctggaggta agttgacgct	660
cgaacgaag cacacggacg ctagccgagt atccgaaagg caagccttat cggaaccacg	720
aaaccgacga acggcacaac gcaacgaaac gtcactccgt gccctcggct caagaatacc	780
gtgacagtcg cagcctcgtg agcgaacgac gcacgcgttt cgccttaccg agtaagtaaa	840
gaaacgatga aagtagtggt atttcaccgg cgatgttgcc atctcccact tatgctacac	900
ctctcatgtc tccttacaat gccagactag agtcaagctc aacagggctc tctttccccg	960
ctaatttttc caagcccgtt cccttggcag tggtttcgct agatagtggg tagggacagt	1020
gggaatctcg ttaatccatt catgcgcgtc actaattaga tgacgaggca tttggctacc	1080
ttaagagagt catagtact cccgcggtt acccgcgctt gcttgaattt ctctactttg	1140
acattcagag cactgggcag aaatcacatt gtgtcaacac ccgctggggc catcgcaatg	1200
ctttgtttta attagacagt cggattcccc tagtcctgct cagttctgag ctgaccgttg	1260
aatggcggcc gaagaggaca tccaagcacc cgaaagtaac tcagagcctc gcagcaagac	1320
ggttcgcggg gaggccaagg cacgggacgg aactcggatc catgaaaccc aactcgtaag	1380
aattaggctc acttcacctc acccaggccc ggcacgtcag ccatgaccca ctctctcgcc	1440
aagcccgaca cgccccgac ctcagagcca atccttatcc cgaagttacg gatccaattt	1500
gccgacttcc cttacctaca ttattctatc gactagaggc tcttcacott ggagacctgc	1560
tgcggatatg ggtacgaacc ggtgcgagcc tccacgtggc cctctcctgg attttcaagg	1620

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ttcgaggaga agatccggac accgctgcaa ctgcggtgct cttcgcggtc caaaccatat 1680
ctccctgcta gaggattcca tggaactcga acgcttatac agaaaagaaa actcttcccg 1740
gatctctcga cgacgtctcc aggtcctttt ggggtacccc gacgaactct cttgcgaggg 1800
cccgactttt tgacgggtcc gctaccgggt tccggaatag gaaccggatt ccctttcgcc 1860
caatgggtgt gccc 1874

```

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<210> SEQ ID NO 10
<211> LENGTH: 816
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

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<400> SEQUENCE: 10

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```

tttttttttt tttttttttt tttttttttt cagagagatt cccatcaacg taaataatca 60
gggtatttat tcacatgtcc ctacgttctt atcatcatgt aaaaggagtt ttgactatac 120
atattttgaa aacatttaaa tggggccctc agaacaacag tggactaagt cacaaattca 180
gcatttttag attaatatat caataaaagc agcaaaatta aatcttccga ttaacaggga 240
cctacacaac ctacctctat atttggctag atgatgctac ataatttgta gctttatctc 300
ataaacataa tgaaaatatg aatgcaaaga ttgcatttat ctcaaaactt agtttttgag 360
cttatgccac tgttgctgat agcctcaaat attaacatgt tgacagacat aacatctata 420
gatgtcta at ttccattgaa acgtctagat gacattttta aaataacgaa ttgtgcatat 480
tcaaaactaca tctatagatg catatgaaat atgacatgaa catacattgt cgtcatcaat 540
atgtttacaa aactcattgt ttccatattg acagtcta at tctatacccc gtatctgcaa 600
aaaaacttaa tttccaattt tcgtggcaaa cgactaacia aacagttatc catctataca 660
caaaactctg atctaaciaa aaaattctag gaacctctaa taccagtc at ctaataacct 720
gtaactgaat atcttttagac ttgataagaa aaaaaaaca gaaaaaacct acttgacaaa 780
tctcttggca gatacgggct attagaatta gacccc 816

```

```

<210> SEQ ID NO 11
<211> LENGTH: 579
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

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<400> SEQUENCE: 11

```

```

ggggctttta catcaaaaat ttcttttagct gttgtcggtt aaggacagc ttacaaaatg 60
aaattcaaca aattagtaac cgcttcaaga agcaaaaata ggaaaaggca tttcacagcc 120
ccatcccaca tcagaagaac cttatgtcc gcacccttgt ctaaagaact tagacaaaag 180
tacaatgtta gcactatgcc aatccgcaag gacgatgaag tacaagttgt aagggggcac 240
tacaaggct agcaagtagg taaagttgta caagtataca ggaagaaatt cgttatctac 300
attgaaagga tccagagaga aaaagccaat ggagctagtg tatatgtagg aatccaccct 360
tcaaaagttg ttattgttaa acttaaaatg gacaaggaca ggaagaagat cattgacaga 420
agagccaaag gacgtttggc tgctttgggc aaagacaaag gaaaatacac tgaagaatca 480
gctgcctcag ctgtagaaac atcttaagtg taataagtaa tttttaataa taaaaataa 540
taaaagttcca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 579

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<210> SEQ ID NO 12
<211> LENGTH: 585
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 12
gggggctggc agtttgctgt cttaatgttg acatttttat atattggaaa aaatgtcgaa    60
agttgaattt aaacaagata tgccccaca agggggctac aatccaatta actataaaag    120
agttccagcc aaaactttat ttggaggatg ggccttaatc gggggctacc ttggcatgac    180
tgcaggagcg gcgtatttat attattttaa cgtaaggca gtaaaaactc gagaacttga    240
attaaagggc gccagcttag cgctgtatcc aatacttatg gctgaaagag accgtgaata    300
tatgaagcaa ttaaggagaa atagagatga agaacgtgaa ttaatgaaaa atgttgaagg    360
atggcagacg ggtacatggt atggtgaacc catctacaag actaaagaca aagatactct    420
tattcatccc ctattccatg aatattacat tcacagttct tacaaggact acactgttcg    480
tgcaaacgtt ggtttgatgt cttaaatttt tattctattg taatttagta gcgaaattta    540
aatattaat tgtaaatatg aaaaaaaaaa aaaaaaaaaa aaaaaa    585

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<210> SEQ ID NO 13
<211> LENGTH: 1043
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 13
ggggagtcgt caacatcaat ttcaagtffc aagaaaaagc aaatcactac gacttgccgg    60
atthttgtagt agtggttaatt ttgtattaaa aaatcaaaat gagttctatt ggaactgggt    120
acgattttatc agcttcccaa ttctctctctg atggaagagt atttcaagtt gaatatgcaa    180
tgaaagcagt tgaaaatagt ggcacogtaa taggcctccg aggtacagat ggcatgtgat    240
tggtgctga aaagtcatt atgtcaaaat tgcataacc aagtacaaat aaacgaattt    300
tcaacattga taaacacata ggaatggcat tttcaggctt aatagctgat gcaaggcaaa    360
tcgttgagat tgctagaaaa gaagcatcaa attatagaca tcaatatggt tcaaatattc    420
ctcttaataa cctaaatgat agagtaagca tgtacatgca tgcatacact ttatacagt    480
ctgttagacc atttggttgc agtgtcatct tggccagtta tgaagatagt gacccatcta    540
tgtatctgat tgatccatct ggagttagct atggatactt tggatgtgct acaggtaaa    600
caaaacagtc tgcaaagact gaaatagaaa aattgaagat ggggaatcta acatgcaaag    660
aacttggtta agaagcagcc aaaatcattt atttggtcca tgatgagctg aaggataaga    720
atthtgaaat ggaactttca tgggtatgca aagatacgaa tggtttacat accaaagtgc    780
ctgaatcagt gtttgctgat gcagaaaaag ctgccaaaaca agcaatggaa gcagattcag    840
aatcagatac agaagatatg taataactac atttagtttt taatatttcg ctgatggtgg    900
ctgttcttac aatatttcgt gtgttatgtt catatattat gtaatactgt gagaatttcc    960
atthcaagga taggtttata actttttttt ctaataaata cataacttta tgtcaaaaaa    1020
aaaaaaaaa aaaaaaaaaa aaa    1043

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<210> SEQ ID NO 14
<211> LENGTH: 601
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

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<400> SEQUENCE: 14

```

gggataatca ttagtttttt tattgaaagc tggaaatgaag ggttgatga aaaaaaaaaac    60
tgtctttatt taatttataa agaattttat ttttaagtta aaaagcttaa attttttttaa    120
aagacgagaa gaccctatag agttttataa aattattaat aagttttttt agtattaaat    180
ttatttatat aataaattta ttttaattggg gtgattaaaa aataaattta acttttttta    240
tattattata ttaattaata attttttgat ccaatttttt tgattataag aataaattac    300
cttagggata acagcgtaat tttattggag agttcaaatc ggtaataaag attgcgacct    360
cgatgttgga ttaaagttha taattggtgt agcagctata ttattaagtc tgttcgactt    420
ttaaaatttt acatgatctg agtttaaaccc ggtgtgagcc aggttggttt ctatctttaa    480
tttattaata ttttttagta cgaaaggacc aaatatataa aataattttt atatttagat    540
aatatttaa aaaaaaaaaa aaaaaaaaaa caaaaaaaaa aaaaaaaaaa aaaaaaaaaa    600
a                                                                    601

```

<210> SEQ ID NO 15

<211> LENGTH: 913

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 15

```

gggggcagtt atttcgactt ttcagtcttg tcataaaata aaattaaaat atatccggcg    60
aggtgttgac tagcggattt ttttagatc aacaatctta ttttataaaa taattagtta    120
aaatgatgca aacagctaatt aatgcatatt atcccgatta ttccactgct ccaatgcaac    180
gtcaaatata cccctatgca gataatggag ggagtgtagt agcaatagca ggtgaagact    240
ttgtaataat tgggtgcagat acacgtttga gtactggatt ttccatttat accagagaac    300
aaaaaaaact tttccacta tcaggcacta ctgttttggg ttgtgcagga tgttggtgtg    360
acactctaac attaaccaga atccttaaat ctgcgatgca gatgtaccaa caagagcata    420
aaaaaacaat gtctacaact gcatgtgccc agatgttgtc aaccatgctc tactacaaga    480
gattctttcc ttattatata tcaaaccatt tagtaggttt agataatgaa ggaagggtct    540
gtgtttacag ctatgatcct attggacatt gtgaaaaagc tacgtataga gcagggtggt    600
cagctggagc tcttcttcag cctctgttgg acaatcaaat tggacagaag aacatgctta    660
aaacatctgg ggaacctctt agtcaggaga aagctctgtc tacccttaa gatgtattta    720
ttctgctgc tgaaagagac atctacactg gagatagcgt acttataaat attattacta    780
aagatggagt aaaggaagag tccttcagtg tgagacggga ttagaagcaa gtggttttgt    840
ttatattttc ttatgtgtaa ttcaaatata ctttctaat aaacaaaaaa aaaaaaaaaa    900
aaaaaaaaaa aaa                                                                    913

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<210> SEQ ID NO 16

<211> LENGTH: 681

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 16

```

ggggatttcg ttggtttaac gattgatagt aactataaat tcaaattaca gatcagatgt    60
atatatatat ataaacacgc aaaaatgctt ggctataaaa tgaaaaatgt aactgcaata    120

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ttagatgacg ttatatataa aaataataa aatctgctgt tgatattgta gttcattagt 180
tttgaataat aagcagtact aactttaatc ttgtgcaaaa ttagttttat tgtaaatatt 240
aatattttca cccaaataag agaaatggat gacgtgcaac tgggtcctgt gagtattagc 300
atgatagaag ataatttata tttaggagga ttggcagctg cgaataattt ggaagtttta 360
aagaagtaca acattactca tattcttacc atagatatat gtccattacc aagaactgta 420
acagaacaaa gaaatttagt taccagattt atacagttgt cagaccaacc aagagaagat 480
ttgctttcat attttgatga aacagattta tttattaatg aaggaaggga gaagggaatt 540
gttttggttc attgttattt tgggtgtttc agaagtgccg ctgttggtat tgcccatata 600
atgaaaaaat accagatgag ttactttgag gcatttgata tggtaaaagc tgaaaaaaa 660
aaaaaaaaa aaagaaaaa a 681

```

<210> SEQ ID NO 17

<211> LENGTH: 1109

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 17

```

gggggagtag ttgtttttat tgtgagatga tttcgaagtt caccctggtt ttcttggttt 60
gcattgtcgc accagcgata ggtgatccac cagttccaga atggagtgcg acttatagcg 120
tagaagggaac tatccatttg ccttatgcag aaatagtaga gcctttccat gcttggtatg 180
atggaaaatc taaaaattcg cgcattgatt actacaatgg gacggctaag acataccaac 240
ttggaggaaa tggaaatggt gtccaactga aagtagttcc attcactaca gaggagggtc 300
taaaccaaat aacgtgcttc cagatcaatg gaactgaaga cgatccagtg actcctcaat 360
cgattttgcc agatttagaa ggatttgaat atcaaggcat acaggagtat ggagatagag 420
aactagaggt atggtttcta aaaactgtcc agttagaaaa agaaaacgaa tacactctat 480
gggttggtcg agatgagcat ggtaaagcta ttccagttaa atatgatatg agaggataca 540
attcgttatt gggaagccac tacgatcatt actatttgct atcacatcg aagtcttaca 600
ggactcacia gattgatccc tccgtttttg aagtagaac taatagtga tgcagaagtt 660
ttcttggttc cggaaatcaa catgttcaca tcatgaaccc catggccgaa tacattcgtc 720
ccgaaaaaag tgagcacgtg gactcaagct ttggcgattt tataaataac cacaacaaaa 780
attacgcaga caaaaagaa cacgttttta gaaaagaggt tttccgtcaa aacgtcaggt 840
tcatcgaatc tgtcaaccga caaaataaag gtaagtgtta tagtagggga gcaaagtagg 900
tgtgctaaat ttgcagtcac tcgagagtta tggcgacctt ttgggttggt attattaggt 960
cctaaaaacca aaaaaagtta agtaaaattt tccatttcca acaatcgttt tttccgatta 1020
tagcgtcatc tatccataat tcgaaaaaat gtctctaata aaagttgctt atttttacga 1080
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1109

```

<210> SEQ ID NO 18

<211> LENGTH: 400

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 18

```

gggggatttt ctctagtttg caggaagcag gaatttcagt aaagaaataa gattaaatg 60

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```
gcagacaaag tagaaaaggt tgccagacca atgaaattcc cttacacatt cagtgcacaaa 120
attgcacaat tcccaatcaa gcactacttg aagaaccaat ggatctggaa atactatgct 180
atttctcttg tagtatgtct tccagtcttc aactcgatta gtaaaactggc caactctcct 240
ggaaacggtg ctaaatgggc agagattcgc agaagagaag ctgctgaaca tcatcactaa 300
gaaaattttt ttatatagtaa ttagtctgcc aattgttttg ttctaattta atttctatta 360
aatacatgta gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 400
```

```
<210> SEQ ID NO 19
<211> LENGTH: 800
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera
```

```
<400> SEQUENCE: 19
```

```
gggaagcagt ggtatcaacg cagagtggcc attacggccg gggtagttct agcgttctag 60
ttctatagtt gttgtgtagt attttctgtg tagtttgta ttttccctat tgtgcatttg 120
tatattttat ttattttatt atatatctac gatcagtaag aacattttac ataaattcaa 180
taagcatata gattcgtgta aaaaaatgcc aaagctatcc aaaaaaaatc aaaaaaaagt 240
aggcgctcaa caagactcgt taccgagaaa tgacagaact actgactgta cctcaaatc 300
acattcacat tctggaatg gtgaaactac ttatcatagc gcaaatcaa attctgttgc 360
tcttgaaagt agttcatcaa atgcccgaat tcaaattagc accatacctc caataaatga 420
taattcttcg ccaaacagct cctttgatca aactgcacct acaagttcaa gtttacctga 480
gggaagagta cactccgaaa gaattaattt tcgtcctaga agagccagtt tggtaacact 540
gagacgtgaa aaagttacag ctttgaggaa gacacataaa aatatgagaa aaaataaagc 600
tgtaacaagt tttaaatctt ttgctcaagc cgaaattcaa catgtatctc ttcccagcca 660
ggagaatttg aaatctcgag gatcaattgt gaatttggtc actaaaagaa aaaacacaaa 720
tgaagaatgt tcatcccatg gctcccttac agaatcagat atgggtaacc aaaaaaaaaa 780
aaaaaaaaaa aaaaaaaaaa 800
```

```
<210> SEQ ID NO 20
<211> LENGTH: 1105
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera
```

```
<400> SEQUENCE: 20
```

```
gggagccctt atttctccta ttgctatata cgcagctgaa acatggactc tcaaaaaaat 60
caatcgaagt aagatcgaag ccttcgaaat gtaggtctac agaattattg taccctgtgc 120
caggagagaa cacagaacca acctgtcaat tctgaaagag cttcatataa aagacaaggt 180
attaaaaaaa gtataccgac cataacttaa ttactttggt aaagtaacga ttactatacg 240
aagaggcaaa tcgttacttt gattactctg attacttcgt accaatcgta tcagagcgag 300
taacgactat tgtatctact ttgattactt cgtatcagag cgaataacga ctattgtatc 360
tactttgatt actctgatta cttcgtacca atcgtatcag agcgagtaac aactattgta 420
cctactttga ttattctgat tacttcgtac caatcgatc agagcgagta acaactattg 480
tcagggccgc gtttaggtca aatgaogccc taggcaattc tctagtagcc gcccttcaaa 540
catgtaccat ttttgcgaaa aaaaacgcaa gcagaatttt ttatttaaata aagaatgtta 600
```

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ttgcacaaat ctcggtgttc ttcaataat gtttagaaat gtgttaaaaa tattctttat 660
tttacatcag gcgtaagtgt acatattact attataagta tgtttgagcg tttggaactg 720
tgtccaatgc atgcgtttta atgcatgata cgtagaaatt gcctgtttgt agccgcacct 780
acttgttcga ttttaaatga gagatgcatt gaaaacatta ctcaagcact atgtgtttat 840
agctttgttt aacaataaaa aaattaattt ttagcgatgc aaataatcaa aaccggtata 900
atttgacatg cactttcaaa tgcggtgaagc agaattgcta ttttattttt taatcaaaag 960
ttattcggat tcaaaaattg caatttttcg atattttgaa agttcaaccg cgtctatctc 1020
gaaaactatg catcctacga aaaaacttta acaacatttt ttgcttagaa tgacccaaaa 1080
aaaaaaaaa aaaaaaaaaa aaaaaa 1105

```

```

<210> SEQ ID NO 21
<211> LENGTH: 936
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

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<400> SEQUENCE: 21

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```

gggggctcat tgtagtagcg ccaggcgcgg aaacgtgagt gctaaaacac agtgatcgta 60
ctagtccaaa acatctttta tttttttcta cttttatata taattgtata gtttcgttat 120
ttttattact tagaagttaa tttttttcga tcgttttata cgcttctggg aaggattttt 180
atacattaaa caatattact tgcttgggta agttatgttt ttttttgaaa tatagcattg 240
taaccttttt taaatctttt atttttttta ttttttcttt ttctttaaca tactactgat 300
acgctgcaga ggtccatgcg ttttcaattt tttaggatct tttgataact tttttaaaat 360
gtaacacatt tagaaagacc gttgaaaagt tcgccctttt agaccgcgga ggcagtgcag 420
tagctgacag gtccgaagg cggggggccc cgacattagg agggataagt agagatctct 480
ctagtccagag ataagtactt actttcgatc ttttcgtaat tacgtactta ctttcgatct 540
tttcgtaatt acctctgttt tccttcattt gcattgtgat tttgtatata tttcttaata 600
ttttacagaa aacgtaagtg tgtctacaaa atgttttgca ttttgtgta aaattaatca 660
aaatatctta aaaccagtag tcaattaaaa aaatatataa aaatgtgtg caataaacct 720
tgcggtatct actgaagtgt ttcacacctg tttgaagtta aatatcaagg tttatttttt 780
ggccgggaat ttaaagggtg tgggtatatt actttttaca attaataatg ggatcaactg 840
attgggtata taggggtgat aaattatacc ttgtagttca atatcttcgt tgccagaaga 900
gatgcaggaa aaaaaaaaaa aaaaaaaaaa aaaaaa 936

```

```

<210> SEQ ID NO 22
<211> LENGTH: 812
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

```

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<400> SEQUENCE: 22

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```

gggaaagcac taaaaaatgc aggatacaaa tttgacattg catatacatc tgccttaca 60
agagctcaga acacacttaa ttcaataatc aaagaaattg gccagagaa tttggaaact 120
ataaaaactt ggagactcaa tgaaagacat tatggtggcc tactggcctt aaataaagca 180
gaaacagcag caaaatatgg agatgagcag gtagctatct ggccggcgag ttttgacatt 240
ccacctccac caatggaacc tgacctgctt tattatgata ccattgtaaa agatgcccca 300

```

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tatgctgatg gtccctgcacc agatcagttt cctaaatttg aatccttaaa gctaacaatt	360
gagcgtactt tacccttctg gaatgaaact gttgttcac aaattaaggc tggaaaacag	420
atcttaattg cagcacatgg taacagtttg agaggaattg taaagcatct agaccagctt	480
actgatgacc aaattatgca gttgaatttg ccaacaggaa ttccatttgt ctacacatta	540
gatgaaaatt tgaaaccaat aaagagtta gaattcctag gagatccaga aactgtgaaa	600
aaggctatgg aagctgtagc tgccaagga aaagccaat aagcattatt tattatttat	660
tgttttaatt tatatcaaaa tcatttattg ttagatattt gatgtgtaat gaataaatgg	720
ttaggctgaa ttgtaaaact cagcagaaat gttatgtgca agacattaaa gcatattctt	780
ctcaaaaaaa aaaaaaaaaa aaaaaaaaaa aa	812

<210> SEQ ID NO 23

<211> LENGTH: 1127

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 23

gggggaagta ttctgtagaa aactgataag tatattgctt ttctcattta tttatgtggt	60
taaatagtga gttagtgttg gtcaacgtag atgataacaa ctgaacattg aataaactac	120
aagaataatg ttaagcataa aaattctgtt atgtatgttg ctggcacacc aatctgcggt	180
agaagctgta tataatgttg gagttggacg agccgattgc acaggaccat cagcagaaat	240
tacttttatg ggttatgcca aatccggtca gaaaggatgt ggtatccatt taaggcagtt	300
ttcaagagca tttgtgatta aagatgagaa cactctagtt gcatttgtga caattgacac	360
atgtatgatg aaccatcccc taaaacaagc ggtaatagat aaattggatc taaaatatcc	420
caatgtattt actctaaaga atacaattct cagtggaaaca cacagtcaca gcacacctgg	480
aggtttcctc aaggatgtaa tgttggacat accaagctcg ggatattgta aagaaacctt	540
taacgcattg gtagcaggaa ttgtaaaatc catagataaa gcatacaaca atcaagttga	600
agcaagaatc ttttacgca ctactacagt aactaataca aacaggaaca gaagtccagc	660
tgcttacctc tataatccag aatcagaaag aaaaaagtaa gtgtaatact agataataat	720
actttaaact ttattaagta taataaaatt aataacgtac aaaatactca aaattaacat	780
ttatttccaa attaccatat aaatataatt ttaataattc tgggactcaa aacattgtaa	840
ttttattttg cttattaata ataataaatt gtacaaataa attctatttg tcaactctaaa	900
cacaataag atgttgctgt tctttacgac agtctcctgg cgactagtgt cataactttt	960
atactcgcat tttaattggc atcattaata gtggagtcaa tggagttttt acttaggaaa	1020
aaaatcaaac aagagaggac tgtttataac ttcattcaga aatgtatcat aaacaacaca	1080
tcaaaaagtt ctactccaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa	1127

<210> SEQ ID NO 24

<211> LENGTH: 869

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 24

gggccaatag tccatgaaa gcagcotacg attattacaa gaaatgttca aagacaggaa	60
attgcttgcc accagtaagc ctccttcttg gcaacaaaaa ggaaggcgaa gttcaactgc	120

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aaccaatcga tctcaagaaa aatccatttt taaacggagt ttatgaagcc ggaagttctg 180
ctgacttctc caggctcttcg tctgagacga aatccaatgg agcctctctt gatagtgcg 240
cgtccaatgc gagatttgcg ataactggag ccaacgatga ggacaacgag gtatctccca 300
gccagaggat tccatgcaaa ggtgatggaa aagtgtgcgt gcccaaggac gcttgcgtca 360
atggtgtggt caccaaacat agaggaagcg cattgcagat caaacaaaat aattatctaa 420
gtaaacattc agatccacaa agccaggcgt tgtagaaaa tgtgaattca aaatattact 480
actacacgag aacaaaagga ttattcagga tatgttacc aaaagaaagg ccgcctactg 540
taaagacata cttgagtcct ttggaacgc attgtaacaa tgtaaattac tacattcccg 600
atgaaaataa cgataccaag gacttcaactg acgatgcttg gacaagatta catatgggac 660
gatecatgat agctctcttt atcatatcgt tcatagctgt ctttgcgtcc ttctgcaccg 720
gggtcactgg atgttggaag aggtctccag gaaatattac agccactgca atacttatgc 780
tgctagcatg tttgttgagt gctggtgcta tgggtctatg gcacggagtg gaatattaca 840
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa 869

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<210> SEQ ID NO 25
<211> LENGTH: 569
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

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<400> SEQUENCE: 25

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ggggagtctg attccggcag cggacggcga ctctgtgaaa gttgatcgct taaacgtttc 60
tacacgtggt gcacgtgctc cgtaccgaga cgacgacgaa gagaagacgc cggcgtcgcg 120
acgcgagtag acgacaacgt ggttgaacaa gtgtggaagt gccggcatgt tgcactgagt 180
gaagtgcacg agttgtgcgc atgtgaggaa aggatgtcaa gggattaaag ggcggcatca 240
tggtgagctg ttaagggtta gtaaattcca tactgctggc gcttgactga gaataatgag 300
taagtgttta atagtgtatt aatatagttt cttgaacttt tattcaggaa agattcaagt 360
aaatgtgata cagtggcggg tactgtgacg taaagagaag ctttatttaa attttaggaa 420
atattatttt taatattatt tttttgatag tttttttata gattttaatt atattgaaaa 480
agttgacatg ttgtgtaatg tctggctaag tggctcggcc aaggccatca aattcactca 540
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa 569

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<210> SEQ ID NO 26
<211> LENGTH: 576
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

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<400> SEQUENCE: 26

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ggggcttttt cacatgcag gcaccaacga caaagccaaa aagagatcca atccactctg 60
tccaagtttt tggcagaaaag aaatcagcta cagccgtagc ttattgcaaa agaggtagag 120
gagtcttgag ggtaaatggc agacctctca gccaaagtga gcctaaaaatg ctccaagaca 180
aacttcaaga acccattctt cttcttggaaggacaaaatt ctctgctgtt gacatcagag 240
ttagagtaaa tgggtggtgga catgtttccc aaatttatgc tattagacaa gctatctcaa 300
aggctttggt agcttattac caaaaatatg ttgatgaagc atcaaagaag gaattgaagg 360
atatccttat ccaatatgac cgtaccttgt tggtagccga tcccagacgc tgcgaacca 420

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agaatttcgg tgggtccaggt gctcgtgccc gctacccaaa atcttaccgt taagttcttt 480
tttagattta atgttgtgtt tcttgatgtg attaagatat caacaataaa cacaattttt 540
tcccgcaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 576

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<210> SEQ ID NO 27
<211> LENGTH: 1118
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

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<400> SEQUENCE: 27

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```

ggggcaccaa ttaatccttt ttaattagta cgtgtatacc tataagaaaa atcaataaaa 60
tacatattcg atagtctgct gctgaagtga caggcaaaga gaaatgaag gtgattcttt 120
gtttactggg gggtgttacc ttagtactga gcactcccggt gtaccaggaa gacttacaga 180
aatattatcc tcaaggatca attccatgcc cattcttcaa gaaagacgcc agttttaatg 240
catcttccga tgatattaaa gtttatttta gaaacaaaga tcatcctgag agttcagtag 300
caatagacat taacgatagt tcggaagtcg atgcgttggg attttcacca aataaagata 360
caatgtttgt tgtccacggc tggcacacgc gtcacgactc gccagtctgc gatgagatat 420
ccaaagctgt cctccagaac gacgacataa acgttttctt aatcgattgg aacaaaatcg 480
ccagcaacct ctacttagta gcttacaaag cagttccagg ggtcgggtcaa ttactaggaa 540
cactcattag aaatttggtc aacaacaata aattggattt gaataaagct tctatcgttg 600
gccattcttt gggagctcat gtcgctggat tggccggagc tgaactcaac ggacgggtta 660
gtaacattgt aggtctggac cctgctctac catgcttctc atacaacgat atcagtacaa 720
gattggaccc ctccgatgca caatacgtcg aggtataaca cacatgcgca ggtttactcg 780
gttttgatgt agatattgga cactcagatt attaccctaa tggcggaaaa gatcaaccgg 840
gttgcacttt ggatgttgta ggaatgtgca gacacagtag atcatattac tactatgcgg 900
aatctttaat tagtggagga tttgtgcaa aacaatgtaa ttgctacaaa gattttaaca 960
acaatcaatg taatggagga acatccaata tgggagaata taatatcaac aaaagtgcc 1020
aaggcgata ctaccccaac acaaatagtc agtcaccata tgcccaacat tgatataaat 1080
gtataataga aaaaaaaaaa aaaaaaaaaa aaaaaa 1118

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<210> SEQ ID NO 28
<211> LENGTH: 955
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

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<400> SEQUENCE: 28

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ggggattaca aactgaactc aacaacctct tttcatcttc gaccggtttg cggcggttag 60
cttgtaaaac atttctgtta aaatcacgaa ccatccgtta aaagaaatgg cagatgaata 120
tttttttgct ttaacctca aaggtaaaaa cagtgaatc tgggatccag aagcgaaggg 180
agcagaggat taccaagggg gacacaaatt gatcattaaa caagctttgt tgggacccga 240
agcccaagaa ggtgaagtaa atgtgtgaca agtagaagct atgacgtgga aagactcagt 300
taaaatccca attgccacac taaaagccgg aggcccaaat aaccaagtat tgtagatct 360
gtcattccca gaccaccag tcacatttct acttatacaa ggtaatggac cagttcacat 420
tgtaggcat catttaattg tagtccgat ggaagaattc gatgaaatgg atgaattaga 480

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agaggaaatg ttggatgatg aagaaggga agaaggagcc gaggaagatg aggatgaaga 540
tgaacccaaa gccaaaaaag caaatcagc gactaacgcc aagggaacaaa ctcccgtaaa 600
aaacaattca aaggctgcaa agaaataaac aagttcatct aatcccaaaa ccacctcctt 660
tgtaatgtta agttagtttt ttaatgtatc tcgggagtgt ttatacatcc attaacagat 720
caaccgtaac aatttctctt aaatataagt ataatatctt atgtttcttg acgtcataag 780
atthttgtgaa agtttctttt attccaggtg taactcttag ttttaattgt atcaatatct 840
ttaagctgga aacgtattta tttcctttga aatcatccaa tttgtgtgta aatatgcagc 900
cctcattaaa ccattttttg tagcaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 955

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<210> SEQ ID NO 29
<211> LENGTH: 422
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

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<400> SEQUENCE: 29

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gggggaaata tatactacaa tgaagttttt aagatcgaca gtgtgctaca ttgccatctt 60
ggcaattctc ttaccctctc gtgccgatga ggttgaagga aggagaaaaa ttttgatggg 120
gcgaaaaagc attaccagga catatcttcg tggaaatgct gttcctgcgt atgtgataat 180
aatccttgta ggaattggtc aactcatcct gggagggata ttgtacgttg cattgaggaa 240
gaagatcatt gctgcacctg taacggcatc atatgcagtg gctagacaag aaccataaat 300
tttatttgtc tagaatatta ttttctaaat atgcatcttt tttaaattat tgtctacgta 360
aataataagt ctagaaatat ataaaaattg tcaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 420
aa 422

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<210> SEQ ID NO 30
<211> LENGTH: 2911
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

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<400> SEQUENCE: 30

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```

gggggtgcga agctaccatc cgtgggatta tgcctgaacg cctctaaggc cgatcctttt 60
ggcttgaaga gttttcagca agaggtgtca gaaaagtac cacagggata actggcttgt 120
ggcgccaag cgttcatagc gacgtcgctt tttgatcctt cgatgtcggc tcttcctatc 180
attgcgaagc agaattcgcc aagcgttgga ttgttcaccc atagacaggg aacgtgagct 240
gggttttagc cgtcgtgaga caggttagtt ttaccctact gatgactcgt cgttgcgata 300
gtaatcctgc tcagtacgag aggaaccgca gggtcggaca tttggttgac gcacttactc 360
gagcgggtaa tgggtcgaag ctaccatccg tgggattatg cctgaacgcc tctcaaaagt 420
cacaagatga gtgtaacgcc acctacagat ctacacaaga aagaagaacc acgatagcat 480
cgacagacag tggtaatggc cgacgaccgc gacgagggaa ttttaaaata cgaaatgttg 540
taaaaggaga ggcacaaaaa agaagagtag atggttcgaa aaatcaatga aaagctagtt 600
gaacgttcag tttcttttaa aaaagaaagt tttgtagatt ttgaaacaac accgcacaca 660
tcttatggaa aatgtaatgt cactcaagtg caattgaatt tgcctgaata tattggtctc 720
gaagttacaa tcatttcagg tcgttgccgc aactctgaat ttttattaat aacggtgcat 780
attgatataa ataaaacata aaactaaaat caaatgggta tgagttagaa aagaatgtga 840

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atcggcagtt cataaatctt tctgaaagta ttaagggtctc ttatcttata gataaatgac 900
aaagcacttc tagtgatgca ccgcaaaata aagggtcaacc tcacgctcgg gtaacctgtt 960
ttcaatagcg actagactaa tagtatttgt aaataggaca gttttatgga cttcaaaatg 1020
tgattctaca atttacgcgg atattaatca aaattcggag ttggcgcagt gatgtgagat 1080
tattgtaatt tctaaacgaa tctatttatg taaattttat tgtgtttgag tgacattaca 1140
tcaaccataa gatgtgtgtg gggccctttt ggcgaatttt gccataaaaa aattaatttg 1200
gagggttttt aactagctcc aagagtgtga cagaaagata tgccgctatt aatattgttt 1260
cgcaacaaat agatcatttt gattacttaa aaaaagtaca atgaatcata ctaagttatt 1320
ttttgttgta ctatccgttg caagataatt tggatagtaa atttaacta attcaactaa 1380
atatattaaa attttcgttc catctacttc cattttcttt tatttttttt tataacgagt 1440
ggatcaacaa aatgagcatt tttttatatt ttaattgtga tttgaaagtg tattttaagt 1500
gggagatgat gatgttcgag tctattaact gtacgttact taccacaatc tattttgtat 1560
ggattttcat acaaaagaact ttagtttggt gattattatt taataaacta cattttattt 1620
aaaagtact gtttaacgaa tcatgtaacy atcacgctcc tgcgcagtaa acaaaatatg 1680
ttccaacaaa cagatgatcg ttcacgcat cgtccttcca attgttcaa caaaaattgt 1740
gatcgtccaa tgacagtgtt gcgacgatca ttttagtact ctgatactat aaaaattgtg 1800
tgttgaaga aacctaatgt aactgcgcca ttttgaactc agatgtttct taggtatgcc 1860
cagggtagta gttcccttaa agaaaaaaaa gtgggaaaat gtttaggttt ctatttatta 1920
acaaatcaca tattggatgg acagtctgca tctttttttg tcagtataga taaaaaatcc 1980
tgttcttata atgctaactt gattatcaaa cgactgctaa gccttagatt gaagcctcat 2040
acgcacccaa ctgcctaatt tagatacaaa attagccaaa ctaaatcttc gaatacccaa 2100
aacacttaaa ttattgccat ccatatgtct agtgtgtaaa gacaaccaga aaaacctgat 2160
tactgatact aggagtgtaa aatataagct gagggccctg acatctgacg agttgatgaa 2220
gaatatatct tcctatagaa actgttaaaa aaacggtaat attaaatgcg aaacacggag 2280
ctaogatgag aagaaaaaat ttggtcctct aaccactaca agaaaggtcc aaaggtgttg 2340
taatatttga tcttatacag tataactcat gatcaacaa cgtagagagc aaatatgaga 2400
acatcaaatg tatgttaata ttccgttggg gtgagttgac ggaattaatt aaaaaaagt 2460
gtaacgacga acagtaatat atttatttat tttgggtgaa caacggcgtt gttttgctta 2520
tatctcgaaa gaggggtgat tgtagcgaa ccgaggattt gtctgcatcg tttgcgtgct 2580
gtgtagagac tggcctccgg accaccacct ttatgtcaac tagttttgcg gttttgagat 2640
aatgaccaga aagggccata cattctgcat ctctttttaa gaaccttttt gtattttaag 2700
aagttgacat aacgagtgtg gcactctggg catcgcaatc tattagtgtt tccttgaatg 2760
aaacattaat cacaatctgt ttaaaggata acatttcggt tctcgaaatc aacggcatat 2820
ggtttgata tcacatgtgg attttaaatg accaatgccg ttccattttg agaaaagcca 2880
tgaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 2911

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<210> SEQ ID NO 31

<211> LENGTH: 1287

<212> TYPE: DNA

<213> ORGANISM: Diabrotica virgifera virgifera

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<400> SEQUENCE: 31

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gggagacaag aggcagctac tattaacgat acatcgctct ctcgttagtg ttcataat 60
acgtgtagtg taacagaaag tgcagttttt tttcaccat gtctaaccgc aacatcccta 120
tcaaaatggg tgacttcagt gttatcgaca cggagttag cagcatcagg gaaaggttcg 180
acgccgaaat gaggaaaatg gaagaagaaa tgaacaaatt cagatctgaa cttaccagta 240
gggaagcgaa caacttcttc agaagcacia ccagcatgtc gtacgaatct gaaacgggtga 300
ctggtggaaa taagtcttca tcgacgtcca gttcaacgac acagcaaagc agcacaggat 360
cagatttagc ccacagagca ccaagtgggtg atgtcagaac atggtacgac gacctcaact 420
ctcccctaat ccaacaggac ggtaacgaaa agagcctaaa attaagattc gacgttagtc 480
agtatgctcc agaagaaatt gtagtcaaaa ctggtgataa taaactcttg gttcacgccg 540
agcacgaaga gaaaacagaa tcaaaatccg tatacagaga atacaatagg gaattcttgc 600
tgcctaaagg aacaaatccc gaacacatca agagctcatt aagtaaagat ggcgtcctca 660
ctgtcgaagc acctctccca gctatcacct caggggaaaa attaatcca atccaacatt 720
aagtaattta aaattccttg taagccttcg aagcgtttat gtccgctagt aaatactcat 780
cgattaatta tttaaatgt aacaactcat gtgactaaca aaatttttat tttatttcat 840
ttttaaaacc tggcaacgtt gtctggcttg tttaggataa gtcacaaatt tagtggtggc 900
tctaagtac ttactgtcta cacagcacia gtcacaaatc gttaaatata ccataaacct 960
catgcatcgt tgccggatgg ttcaaaagct catactatct gtgactatct tcttgatggc 1020
ggtcgtaaac ttgaagggtg attaacatcc tttcaciaag cttaattatg caatgaaaat 1080
aatttttaac aactttatct gtgacaaaaa aattgaagct aatgtaaaat tgtttgggtta 1140
aattcttggt aagggtctatg gttcgatgtt caataaccag caatttcacc gtaggcgtag 1200
tgtaacaaat tgtatcatgt gtaggatatt tacgaataaa ttatttttaa tctcggtaaa 1260
aaaaaaaaaa aaaaaaaaaa aaaaaaaa 1287

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<210> SEQ ID NO 32

<211> LENGTH: 560

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 32

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gggatcacgt gaataaatta caatatctct tcaaaatccc ttgacgcac ccttgtaca 60
caatactgat aacatggtat tcggtataga tggtatcggt attgtggaca ggggcgcgcg 120
ttaagggtatt ttgaagaaat attgtgattt attcacgtga tcaactccgtc tgttaggtag 180
acggaggttat tttatgttcg taacaggtag tctgtatttc ttttaaggca aatatttggg 240
ccgtcgttga tctattgttt ctaaaacctg cctggtatct tcccaatact tttccgaat 300
attgatttag cctttttctt atacagtatg cggcaaaata aacagtacct actgaaatga 360
atattgaaat gtttatgatg atttatatat ctagtatata tgatatagcc ttgcaaactt 420
tattcacgac gacgcatgtt cccgataaac agatgttaaa gatgtcctct ggtcagtgac 480
ggatctacgg ggagggaaaa tgagaaaatt tttccccta acaagggtca aaaaaaaaaa 540
aaaaaaaaaa aaaaaaaaaa 560

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<210> SEQ ID NO 33
<211> LENGTH: 807
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 33
gggggacagt tcaatatgga tccactactt tactgggtca tatttggtac gttaatatgt    60
acgctaggta ttctaggaag ttacttaatg ttttctataa taagagatag ctgttttaag    120
agaaagaaac aaaaagatac tgtgatgga atatatgaac cagattttca tccagcatgt    180
ctgagtaagt tacagtatga taaacatgat gttgaagatt taacgagaat cgaagaaat    240
tccaagacgg ggtttagaag actaagtttt caaatgaag tatttggtaa gcagtttgaa    300
ggattattgg gtgagaaaag acaatctgtt gacaaggaaa gtgatgtgtt tgtatctacc    360
aacactcttg aaaaaagcat tacatcaatt acagaagaag atgaagaatc agacgatagt    420
tttgatcgag atactgtcag cgtagacatt gaagtatcag acgaggttaag agaagtttta    480
agaaccgaaa aagaagctaa gaaggtcgag aaagaaatga acaggtttgc aggtggtaca    540
aacgatttac aatattacga aatcaatgag aagtatataa aattaatgat ttctctttgt    600
gatatggaat gcagctccat cgagtgcaga aaacacaaaa acagagtttt aagttacatc    660
gagcaatgtc agaaccaact caaattaaaa tctctgaagt ctaaataatt atttttattt    720
gcttgagat gtaattatta taaatatatt ttaaatataa gtttagtata aacagccaaa    780
aaaaaaaaa aaaaaaaaaa aaaaaaa    807

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<210> SEQ ID NO 34
<211> LENGTH: 981
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 34
ggggattcta aacttttcga actaacaac aagatggcaa ccaaattttt agttctcgcc    60
gcattcattg cagtagctaa agccggttct tatggatcag gtttcggcta cgccgcgcca    120
gctgttgctg ctacaggatc tcacgatgcc atctctacct actccactgt gcaacatcat    180
gtccagccg tacactccta tgctgctcac gctcccctcg ttcgatgtcc agttgcccac    240
tctacgcag ctcttttggt tcaagctcca gtcgctcacg cttacgtgc tcccgttgct    300
cacgttcacg ctgaaccctc tgcaccagcc cattacgact tcgcatatgg agtaagtgac    360
ccccacaccg gagatgctaa gagccaacac gaatctcgtc gtggagatgt tgttcacgga    420
agctactccc tcgtagaatc cgatggaacc aaacgtaccg tagactacac tgctgatcca    480
caccatggat ttaatgctgt tgtacacaaa gaacctaccg tacatgctgt tgctccagtt    540
gttgccaaaa tcgtagtccc agtagcacat gctgctccag tagctcatgc tgettattgt    600
gtccagcggg ttcattgcgc ttactctgct ccagcagttc atgctgctta ctctgctcca    660
gcagttcatg ccgcttactc tgctccagtt gtccatgctg cccacgctgc cccagttgcc    720
catgctgctt atgctgggcc agttgcccac gccgcttatg cagcaccagc tctacatgga    780
tacgtgggct ctggtgtcga tggttacgct gctcctttgg ctcatggtca tcatgcttat    840
gctgctcatg ctccagtcct ttcacataac ttgtggtaat tctagaaagg aaaaattgta    900
gattttgtat ataaattatt tatactgctt gcattacaat aaaagattgt ggaaaaaaaa    960
aaaaaaaaa aaaaaaaaaa a          981

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<210> SEQ ID NO 35
<211> LENGTH: 1160
<212> TYPE: DNA
<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 35

```
gggagtaaaa ttaaactgca gtgattaaca atgaaagttg ttattatattt cgctttttatc    60
tgcaatattg catttgtagc tcatgtttac ccggaatact taaaacaata tcgctgcaag    120
gcatcttcgg aaaattatag tgaatgcttt ctaaataagc tcagaaatac tctgccctac    180
tacgttaaaag gcattctctga attagatata cctccatttg atccgtttac actacctata    240
tacagtcgca atgtaaacat attgggaaac aagattagtg cgactttcaa aaattcgatt    300
gtaactggac taaggaactc tattattcat aatgctaagg ttgatctgaa taacaactat    360
gcagaaataa gcgttactat tccttggttg gatatggcca cagagtatga tatttctggt    420
gaattctttc aataccact agatgtgaag ggtactttta aaggaaatat aactgacatt    480
caacttttct caaaatctac tctacaaact ttcaaaaata acggtgaaga ttattataaa    540
tttgataaaa taaacaaaaa agtacaaatt ggaggaggcc atattgaaat aacaactaca    600
gataaagatc ttatgccgat agttcaaaca atacaagaat attttaatga gcatcccaga    660
ggcttcttta acttgatatt gccattcaca ttggaatacg cacaagacct actcagagaa    720
tttggaatg aatatttagc caatcttctc gcttctgaat ggttaccgca gtaaacataa    780
atttgaaaaa aatagtagac ttagtagttt aaacaacata gttttttagt taaaaaaatt    840
gaccgtagta ttaataaat ataatgacaa taatgttggt gatgatcagt tgagatatat    900
ctatccgcta ttctatggaa aattccagaa atgcaatgca ttttgaatta tgcccataag    960
tggaagtaatt cgttctagca gcatatagcc tacatgttca aatggactga gaccctatc   1020
ttctgttgac catagcaata catacatttc ctctagaaac acttttttgt gattattatt   1080
tttactttgt gagtattttg tatatgtgaa ataaaaatat tatattttgc aaaaaaaaaa   1140
aaaaaaaaaa aaaaaaaaaa                                     1160
```

<210> SEQ ID NO 36
<211> LENGTH: 721
<212> TYPE: DNA
<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 36

```
ggggtcactt taattgtcag taggaactga gtgctagttc aaggtagacg tacgttgacg    60
agcgtgtagc aaagtgtgtc gtttcggatt ttgtttttcg taggtagatt aatatggatt   120
atagtaagac atggctggga gccattaaaa aatgcagctt ctgtgcatgt cttccagaaa   180
aatatagcaa tgaatgggtt aaaggcgcct cacgcttctc tgagttaact aggacattct   240
tggtattaat ttttctattt tgcttcaagt aatattgtcc tcatggctta gtggcgggaa   300
gcaagatcat attagtcgcc gtttcgcaaa atgaagcata ttccataaat atctgtgggt   360
ataaagtatt ctccaagcga agctccagaa tgctgcagaa tgcaggagct ttatagccaa   420
gtctgaagtg aatacagagc aatatcatta ataagtcatg ttcttaaatt atttctaaaa   480
attataaaaa ctgtcagagt gatgatgata gccaaacttg atttagaaag gaattaggaa   540
taaaagatgc attatttact ttaaatgtga taactcaaaa atgcatggat tatgtttgtg   600
```

-continued

```

aatctgcatg ttgttactt taatttttaa attgtatttt tttttaaat ttaaaaagca 660
tttgacaaag taagacatga aatattagtc caaaaaaaaa aaaaaaaaaa aaaaaaaaaa 720
a 721

```

```

<210> SEQ ID NO 37
<211> LENGTH: 928
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

```

```

<400> SEQUENCE: 37

```

```

gggggttagt atgtcttaga gcattatggt tactcttcca atcattggat gatcggtctc 60
caatgcggta tctgtatat taccacttaa tacaattgc gaaacagaca gaatctgtaa 120
aattagtgtt tcaagatata aaccatctaa agcaacagtt tgccaattgc cttccgtcta 180
atgaacagct tcaaaagctt tataggcttt tacatgaagt actgggttaa tcaaatcaaa 240
gtgagcaggc tgctttagtg atgattgaac ttcttggtac atacactgac aaaaatgctt 300
ctcatgccag agaagacgcc atccgttgca ttgtatcagc actagctgat cccaacacat 360
tccttcttga tccattgtta tcaactaaac ctgtcagatt tttggagggt gatttaatac 420
atgacctttt aaacatcttt gttagtgaat atttgtccac ctacctcaag ttttacaatg 480
aacataagga atttgtgagt gcacaagggt taaatcatga acagaatatg caaaaaatga 540
gactgctttc cttcatgcag cttgtcgaga gtaactctga aatatctttt gatgtcatcg 600
aaaaggagtt acagatgaaa ccagacgaag ttgaaagctt tattattgaa gtattaaaaa 660
ccaagttagt tcgtgcaaga atggatcaat cttcccgaa agtctttgtg tccagcacia 720
tgacacggac tttcggaagg gcacaatggc aacaactgcg ggacttactg cactcttgga 780
ggggaaatat aagtctctgt caagacggta tgaagactat cgcgcgtgct cagctagaac 840
ttatgaacca acaacagtaa tgataatgaa gttttcataa cttttaataa aacgttgaaa 900
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa 928

```

```

<210> SEQ ID NO 38
<211> LENGTH: 1339
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

```

```

<400> SEQUENCE: 38

```

```

ggggaatata attaatcaaa taattagaat tagaaatata tcgttggaac agttgtagat 60
attcataatg gagagtaact tgggttatca aaatgggagt caaagtagag aacaagactt 120
tcaaaaactg tcgcagacca tcggtaccag catacagaaa atatcacaaa atgtgtcttc 180
tatgcagcgg atggtcaatc aaataggaac ccatcaagat tcgcctgaat tgagaaagca 240
attacattcc attcaacact acaccagca gttagttaaag gacacaaatg gatacatcaa 300
agaccttagc catattccac catctctata acaatccgag cagagacaaa ggaaaatgca 360
gaggagaggg cttcaagatg agtacaccag tgcattgaat ttgtttcaaa acgtccagag 420
aagtacagca tacaagaaa aggagcaggt caataaggct aaggcccagg tgtatggaga 480
acccatttta attggatata agtccaagga ccaacaactc atagaactgc aagacaataa 540
ttcgaggcaa atgcaaatgc aagaggagtc aaatctaagg gaattagaag aacaggaaca 600
gtcaataaga cagttggaga gcgacatcaa cgatgtcaac ctaattttca aagaattagg 660

```

-continued

```

aacccttggtg caccgaacagg gcgaagtgat agacagtatc gaggccaacg tggaaagaac 720
caccgacttc gtcagccaag gtgccaaca actccgcgaa gctagtacgt tgaanaacaa 780
agtaagaaga aagaagctga tcatgttgat gatcgctgct ctagttttta ctatactcat 840
aataataatc gttgtatccg tgaaacgtta aaatagtatt atggtaatga tattaaaaat 900
gtgatgattt aaatgattgt ggtaagtaga taggaaatat tcatgaacta cacatcctta 960
cttattattt tatcttattt ggtgaagctc ccagttcctt aacccttttc ttggcaaac 1020
gatataaaac tgtgaaaact ctgttttctt tatattcatg cccttctaga attattttaa 1080
aatttatgaa ataaatatctt cacccttaatt ttattcctaa gtaccaaatt tgaatgtgtt 1140
acaaatttgt tacgttgcca agaataccat accccttatt accactgatg gtccatgcat 1200
tttctaaggt ttgaaccgat ttctcagaac aaagttaaaa tttcttttat ctgagttcat 1260
gggagtgtctc tcgctgcaca acacccccct atccccatta aatttttagga aaaaaaaaaa 1320
aaaaaaaaa aaaaaaaaaa 1339

```

```

<210> SEQ ID NO 39
<211> LENGTH: 533
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

```

```

<400> SEQUENCE: 39

```

```

ggggcctttta tttccgcttg atagtcaaga aaaggtgtca agatgacatg taaaaggcgc 60
aatggagggc gctccaagca cggccgtggg cagctaaagc cagttcgatg caccaactgt 120
gctagatgcg ttcccaagga taaggcaatc aagaagttcg tcatcagaaa cattgttgaa 180
gccgccgctg tgagagatat tactgaggca tcagtatatc aagcttacgt tctccccaag 240
ctctatgcca agctccacta ctgtgtatcc tgcgctatcc acagcaaagt tgtgcgtaat 300
agaagcaaaa aggataggag agtcagaact cctccacaga gaaacttccc tggtagggac 360
aatgctagag ttcagcaaca acaacctagg aagtaaaactg tttcttttagt ttacaataa 420
aatttaagaa aaaataaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 480
aaaaaaaaa aaaaaaaaaa aagggaaaaa aaaaaaaaaa aaaaaaaaaa aaa 533

```

```

<210> SEQ ID NO 40
<211> LENGTH: 535
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

```

```

<400> SEQUENCE: 40

```

```

ggggcctttt cagcagttgt caaagcactg ccacaatggg taaaataatg aaatcaggaa 60
aagtcgtatt ggtcctcggg ggccgatacg ccgacagaaa agccgtagtc gtcaaacct 120
acgatgaagg tacatcatag aaacaatacg gacatgcctt agtagctgga attgataggt 180
acccaaggaa aatccacaaa cgcattggga aaggcaaat gcacaagagg tccaagatca 240
agccttttat caaagtattg aactacaacc atctcatgcc cactagatac tctgtagatt 300
tggeatcaga cttgaaagt gtacccaagg acctcaaaga tgccatgaag aggaagaagg 360
ctagattcca gaccctgtgc aaatttgagg aaaggtataa gcaaggaaag acaaatggt 420
ttttccaaaa attgaggttc taggctgtag atttaatttt ataattgtac actttttatt 480
ttgagaataa aatgtggata aatgcaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 535

```

-continued

<210> SEQ ID NO 41
<211> LENGTH: 788
<212> TYPE: DNA
<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 41

```
ggggaactgt caaatataac cttaataat atttatttac gtgtgtgtct tgtttccata    60
gttttagctt tttttctttt aatttaaaaa gatgagtgc gatagtata actttgaata    120
tgtagacgat gagatagatg ataaaactca caataaacta gtggataacg tttttaaagt    180
taaaaaaagt tcaacatgac aaaagtgcac atagaactga agctgccact aaagtgtctg    240
aatttaactc agtaaaatcc ctttcgaata aaaatttagt gcattgtaat gaattaacga    300
gcgtttttaa gggaaggaag tctcttcagc tgtctaataa aattaaatct acaagtaata    360
tcagcaagac attgcctaaa cctctagaaa agccacaagc tgaacgtatt aaacgagctt    420
taaaactatga gaaagcgaaa ttaaaattgg atagatggga agctcttgtt caggctaata    480
gatcagctgc acaattatcg ttccctttta atagtgatga gaaagtaaag gtcattgaga    540
aacggggcat atcttaccct ttatctttta gagttaaatc ggaccttcag aaaaatttgg    600
aaaatataga ttcacaaata gaagagtatc acatagatag agtagaaaag aaagaagatg    660
aagactatcc acttacacta gaagaattaa aggaaaaaaaa agaaaagaac tagccaaact    720
tcgtgcacac cagagtttta aagaagcaaa agctagacaa aaaaaaaaaa aaaaaaaaaa    780
aaaaaaaaa                                     788
```

<210> SEQ ID NO 42
<211> LENGTH: 444
<212> TYPE: DNA
<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 42

```
ggggaacgaa gtggccattt cttacagata attccacatg ccaaccattc ataagataaa    60
gcaaggcatc gtcgtgttct tgttgaaact ctagtatgct gtatgggccc actatccaat    120
ttccaataat tctaatacaa ccagtaactt tttgtgacac ttctgtatga tctccttgaa    180
tataatcagg gttgttaaca acgcaactga atatttccgt agagggcgct tcaaaaatcc    240
gtagaaatcc gtagtacaaa aatctgacag aaaatgacac ttggcagacc aaaaaaagaa    300
gaagaatgac acttgacata caaaaaaaga agaagaatga cacttgacag accaaaaaaa    360
gaagaataat gacacttgac agacaaaaaa gaagaagaat ggcacttgac acacaaaaaa    420
aaaaaaaaa aaaaaaaaaa aaaa                                     444
```

<210> SEQ ID NO 43
<211> LENGTH: 472
<212> TYPE: DNA
<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 43

```
gagggtttaca tattttcaag ttgtccaaaa atatccacat gtcttcgagg taattgagat    60
ggtagtccag accttttaaa catttttaaa ttcatttggg tgacatatat atattggtgg    120
aattgaatat gtcaaattta tttattactt caatagtata taagtcttgc agctgttacg    180
tttaaaattt gagtagctta cttaactgtc gtatttgaaa agtgtgttgg tcgaatatgc    240
```

-continued

```
gcctcgtag ttatttctag ttgcttttg taaatttga ggatcaaaaa ataaataagc 300
ttatgattaa ttgtttatat gggaggtggg cgcaggtga aatgaaaaaa aataatttta 360
ttaacgtttc gacgcccata tcgggtgccg ttgtcaaaat acaaaatatt attaaaataa 420
acaaaagtgt tgttgctaag cgaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 472
```

```
<210> SEQ ID NO 44
<211> LENGTH: 497
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera
```

```
<400> SEQUENCE: 44
```

```
ggggcttatt cacaattatt aaaataataa atggatatga ccaattatca gtaagtgaag 60
cagaattcat tggatataat ttcatatctg taatccgtct acccgtaaag gaaaccagaa 120
ccaatagtag taattttatt tctgaaatac agggcatgcc tttgtttaca taatatttgc 180
atactaacct ttgaaacggt attcctgaag atctacattt gcttctgctg ctccaactgc 240
gttgaggaca ggacagacac attttatgca atagtgttaat aatactataa aagtatccga 300
attaaaaaaaa atattcttaa aaagcacaaa taaaacaaac aacgatcacg ccacacacga 360
caaggccggg caaggtggcc aagatgcaa gatggccgaa gtgaggctcg tcgttggtcg 420
tttttagtca cgtgatgcca tcgtgatgcc ctctctaagc ggcatgcgaa aaaaaaaaaa 480
aaaaaaaaaa aaaaaaaa 497
```

```
<210> SEQ ID NO 45
<211> LENGTH: 809
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera
```

```
<400> SEQUENCE: 45
```

```
ggggaagtaa ttctgctaaa aattttacac tcctttgat tggaggaaga attacaattt 60
tcattattaa atatctattt gaaaataaat aacaattgca caaggtgtag taaaagggtg 120
ggtcatgaat aaaataaaat attctgggaa taaaatagt tccattgaac ctaagttacc 180
ttagtacaaa ggtgcacata aaaaaagtta taactctttg agcttataaa ataaaaatcg 240
agaatatcga aaaatattag aggttaaaat gggcatttga cattattatg gtaggaaaat 300
ctttaaaaaa atagtagtga aattttcaca gccgataaaa attttatagg ggctttattc 360
ccttaacctc cccccccccc aaacctttat gtacgttcca gttaaattat tatttagtcc 420
tggaggggga tgtgtcacca acacgatatt ttttttctt atttctctga actaattgtg 480
ataccattag ttaaacacaa tatttctaaa acttttttgc tgactatttt gtcgatgaac 540
cagttgttat atgcggcttt ttttcacatg ttatgagagg ttattaaaat tattgtttaa 600
ttattttatt gtagttaaat gtgtaagcca gttcccat tcaaacctgt cagaggtgag 660
ctaagatatt ggttgcgac aatgtttgtg gacatcaggg ccggttttgt ggtttttgag 720
cgccccgggc aaaataaaat ttgtcgccca ttcatacaag aatatacaaa tttactccga 780
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 809
```

```
<210> SEQ ID NO 46
<211> LENGTH: 1728
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera
```

-continued

<400> SEQUENCE: 46

```

ggggagtaaa gaataattcg gtgtttaccc ttattaagtg aagttttttt actacgaagt      60
gtactgtgtg ggagacaaaa aaaaacatga agaatctgtt gttcttgttt gggtttatca    120
gtattttatc agtattgcta gccgcagatg ttgccttggg agacttagat ccaccagaag    180
ctcaacagca aatagaacaa caggaccagt ctcttacta tgcgccaaaa gtagaatcaa    240
atgttcccg c agtaagatat ttgggaaacg aacctcaca tgttctggaa gatatttact    300
tagctagaca gtatcacgga caagacggaa taggaggata cctttatgga tacaacatcc    360
cagatattgc caaaactgag aaaaaagttg ctggtggaga ttaagaggg gcgtacaatt    420
acattaatga tgatggggcc gaaatcaagg tcgaatattg ggacgatgga actggattcc    480
atcaaactga taatgttctt aaaatcttac ccaagccaat tgaagagtct ccggaagtta    540
aagctgaaaa ggataagttt ctagcaagat ggcatgaaga gcccgagaga aatcaacgtc    600
cagttgtctt cccctatgat gctgatggta attacgctag cggaccatta tcgctccagg    660
gacaagctga atttaagaaa atgtttgaaa atcaaccccc aaggtcagta ctaccaacaa    720
cctagctcta gttctggagt ttaccagcaa aacggacaat atcaacccgc tggacaatac    780
caacaaactg gacaatacca aaaaactgga cagtaccaac aacctggaca gtaccaacaa    840
cctggacagt atcatcaatc tgggtcaaatt aaacaagttc aacaaccagg accccttcaa    900
caaggtcaat attatcaatc atctaatacg caatcttctg gtcagcacca acaacctggt    960
caataccaac caactgatca ataccaacaa actggtcaat accaacaacc aggtcaacaa   1020
gtttctgttc agcaattaac caatccta atcaatcgatt aacttgagc atacagtga    1080
agccaaaact cttacgcaaa cccaactcca aacaaacccat ctggtcaata cagccagtt   1140
gcttcaagct ccaaccagta cagccaacaa ggaggatata aacagcctgg acaacaccaa   1200
caaggtgcat atcaacaaag tggaacaaat cagcaaccag gatcatacca acaaggtgca   1260
taccagcaga gtggagcaaa tcaacaacca ggatcatacc aacaggttgg tcaataccac   1320
caatctggac agtaccagcc ctccgataac tcaaaatcaa accaagtga taattccggt   1380
gattacgata aaagctggga caacgagggc caatatgata aaaaatacga tgaagaagaa   1440
ggctccactg ggcccccaaa gggattcttc tataagtttg attacctgt aggaaaaatt   1500
gttcagaaag gagaaatcgc tagagttgga gatctgaaaa atgcgtatag tcaaaataaa   1560
gctgcgtacg aatcccaagt aagttcaggc cactcgggtt cagctgcttc ccaaagcagt   1620
tactcatatg gttcttaact ttaagctgtg ataatgtatt ttatagattt ttaggagaat   1680
aaaaaatata ttactttcaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa   1728

```

<210> SEQ ID NO 47

<211> LENGTH: 962

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 47

```

gggacggttt tacgtgggaa cagcccaaaa cactacaact aaactgacaa ccttccgtaa      60
caatatttta gaaatctttt attgacgcac tagatgcctc cttctagatt ttaagtttag    120
aaaaaacttc tgtgattggc gctctgaacc ttgagaccga cgcgattttt tgcctctctg    180
aatcggaaac attctacaga gcaaagtatc gcgtactaac aagtaactgt cgcaaacgt     240

```

-continued

```

gccacagat tcccgatata gaccacagtg gcgtttcaag cgttactgca attcagtggtg 300
agtcaaacgt tcagtttcaa gttagatatt actcgccatc tgtgtgtgtg ttaagagaaa 360
aaataatttg gaaaagagca tttctataaa cactccggac tgtattggga atgggtgggtca 420
tccatgcatg aaaagtctct gcaaaaacaa tatttatata ttatgtatct tatacaactc 480
atcagtggtc actggttgta aattatattt tattctaatt ttttaaccta caactctaca 540
ttccttggtt ttttaaaata atcgtaaat taacatagaa tttgcaagaa acatgtacaa 600
tgggcattta agatctgctg cgttttgata tagaattccc ttagtggtta ttttattgat 660
ttgattttgt aaactgtaga tgaataatta ttgtagatga tagtttgaat gtatagattt 720
tattgtacct atgtaattta ttatgagagg ataaaacgat ctatatgttg tatacaattg 780
atttaagtaa gtttggtaga tgtattgtcc aatgtagatc gtaaaatttg gtgtaatttt 840
ttatagcata gtttattttt taaataaccc aactgatact ctattgctct attcaaatg 900
tgcttttttt gtctaagaaa taaaatagtt gtgaaaaaaa aaaaaaaaaa aaaaaaaaaa 960
aa 962

```

<210> SEQ ID NO 48

<211> LENGTH: 1146

<212> TYPE: DNA

<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 48

```

ggggattggt gttcaagtca agtcaagttt gttgagtaaa atcaaaactag tttgacttga 60
tgcatctcta atatctgccg taaattgaag gactccagta ttcaatccga atatgtttca 120
acgtaaatgt aaattctaca tgacaaaaac tcagttctta atagatggac acaacatttc 180
agcgaacatc taaatattaa cgatattgaa gaaggttaca acatagaaaa tcaacaaaat 240
ctacatcatc aactacacac tgaagacca acaagagaag aagtatcaac tgccatccta 300
aaactcaaag acaataaagc cctgaatctg ttctgatctg tataaaaagg tgggtgatcat 360
ttgcagcaat ccataaatta atagtactga tatggcagaa tgaactggat ccagaaaagg 420
gaataatacg tccgttgcat aaaaaagggt atcaactgga ttgtaagaac tatataggca 480
ttactctact agcatctacg tataaaatct tcggcaatgt attgtttgaa agactgaaac 540
ttttcacaaa ggatattggt ggtcaatata aatgcggatt cactgctgga aagtcaacta 600
tacatcaaat tcaagcacat agacagattc tagaaaagtc aatagaatat aacatagata 660
cccaccatct cttcgtcgac ttcaaagcag cctatgacag tgttaaaaga actgcattat 720
ataatgcaat gattgacttt gggatccac cgaatttggt taagttgacc caactaacia 780
tgcaaaatgt aagctcgtgc gttagaattc aaggagaaaa ctggacattc tttgacatta 840
ataatggtct aagggtctaa acagggggac gcgctggcgt gtctcctctt taatattcct 900
tgaaaaaggc agtgagaaaa ttaaatatta gaatgaatgg aagtattttt aatagatcga 960
cgcaaatctc cgcattcgct gacgatatag ttatagtggg cagaagtgtg agagacatgg 1020
tgcagtatct taaaagactt gcggacgcgg caagtgaatt aggacttggt atacacgagg 1080
aaaaaaaaaa atatatgttg gtttctaaaa actcccga aa aaaaaaaaaa aaaaaaaaaa 1140
aaaaaa 1146

```

-continued

```

<210> SEQ ID NO 49
<211> LENGTH: 630
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 49
ggggagtcag tgttgcgac gtccagcagt cttccaaaaa ttgacgtgtt ttctggaata    60
aacaatatgt gattgagtg tttttaacct taaaaatcaa aaagtttctt gtgatagtga    120
agtgaataac ttaaaataat agacaatgtt tgcgaacgga caggtagtag gtgatggtag    180
ctgggacctt cgggtttttg tcacagatct acaaacggag aggttgattc gcgtaaaagg    240
agatgtccac attggcggag tgatgttgag gctggtcgag gacctagaaa tttcaatgga    300
ttggtctgac catgcgcttt ggtggcccca taaaaatata tggctgacaa gaacaagatc    360
tactctcgac caatgcggag tccacgcaga tgccttactt cattttactc caatgcacaa    420
aattctcagg ctacaattac ccgatcttag gtatttggat atgcgggttg acttttcaat    480
caaaactttc tccgctgtag ctcaactttg caaagattta ggcttaaggc acccagaaga    540
attgtctctt tcgaagccac tggaacccaa tcatttataa tacaattata aagacctgcc    600
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa    630

```

```

<210> SEQ ID NO 50
<211> LENGTH: 293
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 50
attggtcaac agaaaactaa tagaagaaga taacttaaca aatttaattt ataaaaatacc    60
tagggtaaat ttagtgggag caaacaaacg gacattggca actataaatg aaggcatacg    120
agtaatggta cgactgggca agaatatgta tgcactacaa tgtgtaataa tgccaaacat    180
gtcacatgac atgatagtag gagtggacga attggcagaa aaacatgtag tggtagattt    240
taaaaataat acgatgaaac taacagaaaa aaaaaaaaaa aaaaaaaaaa aaa        293

```

```

<210> SEQ ID NO 51
<211> LENGTH: 1508
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 51
gggtagcaga gaagaggaaa ttgtatctga tgtggtttat gaaaaaagtt gacgggtgag    60
gggttgaaaa tctcgggtta atgacacatg gogattgaca caattaggac ttctctgctt    120
ctctttaact atttctaagt cttcatacag gtccaatttt aggaagtttt tttgtgaaat    180
attatgtaat aacgagacat cttctgggat attaagggta tgtttgtttt ttacaagatg    240
ttgagagaaa gtagaagtgt tttctctttt ggtgtgctct aaggagcgtg aagataagga    300
tctacaggtc ctacctatat atgtagcgtc acaatcagaa cattgtaatc tatacacacc    360
actacgatcc atgtagttag tagggctctt ggaattggtg agacactgac ccagattggt    420
gggcactttg aaagaaatat gagtattatc aactgctctt ttaagaatat atctaattgtc    480
tccagaaaga cgttcatgaa gatatggtaa ggaagcatat gaggggttga aggtcaagtc    540
tctagggaaa gcagtctctc tcaagactct aaggtgtctc ttttgaataa gttttagtag    600
aatattagga tcgtaaccgt tgttgaacgc tatttgacga agaattataa gttctttatc    660

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atagtttgat ggtgataaag gaatagtttc aagtcaggaa tagaatcaaa aataattagt 720
aatatgtagt taacatctgc acttgaaccg ttttatcagt aacatttatt aacaccatgt 780
accgattcaa gtacattttt ttaataattg aaaaaaagga aggatatagt aagagtaata 840
atataccctt atgtttttat caccttatag taaattgtac actagacaaa ttttagttta 900
atgactccta gaatttataa aactcaaaca actttgaagc tgattatctc agaactacca 960
aaactgcact taaacgcttt tacgtgtggc cccctcaatt gtaaaaccaa aatgttaatg 1020
cgggctgaat ccccgcgaca aatgaatcag aagatagtc attctttaa atttagagca 1080
aaaaccgtga aagaatggac taagagctca aagagtgcg caatcactcc tttaggagtg 1140
tagatgccat gatgatgatg ataccttgta taaaggattt taattatttt tgtgattaat 1200
tgtacacagt cgataaaaag aaagagtata aatgcctttt aaatatatta aattttactt 1260
ttccatgaaa ctttagtggt tcaatatcta atcatgaaaa gttcaagtgt cttcaacaga 1320
atattaactt tcagatttgt aatagttttg ggattaatta ttgtattgga gattcgaatt 1380
taataattct tatccacctt accgttacg tccagtccgt ctgctgctac tctattgtg 1440
ataaaagtat aaattggcaa actttatttt tcatctacaa aaaaaaaaaa aaaaaaaaaa 1500
aaaaaaaaa 1508

<210> SEQ ID NO 52
<211> LENGTH: 631
<212> TYPE: DNA
<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 52

ggggaaaaag ttattttttg ataaatttcg aactgtattt gaaaattgat tctatataat 60
aaatacataa aaagattggt tttaataaaa aatggcacac aatattaaaa aactgagtgt 120
ttcaatgagt aaagcgggaa tgccatttcc agtacctaca aagattatta gatttgttag 180
gaaaggttgt actaatagac cttttttcca catagtagtt gcagatgcta gatcagatca 240
acacgaccct tcaatagaac aacttggaa ccatgatcct tcccaaatg aacacaaatga 300
aagattaaca tccttaaaact tcgaaagaat tcgatattgg ttatcgcatg gagcgattgc 360
aacaatcct gttcttgaat tattaggtct tgcaggattc tatcctattc acccaggag 420
ttatatgact gcttgagaa acagggaaaa ggcaaaacaa gcttctgaag ctgctgaaca 480
gaccaaagag gagaaaagt aataacatgt catttacttc tgtgttgtgt gtacatttta 540
gtatgtttta gtagctataa gtctattatt ttgtaaaaag tcattataaa catataaacg 600
caaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 631

<210> SEQ ID NO 53
<211> LENGTH: 114
<212> TYPE: DNA
<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 53

ggggatttta taaatctggt aaacaatgag ttggtcagca taagctccaa agtgtttag 60
caatacagaa tgagttttaa tatctaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 114

<210> SEQ ID NO 54
<211> LENGTH: 597

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<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 54
ggggtctttt ctcagtgaag ccatcttggc aaacgttagt aacgtgaaat aaaacttaaa    60
ttttttcaaa atgggtcgta tgcacgcacc aggaaaaggt attgccagtc cggcattgcc    120
atacagaagg agtgtaccaa catggttgaa agtcacacca gaagaagtaa aagaccatat    180
ttttaaactt ggcaagaaag gcttgactcc atcacaaatt ggtgttatcc tcagggattc    240
atatggtggt gcccagtaa ggtttgttcc tggaaacaaa atcttgcgta tcatgaaagc    300
tatgggtctt gcccctgac taccagaaga tttgtactac cttatcaaga aggcagtagc    360
tatccgcaaa catttagaac gtaacagaaa agacaaggac agcaaattcc gtttgatttt    420
ggtagaatca cgtatccacc gtttggttag gtactacaaa accaagagcg tattggcacc    480
caactggaag tacgaatcaa gcacagcatc tgctttggtc gcttaaatg tgcttttatg    540
ttaagtttat aaaataaaaa tttctattaa aaaaaaaaaa aaaaaaaaaa aaaaaaa    597

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<210> SEQ ID NO 55
<211> LENGTH: 543
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 55
ggggcctttt taacgaaaaa tcgtgtgtaa aggtagcaca cgaataatca tcttttaatt    60
ttccctataa tcctttcagg atggcaatca gaccagttta ccgtcctcaa atcatcaaaa    120
agaggacaaa gaagttcatc aggcacagtc ccgatatata tggtaaacct aagagaaact    180
ggcgtaaac aaagggtatt gacaacagag tcagaaggcg tttcaaggga caatatttga    240
tgccaaatat tggttatggt tccaattcta agactaggca tatgctacca acaggtttca    300
gaaaagtgtt ggtacacaat gtaaaagaac ttgaagttct ccttatgcaa aaccgtaaat    360
attgtgcaga aattgcacat ggagtctcgt caaagaaacg caaggatatt gtagaacgtg    420
ctcagcaatt gagtattagg gtcacaaatg gaaatgctag gttacgtagc caagaaaatg    480
aataagctat tattttgttt aataaaaaat agcaaaaaaa aaaaaaaaaa aaaaaaaaaa    540
aaa                                                543

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<210> SEQ ID NO 56
<211> LENGTH: 1023
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 56
ggggattcag tatattggga tttattaaag agatttctag ccagtgaga agaaattcaa    60
gaaagtggcg aggttcgagg gaaaattttt ttctgccgtc aataattttt tttctagttc    120
acccttggtg aaccaaatta aggacttagt tactaaacaa gtaagttcgt cagataccga    180
aatgtcacag aaagaaagtg aatctgtgga tgctacatca cctctcccaa tgctaattga    240
aaccactgag aaatccgatg gagtcccttc cagatcacca tctgatgaaa ttagtaaaact    300
aagaccagag gaccgctcaa gaaatcagag cttttctatc agaaatatgc aggtgtccag    360
gagccaaatg aaggaatata gagaagcctt tagactgttc gacaaagacg gtgatggcag    420
tataacaaaa gaagaattag gcaaggatgat gaggtcgtta ggacaattcg ctgcactga    480

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agagcttaaa caaatgcttc aagaaataga tatcgatggt gatggtaatg ttagttttga 540
agaattcgtg gatatagcct ggtcagcaag ctccagggcgt gatcccgatc acactatgtc 600
tttgaggagaa gaagaaaaag agctaagaga tgccttcctg gtatttgata aacacaacag 660
aggatatatt gtctcgctag atctccgagc cgttttgcat tgtcttgag aagacttatc 720
tgatgaagaa attgaagaaa tgattaaaga agttgatgta gacggagatg gacgaataga 780
cttttatgaa ttcgttaatg ctttgggtga accaggcaat gaggatagct acgatgatga 840
cgacgatgat tacttatcat ttataacta gaaaacatta agatatatgg tttttatgta 900
cctgtgttcc cagagaactt catccataat caaataagct gcctaataaa caattaacct 960
aattataaag tttaaatata cctatgcctg ctacaaaaaa aaaaaaaaaa aaaaaaaaaa 1020
aaa 1023

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<210> SEQ ID NO 57
<211> LENGTH: 1179
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

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<400> SEQUENCE: 57

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ggggctttat aatttgctgt tgaaaaagat agggctccaa agtcctattg ccaacaaaaa 60
aacaacgcaa gacattaaac aacttttttc aagcccatct gtatttataa aaacagtgcg 120
aaatgtttct gtgggactgg ttacgggaa tgctgggata tctaggattg tggaagaaac 180
ctggaaaact attattctta ggactggata acgcaggcaa aactaccctt ctacatatgc 240
tcaaggatga cagactggcc cagcatcttc ccacgttaca tccacatca gaggagcttt 300
ccattggtaa catgaggttt acgacgttcg atttgggggg ccacgagcag gctaggagag 360
tgtggaggga ctactttcca gcagtcgatg ccatagtgtt ccttggtgat gccaacgaca 420
gctcaagatt tgtagaaagc caggaacagc taaatgcct cctctcagac gaaactctat 480
caaatgtcc aatacttate ttaggtaata aaattgatct ccaggtgct gcttcggaag 540
atgaattacg aactagatcc ggcttggttg gccaaccac aggcaggc aaagtagcca 600
gaaatgatct acccggtagg cctctagaac tatttatgtg ctctatactc aaaagacaag 660
gttatggaga aggtttccgt tggttgccac aatatatcga ttaattatgt atttttccat 720
ttcgttctgt cattgagtta ggatattaat gtttgaggaa ctattggcaa cactgcaact 780
acctgattca tttcagatct taggtacttt acataaatat ctaaatatag atgttgccaa 840
tgtaattttg aacaacagta tacaattca atgtaaatta tataatttta gttaagttac 900
cttcttaaat ggtgtttgag tggctatggt actgaaatag tttgactttt tgtgttcttc 960
gataactaaa aatgatttct tgtggaaagt tacactcaga attacatagt taacttcttt 1020
atcagcagtt gttgtcaaga tttccatttt gagacgattg ttttgtaaat taggtgggaa 1080
tttttaaaat gttggactgt tttttaacat gcttttctca acttttgta caaataatgt 1140
ttgtccaca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1179

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<210> SEQ ID NO 58
<211> LENGTH: 453
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

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<400> SEQUENCE: 58

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gggggaagtt cgtggtggtta ttgtccgtat ccgcctgaca ttctgcccgg cttttcaatt    60
gttttccgag ttcgcgaata cattacgtgg agtggtcgtg gatttgaaaa gttttgcgtg    120
ttttaaatTT tgtgagtga cttcgcggcg acgatacagt tggactgtgc cgctaattgt    180
tgataactgg agataacggc tttgtaataa agtggtgaca gggatctctt cgggacgctg    240
aggaagggtat ttcaatcttg gttttgtcac tttttgaatt tcatagtaat catttttaat    300
cgagttatga aaccttgaaa tggccatttt cgcatttttc aaatttttaa taactcgaca    360
acagtcaatt ttagagaaaa attacaaggg accttttttg ctcagaatga cccaagttat    420
ccgaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa                                453

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<210> SEQ ID NO 59
<211> LENGTH: 532
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

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<400> SEQUENCE: 59

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ggggagtggc aagtttcata tctgtgaatt tgtgtttgt tacattttct ccggcattac    60
agataatcgt tatgaagaag ttccccttag tgctgacatt tgttgcatTT ctgtggattt    120
gggaggctaa tggatttacc gcagaacaaa taaatgaaat tcgtagtatt tgtagtgaag    180
aattaaaaaa aattccacgt caaaaagggtg atatgggttt tccgggaatt cggggtgtac    240
cagctccacc atcttttggg gcaatcggac ctccaggaaa aactatatat ggtctcccag    300
gagcaccctg aatacccggt ccaatgggag ctcccgtgac ggcaggacta cccggattgc    360
caggagttaa aggtgatgta ggttcctgta gcagaaaaata atttgaagt tctgagtga    420
aatttaaaac tattcttact tttgacatat tatgtagata tttgctgttg tatcatccaa    480
ataagtatca ttagaacata caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa          532

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<210> SEQ ID NO 60
<211> LENGTH: 707
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

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<400> SEQUENCE: 60

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ggggacagtc accactcgac ccagtcaaca taagcatcat gaactcttac agtgtggtat    60
ttgcgtttgc attggccgct gttgtttag ccgaaccacc ttctggctac aactacaacc    120
ggcccagcgg ggggtggcgc atctccttcg ggggaagcag cctctccttg gggggtggac    180
tgtccggcgg tgggtgatac acggctgtat cgtctggtgg tcaaactagc gaaggagctt    240
ccgtagaccc acagcttctc gaacaagtcc gtcaaattct gctcaaagaa gaacagagct    300
cttcacagcg cgggtggtcat ggtggtggtg gtggataccc aggaccatct tcccaatacg    360
gtgtccatc tcctcaatac ggagtacca gctaccaata ccgcgtcgtt ggaatcgatc    420
tagagggaat caaacaagcc atccaagttg ccagtagaaa ccaaatctca cagggaacaa    480
gctttggagg ataccccagc ggacctagtt cgataccatc cgggtcttac ggagcccctt    540
actaaggctc tagaactgat ttcagtgtga ataccatctt ttaccatctc agacgggtca    600
tgatgcattc aataccatca agtttcaacc ataccatcaa aagttgaatg tttgtataaa    660
gctttcgtag gttattcaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa          707

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<210> SEQ ID NO 61
<211> LENGTH: 715
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 61
gggacaactg tcaaatat ttt aactcccaac ataacctgta acctgtgtaa gatcttgatt    60
gacacaaaaa atacaaaaat ggtcaaggct tccgagacag ggggcgtgaa gcccatgtcg    120
atagcaggtc gctttataaa cgaacgagaa cgtttactag gaatgacagc tgcagaacga    180
gactttcgca aacagtggct aaaagaccaa gaattgtccc attctgagcc gaaaaatgtc    240
cctgaaatgt ataaagctac ccataatcca atcaggaggc tctacagatt tcctctggat    300
accttaggta aaatgttgga gcctgttttg ggattacaga gtgcttctag agtgagatac    360
ttcacccgaa aatttctttt ggctgttgca ggtgcttacg ccttgaccta ctatgttaaa    420
tacaatacca atgactggac acgtaagaac ggaatgagaa tactcaagtc taacatatca    480
gtacatgaag gtgaccagg ctatcctaga gtatctcaa ggagtaaacc atcagattat    540
ggtgatcgag gattcaatga taacaaatta aacttgtaat atatttatat gaaaatattt    600
agtgttcgtt ttaggatcat ttatttgttg cttgcaaatt ttaaccataa catctttgta    660
taataaagtg caagaactat tgtaagaaaa aaaaaaaaaa aaaaaaaaaa aaaaa    715

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<210> SEQ ID NO 62
<211> LENGTH: 1242
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 62
ggggacataa aatctacaag atctacagta gatacagtgt ttcgtactac aatgataaaa    60
aacaatcttt caaagagatg ttacaagaag tgctcttaaa attatgggaa ggtctagtca    120
aaaaacgaag ctgcgaaccc acccaaaaag gcaccctgta ttcgtaagac ctacgataga    180
cttcaactca gaagaaacga ttctacagaa cctcattcca caaattcgag aagacattct    240
gaatgaatct ttagtttacc agaagaacac gccaacagtt agaggacatg tcgaaaacct    300
tattaatgat acagtcggag atcttaagcc aaaatttctc aactgtgctt taatagcgat    360
atacgccctac aagtatttta aacaggatca caccgaagaa gagttggtca aggtgggat    420
tttgggctgg tgctacaaat tgcaagacct cgccatgatt atcgttgatg acatactgga    480
tgaatcaaaa attcgttaca ataaacctcc cttgtatagg gtatgggaa taaaacaagc    540
tatectagac tctataat ttagaatcagc cgctaacttc ctagttttaa aatatttttc    600
tgatcacaag catttagtta aaatccaaaa ggatctcatc ctaaacatag cgacaactac    660
gattttcacag aaacaagagc tgtaaagta tgaatatagc gaattggaag tttttgaaaa    720
tttgattaag tcttttccgc ttttaataca tgctgttaca tctgcggtgt atttgctgg    780
tatcgatgat ccaaagatcc aatccatagt gaagaagttt tgcgtggata ttgctatatt    840
tggaataaga tatgatgact ttacagtatt tctagaccca aaaactattg gggaaaagga    900
caacacagat atcgtaggtt ttaagataac atggatggcc atccaagtct ccaaaatggg    960
aagcccccaa cagaaaaaga ctttcatgaa aactacgggt cactcagatc ctgaatcagt    1020
tgctatcatt tttgatatat acagggaact caatttagtt gaacatttcg ataaatatat    1080
gatggaattt tacgacgaca tgcttacaca aattcagaac ttgcctcctc aactgccaaa    1140

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agaatttttc tataatatac tagactgtgc tgtagcaaat aagatgtatg cttaataaat 1200
ttaaattatg tcgaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 1242

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<210> SEQ ID NO 63
<211> LENGTH: 1950
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

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<400> SEQUENCE: 63

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tttttttttt tttttttttt tttttttttc gcttagcaac aacacttttag tttatttttag 60
taatattttg tattttgaca acggcaccgc atttgggcgt cgaacgtta ataaaattat 120
ttttttcatt ttaattgtgg cttatttccc atataataa ttaatcataa aaatgccaca 180
aggaaatagc ttcagaacaa cataaagaaa cgattgttgg aaatggaaaa ttaaattaaa 240
aatggaaagt cccactataa atggaaaatt ttactttact ttttttgggtg ttaggacctt 300
cccttcacaa tccaataggt ccccaaagcg ctcgagtgc tgcacattta gcatactttg 360
ctccccacc attattgata gtcaagaaga gtattacaaa atgtgtatgc atacatatta 420
aaaaaaaaat actacgtacc aaagaaatca cgaagaagtg aaaagcaaca gtaatatcat 480
tctcaaaata agtttatcat ccacctttag ccctaaacat agattattat cgaactcatt 540
tagaatttag aatacatatt atgtaaaata aaaaaaccag tataataata aataatacat 600
tttactagtg aaagaacacc aatttgcgtg tggtagtatg taattgttta ggaagatctg 660
tgtgttggag tggtttcttt ttgcacaaga acattcataa ataactcaac gggtcacaa 720
tatgccatcg tggagaatta acagataagg aaaatcaatt tgcaaagcat acaaatcagt 780
caatgttaac ttacaggaca cgatgtgata ctcatatgtt cggttcttct acccactctt 840
ttttcacggc agaagtatgg tcagtaccgt attcagattg caaagttact tacagtacgt 900
aaatccttca ggtggacaag ttacgtactg tataacataa atatatttta aaaaggtgca 960
ttttaagaa aaataaaata tttgaatcac cctatttgta aaaagtaaca atatgggtct 1020
atgaagacag aataataact taattgtgta tcatatatat tcaaacctg taaacgagct 1080
ttttatagta taacgtatta tcaatttggt ttaaattctt tttatagtat aacgtattat 1140
caatttgttt taaattctta gaagattaca aggattccat ataaaaatg aagatatcaa 1200
acaagtggac aaaataaaat acttaggagt ctggatcacg gaagctttaa atccgaaatc 1260
agaaattcga tcaagaatag agcaatcaag agcagccttt ttgaatatga ggaaatttct 1320
gagtaaccaa agattcaatc tgcaaatccg atatcgatg gtaacgtgtt atatccactc 1380
tattcttctt tacgggtgtc aagcttggac tgttaatgct gacttaatga gaaagctgga 1440
agcttctgag atgtggcttt ttaggagaat attgaaaata ccatggaaaa actgtttagt 1500
tttgaaatta gtttttaaat aaaaaatatt ttaaaaatta aagacaaatt attaaactcat 1560
taatcataaa ctttgttttt gatttattta tggacagcct tgctacaaaa ttccctcatt 1620
ccattcattc taacagctct attgcaccaa aaactcatc tcgaacagaa gcttcaacta 1680
acacaggtta gcgcagtgtg caatatggtt gttagcatta aggggcatta accttcaaat 1740
tgacaactca ttctgactga cacaacgtc aaaatgtgac aatgtgatg ctaaatatgt 1800
tggaacacat acatagaagt gataagtagg agttattaca gctgattatg aagggtacaa 1860
ttggaagggg tcctagtgga ctacaaatat cctggctgaa aaacattcgc gactggacca 1920

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 gggttaaacac acagacgttt ttcagagccc 1950

<210> SEQ ID NO 64
 <211> LENGTH: 776
 <212> TYPE: DNA
 <213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 64

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gggtacacat aacctataaa aaaaacatta atttgattta ttttgaagt tatatgttgc 60
agttcaagtt gattctcagt tggagttgac tccaactagt tggagtcaac tccaactgaa 120
atgagcagta aaagttgatt ttaaaaaattt aaatcaactt ttactagtgt gagttgactc 180
ttcctggatc gattcagtaa atgttgatta tacgagaatc gcaagtgcac ttttgatgag 240
tgtgcgtttc tttgtttgga cgttttcaac tacttattag tatggcctgt aacgtcgccc 300
cgttgggtg aattattctg attcgatttt ttgcacaaac ttactcaaag aaatacatcc 360
gtataacaat cettataaca aatacacagg gtgtcacgcg gtagcgcggt cgaaaaattg 420
tttaaccaat tttgttgtag caaattcaca aaaataattt ttatctactc tatctcattt 480
atgtaaatca gcggttctca atctgtggta catgtaccac tgggtgtaca aatcattatt 540
tgcggtcctg ccaaagacaa accattttca tttccaataa tgacacgagc cgtctcaccg 600
tgctcggag agcacgttac accgtcggtc cccctgggct agtgtacatc gacactagtt 660
acttgaaaca gggttaaaga tgtaattggc gccggaactg tccgaaaggc aaaaatgcca 720
tacgatatca tatattatga aagtcggaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 776
  
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<210> SEQ ID NO 65
 <211> LENGTH: 1191
 <212> TYPE: DNA
 <213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 65

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ggggacaagt ttttttggat ccatcaagtg ttttcaaat ggctacacac ctagacgtgg 60
ataaaattat tacaaaactc acctccaaag aggttcggga gagcaagaaa atcaaaactaa 120
taagcatatc tgaatctgat ataaaagcgt tatgtttcaa gtctatgagc acatttatgt 180
cacaccccat gctgctcgag ctagaagcac caatcaaagt ttgcggtgat atacatggac 240
aatttctcga tttgttaaaa ctgtttggat ttggtggttt tcccccgac tcaaattact 300
tattcctcgg agactatgta gataggggga aacagtctgt agaagtcata tgcttattgt 360
tagcatacaa aattaaatac cccgaaaatt tcttcttact gcgaggtaat catgaagcat 420
ccgcagtatg taagatatac ggattttttg atgaatgcaa aagaagatat agcactaaaa 480
tattttaaact atttaccgat gtttttaaca cattgccggt ggctgccatc atagacgaca 540
aaattttctg ctgccatgga ggcttgagcc cagatctctt acatatagga caaattcgaa 600
atattcagcg tcctattgac attcctatto aaggtttact ctgtgattta ttgtggtctg 660
atcccagtac cgagcctggt tggacggaaa atgacagagg agtgtcattc tcatttggtc 720
cagatgttat taataagttt ttaaggaaac atgactttga ttaatttgc agaggtcac 780
aggttggtga agacggctat gaattcttcg ctacagagaa attaataacg atattttcgg 840
ctccaaatta ttgtgtgata tttgacaacg ctggagcgct tatgtcaata aatgaaaatc 900
ttttgtgttc atttcagatt ttggagccaa caaaacatat tgaaaaaaag aagtgattta 960
  
```

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aaaagtgaat tagatttatt tatggatatt aatttaagta ctaagtagtt acttattgac 1020
tggtattttaa aaacagaatc acgtaaagta acaaattaaa aaaaaaaatg taaagtattc 1080
tgctcgttac atgctttaca tggtatttgc atgacctttt acgaaattct gttcatagtt 1140
gttaatagat aataaagatg caaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 1191

```

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<210> SEQ ID NO 66
<211> LENGTH: 854
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

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<400> SEQUENCE: 66

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```

tttttttttt tttttttttt tttttttttt atagtgtaaa actgattttt ttattttaat 60
atataccaaa acataccaaa gcttaaaaaa taatcaatta accttcataa aatttgggca 120
attcattttc taaaacaact ctctgttcaa taccagcttc agtgatgatc cccagtctga 180
ctacacctcc tgaagaacca tctcttgaca tggcaagtgc caatgtattt gtgacaaaact 240
tcacacattc ttccttgcct atattgggct tgaagttggc atctacgtaa ccataaacat 300
aactggaacc tgatcctccg attgacactt cttgtctaac acacatccca ccaattggta 360
tggaatatac ttgtccgctt ttctttttat cccaacctgc taccagtata ccagccatta 420
gcgaatctct ataattgtag caaagtctt ggaaaatggc ggcacctact tgtactttgg 480
gttcttcacc aagttccata ccatgaaaaa taagatgata agcaacaatg tctgcaattg 540
cttgtgtatc tgctgcagat cctgaacgac aacagtatat atggtcagtg actttgggtga 600
gtttgtctgc taccgggttt gcaatgtagg cccagtagt tgtgcgagaa tctgctccta 660
taacaacgcc tccatcaaac tccgcggcca taatagaggt tctgtactg tgagcggcat 720
ctctccaatc attaggacca gtcattgcac catactcagt cataagaggc attttttaca 780
agtttaatga aaagaataca agcttagaaa aattacactt gtaatcctgc aatgcaatat 840
tttgccagtc cccc 854

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```

<210> SEQ ID NO 67
<211> LENGTH: 1162
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

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<400> SEQUENCE: 67

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```

tttttttttt tttttttttt tttttttatt ataactatct atattttagt taatacatct 60
taaaatacaca gtacacatta tatacaacta ttaattcaga tttttttcta tccagtcaac 120
aaaagtagta actctggtgt agacaccggg atatcccttt tcagcgcctc taaatccata 180
ggaaaccact ccaatcagat aatatcttat aaattcacca tcaaaactgc cccaaattaa 240
tggaacctct gaatctcctt gacatgcctc ttggcggcca tccgccgctc ctgcacatag 300
agttctctcg tcaattgttg ctttagcccc aaaggcggca gcgcattttg atgtgtcaac 360
tactggaatc tgggctattt ggagggccga acttgaaggt ccattataat atgtggctcc 420
ccaaccagca actacagctg catattttac aaaactttgt tttctgaaat tctgtcaat 480
tggttagacat acaggccata cccaaggatt ggtgggggct ctttccaaag taagaattgc 540
gatatcactg gtgtatttca cgggaactga gtcttcgtga actttagctt tgatcaatgg 600
tatatcttct ggttctgctc catcattagg attgtttaaa tctaagcttc ctaaagcagc 660

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gacatataag tctttcttgt tgtgtacaca gtgagcagct gtgagaatat gtctttctgt 720
aatgagtggt cgcacacaca accatcttgg ctttgaaggg tccctgctat ttctataacc 780
caaattaaca atgaatggta cctcatgtaa tttggctgga attccaccta caactctaaa 840
gtttgttaca ttactaacac cacatttctc gttattttaa acggcaccaa tgatttttgt 900
atcggttgct ggttggttag gttctggttc tggttctggt tctgtattgt ctgttgggca 960
acaaacatat actacagctc caaatttaca tgttgaacgt tgcagatatt ggcgcgtttc 1020
ctgattattg cttcttggtt taagcaaatt gagcatgtat ttacattcgt atatactttg 1080
acaaattcca tattcattcc tagctgtgta acagggtca ccttcttcaa cagccgcgtg 1140
agcaacacta aacaaaatcc cc 1162

```

```

<210> SEQ ID NO 68
<211> LENGTH: 1186
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

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<400> SEQUENCE: 68

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ggggcaaaact gtaagtatt atattttgca cgattgaaag acatttacta ttagcaaaaa 60
tgtctaaaga cggggaattg cagatgggga tgcgatgtgt gaagtacatg atttttgttg 120
cgaattttat gttcatgtta gttggattgt tgctgatac aattggatat accattaagg 180
ctatctacac cgatttcgat gctttcctta gcagccatag ctacaaagca tccgacttag 240
ctatagctgt tgggttcgtc attctagtggt ttgctttggt tggttgtgca ggagcaatta 300
aagaaagtgt tctactggtt aatctatacg ctttactact tcttgtaata gttatcctgg 360
aattgaccgt aagtatcatt gcttacaaat ccaggagtca cttggaagaa acactttctc 420
aggatatgtg gattagtatg gagtattaca tagccgatac tggatatatt tgggatgcaa 480
cacaatactc gttgcactgc tgtggagtac atggtccaaa cgactgggac agatttaaca 540
gttcagacta caatctcaca gtcatttata gttcacaaga cgactcaaca agttcagact 600
tgccacaaat aaattaccca ggagtttacc aagtaaccaga gagctgctgc agaaatacca 660
aatgccaaag tatcgcttct ctttacatga gaggttgctt accgaaaatc cactatataa 720
tctcgcaaa tgctcttctg cttggagttg gggctatgtg cataacattc attcagcttc 780
tcggtgctac atttgcccat cttctggcca gatctattag aaaacttaaa acacagattg 840
aagtggaaag atcaataaga agacaacaac tgtacgagtc gcttgcgaaa tctaacacac 900
aagagaaagt tagtccagtc ctatacgtgg cagagtcttc tgaagcttaa gaattcgtcg 960
tgtgttatat ataaaaataa tgatttaaat atagatttaa atatagatta aaccattgtc 1020
catttcatta cactcatgta tattgtgtta gtgtttacag ataagttata atatatacct 1080
ttctgtttt tgtgtattct ttactaggtc tatgtatgta gattctttaa atgttaaata 1140
tagaataatt ttaactgaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1186

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<210> SEQ ID NO 69
<211> LENGTH: 1002
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

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<400> SEQUENCE: 69

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tttttttttt tttttttttt tttttttttt ctttaataaa tagtatattt tgtaaatttt 60

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tttatcttac ataatacaaa aaatatatac attagtttta tttatgtttt atttatattt 120
caattattat tctaattctt cttcttaaca tcgtcacctt ctggattttg gtgttttgta 180
aacgttagga atacctgttc tagactactt tgtcccaaag aatagtcttc aatattcaga 240
tcacttcgct tagctctttc taatatacca aacatagtgg accatgccat ggaagtgtcg 300
gttatataat aatacaatag ttcttgatgt ttctctctaa gatgagcata aggaaattta 360
tctttgatat acttctccag tgactctgta tctgcatgta ccagaccacc gctctctggc 420
aatttcttta gttttatggt taaggtgtat cctccgcaa atttgttttt aagatgctgt 480
gtggatccaa gacatttgaa attgccgttc accataatgg ctattcgagt gcacaaagct 540
tcacattctt ccattgctgt agaagttaaa acgatgcact tgcggtgtc tcgaattttg 600
cataatgaat cccacaggta acgtttcgtt gctggatcca tacctgttgt aggttcgtcc 660
aaaaatagta ctggcggatc ccctatcaac gacaaaacag tacttaactt cctcttattt 720
ccaccgctca tctctttaac tttctgtcc aaatgacgat gaaaatcgaa gtctcgagac 780
aagaaattcg caattctttg ggttctttta aactctatct ctctgagtag gcagtacatg 840
ataattgttt ctcttgctgt catatcatcc agcaaagcgt cgaattgagg acagtagccg 900
atgtttcgtt gtacttgctt cagttgcgtt tttacactct ttccttcgat ccatgtatca 960
ccgtaagata cagtttcctc tccgctcctc attttaaatc cc 1002

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<210> SEQ ID NO 70

<211> LENGTH: 1322

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 70

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gggtatatga ccacattgtc aactattaga aagattctgt tgccaaaaat aattctagac 60
ttttagtagg tataatactg ttgtaaggta ttacaataca tagggtagta ctactgcttc 120
ttcttgtagt tccttatctt atcggaggtt ggcgatccgt accttattga cggtgctct 180
gaaaatatct actgagctgc aatctgcaat tataccactc tcttaggttt cttagccagg 240
atatttaate ttttatctta tccttaattt taccttgcct tttactacaa cacaggtagt 300
aaaaatgtga taccaaattg gatagtttct ttctgaggtg ttactctata tattactgtt 360
gaaatatagt ataaatatgg acatcttccg aaaacaacta gacagaatat gtatactaaa 420
ctcacagtaa agatgcacga gaaataaaca aaccaagaca cgtttaatgt tacgaggagc 480
actccgaat cctgatttac atctatctat ctaattagcc tctttcggtc catctttgga 540
aatgaacctg aagaaaccca atccttttct attattctct gtctgtcgct atagtcattc 600
acctagagcc cactgcttcc ttgatcatct ctgtccatct catttggggc tttttctgc 660
ttagtttata ttcccatggt ctccaattta taagaatttt gttcaatcga tcttctttgt 720
gtcttatatt gtgtccggca aatctccatt tcaattttgc aacttcttgt ctaacatccc 780
taacttttgt tttactctt acccaactcg ttcttttttt tatecattaa accttgatta 840
cacgtaacga gtattgtagc gagacagtgt tctcgcccg gtgcttgttt ggtataaaca 900
tactaacgag tacttgccg agcactcgac ccagtcatat ggcgagacag tcactcggat 960
ctgtttatac atatttacta agccgagctc tcgacctccc actettcaat cgtatactcg 1020
ccaatccact gggtatgtgt aaacaacact cgctgtgtaa ctgtacatgt taccattacc 1080

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acttcatcag aggagacgac ttgtgttaat caatgttatt tgggattctc aaaaatagct 1140
aacaaatgga actcagatag gacaataaag tgtagtttaa ttctacagat aagtcacacc 1200
cgtgcttatg aaattataaa tatttggagt ataaaaataa acaaaaacgt gatgcagcat 1260
ttaaatattg ttggttttta aacttaagga gtaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1320
aa 1322

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<210> SEQ ID NO 71
<211> LENGTH: 761
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

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<400> SEQUENCE: 71

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```

gggggacata tgggtgacata actcattcaa aatccataaa aaagtttcaa aatgagttta 60
ggagttcgtg aaatatatttc agtaggctca aaattagtaa gaccaagtgt ccagattggt 120
ggtc aaagat gttgctctag cggctctaaa gatggatatt tctatgtaa cgacaaagaa 180
cccagtatgg agtttggggc tatcacagat cgtgctgccc aaacaatgtt ctttactgaa 240
ttattcagag gatttgggtg tactttggct cacattttca aagaaccagc aactataaac 300
tatccctttg aaaagggacc tctcagtcct agattcagag gtgagcatgc cttgagaagg 360
taccctctg gtgaagaacg ttgcatcgcc tgcaagttgt gtgaggccat ctgtcctgcc 420
caggcaatca caattgaagc agaagaacgc gcagatggct ctagaagaac cactaggtat 480
gatattgaca tgacaaaatg tatttactgt ggtttttgcc aagaggcttg tccagtcgat 540
gctatagtag aagggtccaa ctttgagttc tctactgaga ctcatgaaga acttctctat 600
aataaagaaa agttattaaa caatggcgac aaatgggagt ctgaaatagc cagtaatat 660
catgctgacc atttatatcg ttgaaaatat atagaaaatt gtaaaaagtt gtagaatata 720
tcttattaaa caaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 761

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<210> SEQ ID NO 72
<211> LENGTH: 2041
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

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<400> SEQUENCE: 72

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```

tttttttttt tttttttttt tttttttttt gataacgatt tctaaagtgg aaatcgaaat 60
gtcaaaaaaa cttaatttca aagtaaagtt atggtcatt ccaataaaaa aacagtaaat 120
ttcattgtgt atataatttt gtaatgtttt tgtattcaat caaaccaaaa ataaccact 180
aacaaaaaaa atagagtctt ttaccacctt ctccattaaa ggagattact tcactacaca 240
aatgctgatg gatgtggcga tgattgaaat gctcgaaacc gctacttgac caaatacgtg 300
tcgtttgggt ggtaaagctc gtaatccgga attacggaat attggaacc aattattaac 360
aagatgcttt gatacatcac agagctatgc taaatagttg ctaatgttat tcagcaataa 420
cattatcgat gggatgactg aggtcgatat taccattgct taaacacagt attgaaaaat 480
ttgtttcata cattatttaa atagtaataa ttaaattgta taataatata cagtgatgag 540
cacgctcctc ctccctctcc tctcagtcg tttcctcatt tctgagtgc gtgattccct 600
ataatacgat caactatctc ttccgctcgg cttctgtcct gagcttcct catggattca 660
gagaatgttt ttccactggc ttctgtact tggtcctgcc atcgagcagg tgagcgacct 720

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ctacttctgc gctcttcaac cttttccgaa attataagtc tctccagatt atcatcactt 780
cttgcaatat ggccgaaaaa ttttaaggcg gtggagaggc aagtagagga aagtcgagtc 840
tgaatattaa gctcttgga gattgagtga tttgttctct gttccgtcca tgagatccga 900
agcattcttc tccagcacca catttcaaag gcgtcaatcc tttttctgtc gtccgatttc 960
attgtccatg tttcggatcc ctaattaaat atgggaaaaa ttaatgcacg tactaatctt 1020
atthttgggt tcttcgacaa ggagcgatct tccagattt tcgataatcg actcatagcg 1080
tttttggcaa tgccattct cctacgtatt tctgtttcac aacatcctgt attactgatg 1140
taggatccta gataatcgaa ctgcgttaacc acttcaaact ggtctaaggc ccgtgttggtc 1200
tgaagtgaat taaatattg ttattaagta tattcaaatg ggaaataagc cacaatttta 1260
cctaaaaatg attttattaa cgtttcgacg cccaagtcgg gtgtcgttct caaaatacaa 1320
aataatacta aataaacaaa aatggtgttg cctagtaaaa aattcttcca ataatttatt 1380
taatctgact catttatatc ggcaattcag acacgtatta tacattttaa agtagacgac 1440
tttaaaatga tattgccaat attgatgagt tgcgttctcg ggactatgaa tttaaatatt 1500
ctactatcat aatttttgtt ttttgtttat tgatcttgag accacatcta ttgctttcgg 1560
cttccactag ctgcagcaga ctggacattt cttcttcgga tgcagttatt aatgggtgat 1620
catctgcata tctgagattt gagatcttct ttctcgcat agaaataaccg ccattccatt 1680
tgctcgatgc ttttctcatt atatttccc catataataa ccatagcgcg ctaataaaca 1740
cctatatatt tctatttcta tatctatcta tctatccttt ttcagccaa cgtctgcagt 1800
ccttctgtt ctaccattct ccattcttaa cgtctcgtct ttccatggct tcgtacactt 1860
cctccctcca cgatattcgg ggtctaccto ttcttctctt tctattggg ctccaatccg 1920
taatctttga tatccacct gtatgatctg ctcttctcac atgtccatac caaattgaac 1980
gtttttcttc gatgtagttg attatgtctt gttctagtgc cattcttcgt tttatctccc 2040
c 2041

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<210> SEQ ID NO 73
<211> LENGTH: 523
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera
<400> SEQUENCE: 73

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gggggtgtag ctttcgcgag caaaaagata ggtggttagg cattattttc taaaaaccac 60
atggatgaat tgttggaaca ttcagcccta gaggtgaaa aatttaagcc aaccgtagta 120
aataagctta ttgatctaaa ttatgactta ggaagccttt tagcacaaga cacaaatgaa 180
tttgatacaa atttattaag gaggcagaag gaagattatt tgcttaattt agctagagat 240
aacacccaat tactattaaa tcaaatatgg gacttaacta cagaacgcct agaagaagct 300
attgtagtga aattaccact tcaaataact ttattaccta ggatgaaacc actacctaag 360
cccaaacctt taacaaagt ggaacagttt gccaaaacga aaggtatata gaaaaagaaa 420
aaatccaagt tatcatggga ccagcaactc aaaaagtggg tacccttata tggatttaag 480
cgagcacaag ctgaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 523

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<210> SEQ ID NO 74
<211> LENGTH: 473

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<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 74
gggaaagtga attcactaac tatttgagta atttaaatgt caattgacct tagtttacca    60
gagctgccta tattacaccc aaggattacc gttgtgggag tgggtggtgc tggtggaat    120
gctgtgaata acatgatcca atccaatttg caaggagtaa atttgttgt agcaaatacc    180
gatgctcaag cgtagagaa gtcattatgc gataaaaaaa ttcaactggg tattaactta    240
accaagggtc ttggtgctgg tgccttgct gatgttgca aaggtgcagc agaagaatca    300
atcgatgaaa ttatggagca tataaaagat agtcatatgc ttttcacac agcaggaaatg    360
ggcgggtgga ctggaaccgg tgcagcaccg gtaattgcaa aagcagccag agaagcaaga    420
gccgcagtta aggatagagc gccaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa        473

<210> SEQ ID NO 75
<211> LENGTH: 409
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 75
gggagaaatg gttactttga acaagattta gtactaccaa atgttagtgt atatattatt    60
ctgcacgcat taacaattta tggattttat agaataacta ctactgaagt taaggggtca    120
gccatattat tcagtacttt tattggcatg ttggcaatat taggggtcac agctggagcc    180
catcgtcttt gggctcatag aacttacaaa gcaaaactgc cattacgagt atttttaatg    240
ttgttgaga cagcgccct tcagaatgat cttttcattt gggttagaga tcacagaatg    300
caccacaaat atacagacac caatgctgat cctcacaact cgaacagagg attcttcttt    360
tgctcatgtt gatggctatc aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa              409

<210> SEQ ID NO 76
<211> LENGTH: 1532
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 76
ggggaagaaa cgtcaattga atcaactaga cggtgatgtg ttcagtaatt gaatgtaaaa    60
tttaaaataa tgttgaaatt aatcaccttc atattcataa tagtgaccgt caatgcagca    120
gaaagaatca acaataatth aatttataaa aatgtggata gaaccataga tttacgtca    180
cagttagtaa aaatcaccag caccataact cttgaaaatg ccggcgcaga ccctatcaag    240
aattttctac tggcggagca accaaattta gttggacaga tagcatttaa aggtgccaaa    300
gactctgcc aagcaagattt aaacgtctta acagcccaag tagaaaacca gagcgataag    360
agattccaca aagttatctt gaggcagaat ttggaaccgg gccgtactgc aacagtgggtg    420
gttgaagaaa tactcattaa aagtttaatt ccatatccac atagtatttc ccagaaagag    480
aagcagttag tgaggtatth ttgtaatcat tatatttata caccatacac agtggttaaa    540
caaaaaactg atgttacatt aagctctaga agtattgaaa attattctaa attgaaacca    600
gttactcaga cagatagtag aatacattat ggaccatag gagaaattgc accttttgct    660
gtggatgaac tgatagttta ttacgaaaac aatgctccat ttttgacagt tgtccatcta    720
gatagaacaa ttgaaatata tactgggggt aacattgcag tggaagagca aattgaaatt    780

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aaacacacag gagctacatt aaaggggcca ttttcgagat atgattacca aagagacact    840
agtagtacac atcacagtat taaatcatac actactgttt taccagccac tgctcatagc    900
at ttattaca gagacagcaa tggcaacatt tctacttcag ctgtaaaaca ccgtaaggat    960
tggatagaac ttgaactgag accaagattc ccactttttg gaggttggca aagtctttat   1020
actctcggct acagtgtccc cagttaccag taccttttca aggctgaaaa tggagataat   1080
gtattagcta tgaggctcat tgaccatgtt tttgacgata tgtatgttga agaagttgtt   1140
actaacgtag ttcttcctgt tggagtcact gatatacaaaa ttcgaccacc ctatgatgtg   1200
gagagactat cagatgatgt tacttataaaa tatttggata accttgggcg taaagttata   1260
agactgaaaa agagggacct gattgaacaa cacattcaag atttgaaaat tacctataaa   1320
tggcaaccac gattgttgtt acatgagcct ttgctgttat cgttggcact ctttattttg   1380
ttttagctg taattatctg ggtccgattg gacttttcac ttgcagtgcc tgagcacagc   1440
aaaagagaat aactttttgt acatctatat taacattttt tgttaaataa attatgagat   1500
tgaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa                                1532

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<210> SEQ ID NO 77

<211> LENGTH: 107

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 77

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ggggatgact tcaatctttg gctatcgagg gccaacgagg aagaacgaga aagaggtggt    60
aaccatgggt acgtaagaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa              107

```

<210> SEQ ID NO 78

<211> LENGTH: 985

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 78

```

ggggattgaa aggtggtacc gggactgggt gagaggctag ctagatacat acctacctca    60
tgtctctttt taactaaetc ttcttgtatg tgtacgctat ttttaaggctt tatgcgcaca   120
ttgatatact gtagtgctat tataggattt tgtttatttt tcattaaaaa tgggtagaag   180
acaaaataaa taccaagatg tatccgagga tctaccgaa agaggacctg tggagagtct    240
gatctactgg cgtgatccca agaaatctgg tccagtcttt ggaggagtcc tcgtagttct    300
actcgtcttc acatattttt ctctaatacag tgtggtagcg tacgtttcac tcatcgccct   360
cggcgtcact ttagctttta ggatttaca aagtattgta caagctgttc aaaagactgg   420
tgatggacat ccattcaaa aatatctgga acttagaaga ttattcttgg tcgaagattt    480
ggtagattcc atcaaatctg cagtattgtt atggactctt acctatgttg gacgtggtt    540
caacggaatg actctaatta ttctcgtttg ggtcgccctc ttcactcttc caaaagtta    600
cgaagtgaat aagactcaaa tcgatgccaa tttggagatt gtteggacaa aattggetga    660
aattacttca aagataaagg cagcaatacc gatgggcaag aaagccgaag aaaagaagga    720
acaatagatt taacaacatc tatcagacta tattactata catatattaa tttattgttg   780
tttctttatt ccattaaacg ttcttatgta atgtttctaa atataattag tgtacatata   840
taagatgtta ttttaatgtt tttttatttg aattttttga tgttatttat ttcttghtaat  900

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acatagagtc gaagaagaat atagaattta acataataaa tgtgttcgag agaaataaaa 960
aaaaaaaaa aaaaaaaaaa aaaaaa 985

<210> SEQ ID NO 79
<211> LENGTH: 1829
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 79
gggggtatat atcaatgata ttacatatcg acctacgttt cacttaatgt tttgatttga 60
cttgttttgc aataaatcat gacgtttgtg caaagatata atggaacagc tatgaaataa 120
ctaaaccaca ttcaaatagc aaattcccaa ctaaacctct ggacaaaatt aacgcaccac 180
tttaattaat ctaaatatat acaatatgaa cacaaaataa aactaagtta cactggaata 240
ataataataa acacctacaa ataagtccaa catgacttta tcatgacctt aatttgcctt 300
atgtttcttt aaaaatttgt ttttgccgga aatgcgtaaa taagctagca taactctaaa 360
ttgcaaaaag aaaaaatca gttaaagtaac acaataaatt gcactctgggt caacaataat 420
accgtgtagg cccacctaca cggagactgc atttatgcgt caaagcatgc ttgatataca 480
atgttcaaca aaagcttgcg gaatatcttc ccattcttca ataacggcct caatgagttg 540
gttgtgattg acaatagggg gtctacaact tctaactctt ttttgagata gttcgataga 600
tgctctatag attgatgtcc ggactgttag gtggccactc taataataga atatcaatat 660
catgtaggta accaataaac tgctgagcca catgaggacg agcgttgtct tgcatgaata 720
aaaaattagg tccaagaaac ggagcaaaaa gcattacatt ttcgacaata atgttgtcta 780
agtaataatg ggcattcata gacctcgta cgtatggggac caactccata cgagcttaaa 840
aacaatttcc ccccaaaaca ttttagagcc accaccaag gtagttagg agagatattg 900
cagctggcaa acctttctcc tcgccttcgc cagacttcgc cagcttttag gcgttgtaca 960
ggacttatat tatacatata cgtaaaattt tctttttatt aataatatag tgaatgcat 1020
aatatatagt tattttggga taaattagga ttaattattt ttaatacaat tagtaatta 1080
ggtctagttt ttcgtaatat tcatttcaag aagcatttac ttgacaagtt acttgatatt 1140
ttaactactg ttacatttta ttttttttga aaataaatga actttgattt aaatacctag 1200
atagaacttt taaaagtgt ttacgatttt tatttacata ataactattt ttaactcaat 1260
gcgagtacat atatacataa atctattttt aacttgaacg gatcaaaatg ttatatcagg 1320
cttttatatt gcataaagta tattacattg tggttacctg acctgaaat tacgagtcag 1380
aaatacatat atcaggaatt tgctgaatag agttttacgc attacataag acataaaaaa 1440
tgactgaaat tacacactag gaaagggtgaa ttagaattta atggaattac gataatgaag 1500
aattttgaga atatatgtga ataattattt tgaaaatata agaaacgaca aacaaatcaa 1560
cgttttaaag aagaagaaag gaaaatacaa acatgatgga caagaataag tttcacggaa 1620
aatatgagtt ccgatattat gggacogatg aatcaagatt tagagaattt tttacaagg 1680
acaagacaaa gagaagaatc ctaaaaagga aaataaaaaa aaaacatga agataacaaa 1740
gaaaataaaa ttatttatgt acaaggatat acaagaattt ttatacaatg attttaagaa 1800
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1829

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<210> SEQ ID NO 80
<211> LENGTH: 1307
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 80
gggaataaaa aatttatttt atttatattt ttattttattt taaaaataa aaatattttt    60
tagtaaaagt aaagaaaaat tttatttaaat gatagttaat tagtattgtg agagaatatt    120
ttatttttat aaaagaaaaa tttatttttt gtacctgtgt tatcagggat tattaattaa    180
taattatata tttattattt tcgaatttaa aagagctaaa aaaattaaaa tttttattgt    240
aaaaataata ttttaataaa tttttttgta atgaaatggt attcgttttt aaatatatct    300
aattttttta gaaataaatt aaattttatt attaacaata tatttataat taaatatttt    360
tatattatta atattaaata tttttaggga tgagcttaaa aataaaattt tattaaaatt    420
taatttttaa ataaaaatta ggattaaaaa ttttcattat ttaaaatatg ttattattta    480
tttttatata ttattatttt tattttttta taatttttta ttaaaatata aatttaaatt    540
atttaaaatt agtaatgatg ataattattg tattaaaaaa ttgtatattt agtaaaaaata    600
tataggttta ataaaggaat tcggcaacat ttttttcacc tgtttattaa aaacatgtct    660
ttttgtatta aatataaagt ctcgcctgcc cactgattaa tttgaatggc cgcggtat    720
tgaccgtgct aaggtagcat aatcattagt tttttttatt gaaagctgga atgaagggtt    780
ggatgaaaaa aaaactgtct ttatttaatt tataaagaat tttattttta agttaaaaag    840
cttaaat    tttaaaagac gagaagacc tatagagttt tataaaatta ttaataagtt    900
tttttagtat taaatttatt tatataataa atttatttaa ttggggtgat taaaaataa    960
atttaacttt ttttatatta ttatattaat taataatttt ttgatccaat ttttttgatt   1020
ataagaataa attaccttag ggataacagc gtaattttat tggagagttc aaatcgataa   1080
taaagattgc gacctgatg ttggattaaa gtttataatt ggtgtagcag ctatattatt   1140
aagtctgttc gacttttaaa attttacatg atctgagttt aaaccggtgt gagccagggt   1200
ggtttctatc tttattttat taatatattt tagtacgaaa ggaccaaata tataaaataa   1260
tttttatatt tagacaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa                1307

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<210> SEQ ID NO 81
<211> LENGTH: 730
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 81
ggggattcct ttgtgaatgt ttgcttcgct ttctcccggt taccgttccg tgttgacacc    60
gtagaatatt gactgatctg tagtttgaat tattttttta aaacaatgat gtgttcatga    120
actattttct ttgttaatgt gtaaatgttg caacaagctg atctaaaaata gagagcaatg    180
gaatctgcga tggaacagtg cgagaccaag cctttggaaa ctctatcaag tacattaaag    240
atgtttgaca cttttaaatc tacggaagaa gaccatgaat cagacgagga aagctttcat    300
cttcggttat taggatgtga tgatgaagcg gaaaacggca tggaaatatt tgaactaaac    360
gaagaagatg aagatgccat actaaataag ttcgacacac gcgatgaagg aatggacgtg    420
gatgaatgca gcaacaaaaa agacagcgat gtttctaaaa acaatgttgt agatgaagtt    480
aaacttagtg aagaagagcg aaagctagat ggtatagata atttaataa agataatcgg    540

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atagataatt taaatggaga tgatgaatta ttaggaaata atgagatttt agaagataaa	600
acaacagaaa gtacctctga tgataccgaa aataaaatcg aaaatgaaat aaatgaaact	660
gagcctgggt gtgaagaaga ctcaaaagag accaatatta ccaaaaaaaaa aaaaaaaaaa	720
aaaaaaaaa	730

<210> SEQ ID NO 82

<211> LENGTH: 1761

<212> TYPE: DNA

<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 82

ggggagtga tgagctttca ttcgtttcgg cgagggatta gattttgtac tctgaattg	60
ggtcagggtta tttggcgcca tgaatcttct tggaaaagct ctcgtttttg tattgatggg	120
taagtacaca ggaaatttgc taaagaaaat tttgagcgtt cggttggggag ttgttagact	180
gaaaatatta aacagcttac atagcaacac ttacacgact ataactatta ttttaagctt	240
tttataaatc cttaaaaacg ttcaaacata aaataaaata ttggtattga taacggtata	300
ttatattttg cattttttgc ttttaagctaa ttgatggaaa tagtatccat atgttttagt	360
cttttaatgc cctattatac ctgttgcata actttatata atttagaaat atcttatcgt	420
gatcattttc tgtttaatcc tgtccaggga ataaaatttt tcttgggact ttcaataatg	480
caggatatctg acaacttttt tagttatgta ttgtagaccg atagaaagaa aacctgcctt	540
gtatcctgtc gagtgttcgg agctgccttt taattattac tattaacaat ttagtgcaaa	600
aaacgcgatt ttttttcgat ttttaacata aattaaaaaa atagattttc cagaatattg	660
aaaaagcttc aaaatggaga ttttttaaa tgaaaatctt tttttgacag atacttgcac	720
tattttattg ctgttttccc ttttagtaac accttaatat gaaatttaa aaaacttatt	780
ttttgacgtt gttttgcaac attttcattc acctttataa aaatgttgtt tagctcttta	840
cttttaactg ccgaattttg ttgcatgttt tgttgaattt tgattgtttt gtgtgaaaat	900
ttgaaacata aacgggcttt tgaatttgat gactgctggt gaagtaggta ttgagactta	960
gtttcttatt ttacacatag ctattaacaa tattgggtatt gaatgataga taaaagtatt	1020
tctttttacc acagtcagat tttttatata agtgtactat tttgacggta tacaccacag	1080
tgacgggata caccatttta ccacagttag attttttata caagtgtact attttgacgg	1140
tacacatggt catataggta tcatctttct tcttagcttt ctatagtcca tgtatgggca	1200
tggcctcctc taactgatcc catcaatctg taccctaagc aacttacttt caatttgctc	1260
tggctattgt cagagataac tagaagaaga atccgaataa cttcggcagc agtatgaaga	1320
ctgggtgttg tgttgaaaa caaacagata tcagtataaa gaaaatgata ttcaacaact	1380
agttgtattc tgccagttat gatctatgga gcggaaacta cgacacttac agagttatca	1440
gccaacagat taaaaacacc acgcagggcc ttgaaacgag ctatgtctgt gagagaacat	1500
aatatatgaa atgaggacgt gaaaagcagg gcgaatgtgc aagatgtaat tggaagaact	1560
gcccataatga actggaactg ggtaggacac ttggcatggc aaaacaacga aaggtgaacg	1620
agaaacattg tactttggag accacgcgag ttcattcaga gtagtagaag aagaccagaa	1680
aaatactggc tagacgacat caaagcaaaa gtgggagaca ctggcaccaa caaaaaaaaa	1740
aaaaaaaaa aaaaaaaaaa a	1761

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<210> SEQ ID NO 83
 <211> LENGTH: 557
 <212> TYPE: DNA
 <213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 83

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ggggagggtat tctgagtttg ggtatttttaa attgataaag tagctagtta agtaagaaga      60
caaaatgtat aaagtagctg ttttagtttg cttccttatt gcagcaataa atgctagccc      120
atacggaaact tatgggcatac aggataaaca tgtccaacca gttcctcatg ttcttgacca      180
tccccacggc tccccaggcc atgaggaaca cggcggatat ggtcctcatc atggtggtca      240
ccaagattat acgcacgggt ctcattggtca tgaggaacac ggcgaacatg gttctacca      300
cggtggtcac caagattata cgtacgggtc tcatgggtcat gagcaacacg gcgaacatgg      360
ttcacaccat ggtggtcaac atccccgtgc atacgggtcct catggtcatg agcaagagca      420
ccaacatgag tctcaccata cgtacgggtg acaacgcatat taataattgt tataatgtaa      480
catgtttgac tgttctttta atttaataaa ataataatat aaattgcaaa aaaaaaaaaa      540
aaaaaaaaaa aaaaaaa                                     557

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<210> SEQ ID NO 84
 <211> LENGTH: 486
 <212> TYPE: DNA
 <213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 84

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gggataagaa attggaatta agcccaaatt ctctcgaaac aatttttgtc gtaacattat      60
gctgtaataa ctgttgaaaa gtaattggtg aaattcggta ttttagata tttatattaa      120
ataataattc gtaggtgaat gcaagttatt atctagaaaa tttgaaggta acaatatagt      180
ttcattagaa tcatttcagt aactcttttc gcaatttttg tcttaaaaat aattgagaaa      240
cgctgtaggg ttaaaaattt aagttacaag aagtttagatt ttaggtgtag gcttaatgtt      300
ttgttttaaa tactgctctg gatggtgcag tgaagatgaa cgtaaaaaga aagtaagccc      360
aaattctcaa ttgaaaaatt tttactttca tattcgctgt ggcattgagt tgatgtgaag      420
aaatggtgga aataaaaatt ataattgtat atatacaaaa aaaaaaaaaa aaaaaaaaaa      480
aaaaaa                                           486

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<210> SEQ ID NO 85
 <211> LENGTH: 492
 <212> TYPE: DNA
 <213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 85

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ggggattttt tagacatttt gatattttgt cggtatacac gtttcgtgtc tcaagactta      60
aaaatgcgtt acgtggctgc ttactttatt gccgttttgg gcggcaaagc ctctcccaat      120
gctgcagatc ttgaaaaaat cttgggatct gtaggtgttg aagctgaagg agaaagagta      180
aagaaagtca tcagcgagct cagtggaag tctgttgaag aactcattgc tcaaggctgt      240
gaaaagtga gtcctatgcc agttggtggt ggtgccccag ctgctgccgg aggtgccgct      300
gctgctgctc cagctgctga agaaaagaaa gaggccaaga aggaagaaaa gaaggttgaa      360
tctgaatcag aagacgacga catgggcttt gctctattcg actagactca ttagttgtaa      420

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gatcaacctt gttttgtacc ttaatatata ttttttaagt caaaaaaaaa aaaaaaaaaa 480

aaaaaaaaaa aa 492

<210> SEQ ID NO 86

<211> LENGTH: 444

<212> TYPE: DNA

<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 86

gggagcactg ataaaaaaga tgggtgctgc acttcgctta acatgaaatt ctgtctattt 60

taatatagaa gtctatggga agaacctgga caagagatta tgtccagcag tgaattaaaa 120

tgaccatatt aattactgac agttttttta agaaatgttt ttttagtagt agtggtttata 180

attttaaagt ctttggtgtt tggaaattgg cctacacatt gtcccatgta cctatgtgaa 240

acccacgata aaaaatatcc catatgtttt tgtacaaatt acaactgtag ctataattct 300

tctatttgac tgatcacatc ctttgacata aagaaaaaac ttaacctga ttatgatcta 360

ttcttaaacg aagcaacatt attttattat acctatcgct tcttatagtc ttacaaaaaa 420

aaaaaaaaaa aaaaaaaaaa aaaa 444

<210> SEQ ID NO 87

<211> LENGTH: 340

<212> TYPE: DNA

<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 87

gggcattcac aaaattaggc ataacgtata tggtactagg tctcaaattg cacctaaatt 60

tcctaaaaac attagtgaat tccatacggt attaaattct gaagaaataa aaactaatag 120

ggggaacggt ttcttataaa aaatgacgat aataatcaga tcatgtcttc gtgtgaaagc 180

aatttttttg atttaagaca aatatcgaca ttttatattg acggcacttt tgaatactgt 240

ctaagacagc gattctcaat ctgtgtgtaca tgtacaactg gtgtgtacaat tcattacttg 300

cggtgtgtaca caaaaaaaaa aaaaaaaaaa aaaaaaaaaa 340

<210> SEQ ID NO 88

<211> LENGTH: 1447

<212> TYPE: DNA

<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 88

tttttttttt tttttttttt tttttttttt cttagtacta gataggattht atttatctgc 60

ccagttacaa aatagttata gtaagtaaat ataacaaata ataaataatt ataaggtgtt 120

ataagatctt aaaagtctgt ctggcagtta caaccacggt cgcataattat ttaagaactg 180

caaagatgta aacacagtac aaacaacatg aaaaatagct tattaggtat gaattgatta 240

aatagcttag aagcacttgc ggtggacaat tctggggcgg gattogtctg attcttgttt 300

ggagatccac atctgttgga aggtggagag ggaggccaag atggatccac cgatccagac 360

ggagtatttc ctttctgggg gagcgatgat cttgatcttg atggtggatg gagcaagggc 420

ggtgatttcc ttttgcatte tgtcggcaat acctgggtac atggtggatc ctccggagag 480

aacagtgttg gcgtacaagt ccttacggat atcaacgtcg cacttcatga tggagtgtga 540

tacggtttcg tggataccgc aagattccat acccaagaag gaaggttgga agagggcttc 600

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tgggcaacgg aatctttcgt taccaatggt gatgacttgt ccatcaggca attcgtagct	660
cttttcgagg gaggtggaag cagcagcggg gccatttcc tgttcgaagt cgagggcgac	720
atagcagagt ttttcttga tgtcacggac aatttcctt tcagcggtagg tggatgaatga	780
gtaacctctt tcagtaagaa tcttcatgag gtagtcggtc aagtcacgac cggccaagtc	840
caaacggagg atggcgtggg gaagagcgta accttcgtag attgggacgg tgtgggtgac	900
accatctccg gagtccaata caataccagt ggtacgacca gaagcgtaga aggagagtac	960
ggcttggtatg gctacataca tggcgggtgt gttgaagggt tcaaacatga tttgggtcat	1020
cttttctctg tttgccttgg ggttgagtgg agcttcagtg aggaggactg ggtgttcttc	1080
tggagctaca cggagttcat tgtagaagggt gtgatgccag attttttcca tatcatcca	1140
gttggtgatg ataccgtgtt caatgggta tttcaatgtg aggatactc ttttgctttg	1200
ggcttcatct cctacgtatg agtctttttg tccatacca accatgacac cttgatgcct	1260
tgggcgaccg acgattgagg ggaagacggc acgggggtgcg tcctctcgg cgaatccagc	1320
tttgacata ccggtacct tgtcaacgac aagagccgca acatcgctgt cacacatgtt	1380
gtcttttgtg gttgatcact gctcactaga cagaaaaaca cagctaataa gcttgaatgc	1440
gaccccc	1447

<210> SEQ ID NO 89

<211> LENGTH: 1444

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 89

gggagtcgca ttcaagctta ttagctgtgt ttttctgtct agtgagcagt gatcaaccac	60
aaaagacaac atgtgtgacg acgatgttgc ggctcttgtc gttgacaatg gatccggtat	120
gtgcaaaagct ggattcgccg gagatgacgc acccctgtcc gtcttccct caatcgtcgg	180
tcgccaagg catcaagggt tcattggttg tatgggacaa aaagactcat acgtaggaga	240
tgaagcccaa agcaaaagag gtatcctcac attgaaatac ccattgaac acggtatcat	300
caccaactgg gatgatattg aaaaaatctg gcatcacacc ttctacaatg aactccgtgt	360
agctccagaa gaacaccag tcctcctcac tgaagctcca ctcaacccca aggcaaacag	420
agaaaagatg acccaaatca tgtttgaaac cttcaacaca ccgccatgt atgtagccat	480
ccaagcggta ctctccttgt acgcttctgg tcgtaccact ggtattgtat tggactcgg	540
agatggtgtc acccacaccg tcccaatcta cgaagggtac gctcttccc acgccatcct	600
ccgtttggac ttggccggtc gtgacttgac cgactacctc atgaagattc ttactgaaag	660
aggttactca ttcaccacca ccgctgaaag ggaaatcgtc cgtgacatca aagaaaaact	720
ctgetatgtc gccctcgact tcgaacagga aatggccacc gctgctgctt ccacctccct	780
cgaagagagc tacgaattgc ctgatggaca agtcatcacc attggtaacg aaagattccg	840
ttgccagaa gccctcttcc aaccttccct cttgggtatg gaatcttgcg gtatccacga	900
aacgtatata aactccatca tgaagtgcga cgttgatata cgtaaggact tgtacgcaa	960
cactgttctc tccggaggta ccaccatgta ccaggtatt gccacagaa tgcaaaagga	1020
aatcacccgc cttgtccat ccaccatcaa gatcaggatc atcgctccc cagaaaggaa	1080
atattccgtc tggatcgggt gatccatctt ggctccctc tccaccttcc aacagatgtg	1140

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gatctccaaa caagaatacg acgaatccgg cccaggaatt gtccaccgca agtgcttcta 1200
agctatttaa tcaattcata cctaataagc tatttttcat gttgtttgta ctgtgtttac 1260
atctttgcag ttcttaaata atatgcgacc gtggttgtaa ctgccagaca gactttttaag 1320
atcttataac accttataat tatttattat ttgttatatt tacttactat aactattttg 1380
taactgggca ggtaataaaa tcctatctag tacgcaaaaa aaaaaaaaaa aaaaaaaaaa 1440
aaaa 1444

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<210> SEQ ID NO 90
<211> LENGTH: 993
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

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<400> SEQUENCE: 90

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ggggagttcc tgtctagttt tgttgctgaa tgttatactc gtagaattga ttgaatcgaa 60
aaaaatattt aaaatgaaat ttaaattttc cgctgatgat gtaattgctg agaaaagaac 120
aacacaagga aatataaatc ttattaaacg atggctgttt gcagccgatg aaaaatatgt 180
accatctaaa ttatcagatg aattcatagt tctgtttcta ttgtcttgta acaatgacat 240
tgatgtgact aaaaagacta ttactgccta ctataaatta aggaaagacg cacctgaact 300
gtttgatgac agaacttccg agagagaaga tattcagaaa gccttaaaaca cactgagaat 360
ggtaagcata ccaaatcgga cagacgaaaa ctatcaagta gtgtatctta gtctaaaaga 420
tacagatagc agtaactttg aactgaatcc cgttatgaaa gcctcattaa tgctaataga 480
tatagaacac cacaatagcc caccagatgg agttatgttt ctagctgata tgaagggtt 540
cgggttttta caccgcttta aattgaatcc aatctcgta aagaaatatt tcaattatct 600
tggagaagga ataccaactc agttcaaagg aatgcattta atgaacggaa attatttcgt 660
ggatcaattg ttgagcattc ttaagggttt tatggcttca gaccttataa agagggtaat 720
catccatcaa gtaggctgga atccggaaga agcattccca aaaaaatgtt taccaaaaga 780
acttgaggga gacctagaat cagaagacgt actttgtgaa cggacattac cgctgttcaa 840
ggatcgggaa tatttttgga aggcggaaga ggaactaagg aaaagtgtac ttaataaaaa 900
atgcgttaca tgtaatagta ttaaggaatt acaattattt ttggaataaa tatttatagt 960
gccaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 993

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<210> SEQ ID NO 91
<211> LENGTH: 989
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

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<400> SEQUENCE: 91

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tttttttttt tttttttttt tttttttttt ctcttccgt attaaatcga tcagttcttt 60
agctctcctt actttttctt cccctgacag ttctgcttct gcctottctt tagtgctgt 120
agtttctttt tctgttttaa cttcttcaga ttctgtatct actttaactt ctttatectc 180
cttatttttc tcggctaccg taacttcttt acctttcgta ctttctgcgt tctcttcttt 240
tgctggttct tcttcttttg ctggttctgt atgcgtttct gacggactcg gttgctcttc 300
ggggggttta tcttcgatg atttttcaat ttctgtttcg gaggggctca attcttcttc 360
ggggggactt tcttcggacg tattcagagc attattatca ctttcgactc gtggtgtctc 420

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accagcttgt tcatgtgcc ggaagtttcc tgattcagct gaaatagaat gaactggggc 480
tgtactgaat cctgccttgt tcaagacatc atccacttta gcagaaactg tttctaaatt 540
agtacttctt gtaatgatat ctaaaggaa acccttctga ccaataaaat atatcgaggg 600
tacactcggg tctttataaa ttctgctaaa ctgctgggtga gctgtagagc ccgcaattac 660
tttgatagct acaaagtgat cttgttccag tttttctcca aggtcgccat tattgatgag 720
gtctgttatt ttttgtgact ttctgtcagt accttcaata tacactacaa aaacggctcc 780
tttcgattta gaaaaagcaa ccgcatcggc tatttctcca ctgtaccact tcattttaaa 840
aaaaaataag ttagtttaga cttttacaac aataaaatac tagcagactt ctaacaatta 900
aaaaagtaca catcagttat cgcaactaca aacacaaaat acaattttta acgtcaccgt 960
caccggtcac aatctgtcat gtactcccc 989

```

<210> SEQ ID NO 92

<211> LENGTH: 817

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 92

```

ggggatggcc ttttcgggtt caccgcgtcg ttcagcaaga gcttgcgatt tttatTTTTg 60
aaaaatagag agtattctct aatatttaag gacagcatgg aagacgattg ggctgtggat 120
aatcagagtg gtggagtgtg cgcctcaaaa attgcagaac tacctgaaat taagtgtttc 180
gctagatgga actgcgatga tgtccaagtt tcagacatgt cccttcagga ctacattgca 240
gtgaaagaaa aaaatgcaaa gtatttacc aattcagctg gtagatatgc tgcaaaaggg 300
ttccgtaaa cacaatgccc aatcgttgag aggttaacaa actctctaata gatgcatgga 360
cgtaacaatg gtaaaaaatt gatggctgtc agaattgtta aacatgcttt tgaaattatc 420
catttactaa ctggagaaaa tccattacag attttagttt ctgctattat caattcagga 480
cctagagaag atttactctg tattggtaga gctgggtactg taagaagaca agctgttgat 540
gtgtcaccct tgagaagggt taaccaagca atttggttgc tctgcacagg tgctagggaa 600
gcagcattcc gtaatatata aactattgct gaatgtttgg ctgatgaatt aatcaatgct 660
gccaagggat catcaaatc atagtctatc aaaaagaagg atgaactga acgtgtagcc 720
aaatccaacc gttaaattta tttctcattt tatattttat ttccaataat aaatatggat 780
aaaacacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 817

```

<210> SEQ ID NO 93

<211> LENGTH: 1186

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 93

```

tttttttttt tttttttttt ttttttttcc gcaatgcgga gacaaattta taaaaagagg 60
acttgtgcaa aatattgtcg aacatgtcaa aagaaccaac agaaattgtg ccatccactc 120
cctatattaa ccaaaacagc agtacaaaga aattaacgtt tatttaaata atatctaagg 180
atTTTTctta ataaaatgac aacacagtggt caaatctata agcgctaata tattttataa 240
ctttttctaa gtttggaacc aaaagtgtat actgtaaatg tttatgttta tatacagtgt 300
gtcattttaa gtagaaacat ccctgtaaca ttgaaatcc ttaaacattt caagagtttt 360

```

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tttaataccg tgtgtttact tttaaattag atatagatag gaatacatcc aatacatggc 420
aacactgctt cctcgtttcc cacacctgag tcgcgccaat tgactcagtc attcgtcgat 480
tctacagtag caatgcaact tattctcata aaaaatgttg ccgatttttag cgattccttt 540
agtctcctat ccctaatacg aaactaaaag tatggtaaag taataaaaaga ggtaattcgg 600
gacaacattt aaagggttca tttaaagtac catatcataa tcatcatcat cagcctgttt 660
taaatccagt gcaggacata agcctctcct gtttgatcc agaggccgtg cctctcctgt 720
acgggtttgt gtagtatgga tccaattttt cgttatcttt catcatcttc caatcgtgta 780
gggtgtcttc ctctctttcg gttatctgtt cttggatcc attcagttaa cttgcgtgtt 840
caccttctat ctttcatcct tgccatgttg ccagtccttc tccatttttag tctgcaagct 900
ctctccacaa aatctgtaac tctagttttg tttcgtatag cttcatttgt gatcttgtct 960
tttattttta ctctatcat tgaacgatcc atttttcttg tgctattctt agttttaaag 1020
cattcttttt gcagacagag tttctggatc ataggtcatt actggcagaa cagactgatc 1080
gaagactttt actctttaga ttaatcggtt cattgctgcc tttaaatcag tttttaacag 1140
ctccatatgc tgcccatcca tgtgtctatc ttcttgatac atcccc 1186

```

```

<210> SEQ ID NO 94
<211> LENGTH: 1033
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

```

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<400> SEQUENCE: 94

```

```

tttttttttt tttttttttt tttttttttg cgtagtctga cattgcgacc aggtttttgta 60
gacgtcttga actatttttg ttatttttta attgttgaaa tctaaataga gcggattgaa 120
tattatcatt tactaccctg tgacaataat attattattg tcacaaaaca gtaaacataa 180
atattctcat tccaatgttc gaacaacaat gaatgttaat atagaccagg actaatctgt 240
aaaaattcgg atggcattaa aatttttgca gataaagtta ggtgacacct ttagtaataa 300
taattgaccc atgctccctc tcaaacataa ccggaacatt aataaaaaat caaaatattt 360
aaaaattcag aaaaagatcc atttttttct gctttctttg cttatagctt taaaacgggt 420
cgttctggaa caaatccgta cagaacaaaa acagagacaa tgaatcatg tatgatgtac 480
gaccggtcaa aaatgtctta aggtattacc tttctgcaa aatagcaata aacacaaaat 540
aagggggcaa aacacgcgtg ttgttattca atgtctctta accacttttg tggcagttag 600
aaccttagta atccgcttag aaaattctta tagcttagtt aaatggtcta ccaaatttca 660
ctaaaatcga ctaacagat tctgcataat aaatttgcaa tataaatggt tttaaaaaag 720
ttcaaatttc aaaatctttc tgaacaaaaa gtagacaatt tagtagttgg ctaatttttc 780
cacatacaaa aaggcactcc acccatctaa tacacccac agcatcaaaa tcggaccatc 840
taaggggcct cagcaatgtt tcaaaaatc taacaacttt ccggctcata aacaaatagc 900
tttgtttaat aataaaaaaa taataatttt tagcaacgca aataattaat accggtatag 960
tttgacttaa tcttttaaat gctgtcagca gaattgctat tttatttttt aatcaaaagt 1020
tatoctcggt ccc 1033

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<210> SEQ ID NO 95
<211> LENGTH: 551

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<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 95
ggggacatta atttcaagcc taggttctgg agaattattaa ttaacatttc ctgcggtatt    60
gttgatgaa cattagataa gagaagacgt tccgatggag tgactaatct acgtgttaga    120
agtacttcat tatttatttt tatggatcct accttattta gaaagtcac aactacagct    180
ttacttgaaa gataaacgca tactcgggta ttagagattc ttgatgaata aataatattt    240
tctggttgga cgagtgggtcc tagttgcaaa agataatctt gcaattttgc gccattaatt    300
gaactgaaga tgatggcttg ttctttcact ggtaattttg gagtagtttg ttgagatgca    360
atagtagagt acattagagt gttttgagaa gtggtaggag tttccattgt tgataaagta    420
ttattcatca ttaattgtta cttgaacgat ttattataaa catatttagt tagggttata    480
atatgtatgt tgtgactggc tgaatcacta atgtgtatgc caaaaaaaaa aaaaaaaaaa    540
aaaaaaaaa a                                                                551

```

```

<210> SEQ ID NO 96
<211> LENGTH: 1050
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 96
ggggagaatt tatgaatata ggtaagcctt aatacactaa ttaagagtt taataattgt    60
atattatttt caaaaatggt ttaagtgtgt gactttgtag agatattggt ctgtgatctg    120
agcaggtttt gcacttgact ttttgagaat tgctacaaag gtcgattgca gcaattgtca    180
ggcgattgtg gaagtctgat atgataaatt aggagttcaa ccattacata aatatcatct    240
tcatcaatga gttttaataa ttcatgtgtc acatcttctg gtccagtaac tttgctatct    300
ttagtgttct tgatgacata gatgacttct tctcgtaata atggtggttg atatcctcta    360
tggtttctag tgacagtttt tctctttcct cattaattaa ttcttgaatg taattgatcc    420
agtgacacat tctctccaat tatatcagta ataattcatc atataacaat tcatcatatt    480
tcttcatca tttttgatgt tatttctatt aaaaatgtcc gtacctacat tatcctctc    540
ctctccctc atcctttatc cttcgtaagg atgtggtgac gttatggtat ttgacgaatg    600
gtttctatcc attcttctct ctcttgggcg cgggtgtgctg cctcagacag agagtaaccg    660
gtggcgcat ttttttggtc tgaccatcgg agtggctatc ttctctgagt tcttttacc    720
tctaccttg cttcaaccac caacctctcc atgccttctc ttctgtctgt aatgtgtcca    780
aagtacctca atatttttg gttgatgatg gtggaagcc tagtggtgat gtcgagttct    840
gataatattg agatatttgt gcgatgtgct acattatcca tattacactt aattaaatgc    900
acttttaaaa catttttttt tataataatt atgtaggtcg tttttttaat ttatcattaa    960
gctctaatac agttgagaga agccgaacct cagctatgta tctaataatta tacagtatgg    1020
tacaaaaaaaa aaaaaaaaaa aaaaaaaaaa                                     1050

```

```

<210> SEQ ID NO 97
<211> LENGTH: 1391
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 97

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```

gggggaaaaa atgtttggat acaatgtatg tatacaagtg ggctttgatg atgtgttatt    60
gtgttttaag tgctaaaaat atttttttat attatgttca caaaaaaaag catgtgtgtt    120
ggtgacattg ttaatcctcc tgtcagttaa gtcctttatt catcttaaac aataaacttt    180
taaaacatga gcttcaaaaa agagcataaa tgattattat tttaatgctt ttcaaaatgg    240
ggttttagat gtacacgata tatattatgt tttgcataaa tgatactttt attatatattt    300
tattatttgg tcttacttta ttgtagttat ttttttgata tttttttgtt cttactttgt    360
tatttttttg tagattgtta atttgcaact aaacgatcta cttataatag cgtagtagta    420
aattaacaaa acgaaccta atatctacca cgagttaact ggtaagacc atacagaaat    480
aaataaattg cttaattgca attaaaacag ccgtaaaaa tgataagaaa attaagaaaa    540
acaatatttt ttctaataat aaagtaataa aggcagtttt tgtttttatt ctattcagag    600
ttggaccacc atctccatat agctatttca gcaccccatg catctttagt gaagctatgc    660
agtcacaact ctgaagcgaa tattaacaac cctgaatatt taagggaac catcgcgata    720
caatgattcc accttttgag acgcaatcta gcgacatctc tcgcaaacg aggaaaacaa    780
cgaaaagccc tagatacaaa gtttactact ttttaacaaa ttagaataat tgaataaaaa    840
atataataaa caatatttta aatccacgaa tttcgttaat aaactgcttt ctggctgcat    900
cctgtatatc tggctattta tatttagctt aatatttttt ctcttttaat atttggttca    960
agatatagag tgttttagaa caaaattaca ctaagggcgc tcgcaaacac agccacttgt   1020
ggccgccacc ggtggcagtg ctgactgagg tttgtatgta ttttaaatgg attcggccca   1080
cacactatgt ttccggtgat cttcgagcga caagccacga caagctatgg cgttggccgt   1140
ttctggctac atgaagtcgg tggcgatcac aaaacagcca ttcgtccaga gagagaaaga   1200
gttaaaacaa catcataaga aagagcttgg atacaaaaat aggcctaccag aatatatgaa   1260
ataaatagtc ggtctgttta gccatgaaga ggaaatggat gaagaacaac tacggaaaca   1320
aactgtaact cctaacttca aaattaaaac accatgtatt gaaaaaaaaa aaaaaaaaaa   1380
aaaaaaaaa a                                     1391

```

<210> SEQ ID NO 98

<211> LENGTH: 515

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 98

```

gggggttact tacctgtaaa cgaatcattc ggtttcactg ctgatttacg ttccaacact    60
ggaggtcagg cttcccaca atcagttctc gatcactggc aaatcttacc tggtggccca   120
atggaaccca gtaccaaacc ctatggaatt gtgcaggaca cacgtaaaag aaagggctct   180
aaagaaggac ttccagacct ggcacaatat ctggataaat tataaacaac taagaaactt   240
aatttatgta cagattattt aataaaatta tttcaattta ctcaacggtt tttatagtta   300
attgtatttt tgatattttt attctgataa gttttcagtt ctctcaaatt gatggcaaca   360
ctagaaatga aataaactaa ataatctgac taatatttta tgtttgctat atatattttt   420
gttaacagtc cagatatatt tatatttatt aatttgacat caaaagtaaa tctgatgaaa   480
cattgaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa                                     515

```

-continued

<210> SEQ ID NO 99

<211> LENGTH: 580

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 99

```
gggggatgta tacattactg aatattgttt gcttaagtaa taataataat acaaaagagt    60
catcatgaag ttcttggttt tcagcttggt ctttgctggt tactatgcaa atgcagctat    120
tactcccgaa caagctgaga agatcaaaag tttccacaaa gaatgtcttc cagaatccgg    180
agttaatccc gaattgggtc aaaaggcaag acaaggagat ttcgccaatg acgacaagct    240
aaaagcacat atcttctgcg tctccaagaa gatcggtttc caaaacgatg ccggtgaaat    300
tcaagtggaa gttctcaaag ccaaagtggg tgctgcctta gaagatccag ctcttgctgc    360
ccaattgatc ggacacctg ctaagcaaca agcaaatgga ccgaaacag cctttgaaac    420
cataaaaatgc tatcacgaaa agacaccaat tcattcttagt attatttaaa tattttgatt    480
ttgttataat ataaaaaact tctttttgaa gagttgttat aaaataaatt ttttatcatt    540
atatgtacag aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa                    580
```

<210> SEQ ID NO 100

<211> LENGTH: 913

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 100

```
ggggagtgtc aacaatgatt tatagcagat atctgtggat tgtgtgtgta gtgttatcac    60
tattttatca gacaaattgt gaatgcccta aaatatatac tcgcaatgaa tggagcgctc    120
gaaaagcatt aagtaccaga ccgttaagag aagatcctcc accatatgtg gttgtccatc    180
attcggccac tcgctcatgt ttttcagttg aagattgttc aaaacttgta aaaagcatcc    240
aagattacca tatagatcac aatggatggg atgatattgg ttacaacttt ttgattgggtg    300
gtgatggaac tatatacgaa ggtagaggat atggtttaca tggtgcgcat tctattccat    360
acaacgcaag aagcttaggg gtttgccctt taggaagttt taaagatagc aatcctccta    420
atgtacaact gaaagcattg gaagactttt tgtcttgctc agcagctgat cacaaaatta    480
ttgcagatta tcaccttate ggacatggc aagctgataa aacagaatgt cccggggatc    540
gagtgcattg agttatcgaa aaatggcctc attttgaagc caatccacaa gatgcttccc    600
caaagaaaact gtaaacatag cgaagttacc ttttctctta tggaaataaac acctctctat    660
cgcaatgttt ttagattaca attattaata catgtaaata tttaaaagac tgtatatcta    720
ctcactatctt aaagatgtgc gaaaatatat cactatcttt aaaaaaaaaa aaaaaaaaaa    780
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa    840
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa    900
aaaaaaaaaa aaa                    913
```

<210> SEQ ID NO 101

<211> LENGTH: 569

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 101

```
ggggaggcgg tcgacatggt tttttttttt tttttttttt ttttacatct atccacatct    60
```

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tatttctcaaa ataaaaagtg tacaattata aaattaaatc tacagcctag aacctcaatt	120
tttgaagaa ccatttggtc ttctcttgct tataccttcc ctcaaatttg acacgggtct	180
ggaatctagc cttcttcctc ttcattggcat ctttgaggtc cttgggtaca actttcaagt	240
ctgatgccaa atctacagag tatctagtgg gcatgagatg gttgtagtgc aatactttga	300
taaaaggctt gatcttgac ctcttggtga ttttgcttt gcccatgcgt ttgtggattt	360
tccttgggta cctatcaatt ccagctacta aggcattgct gtattgttta tctgatgtac	420
cttcacgtga ggttttgacg actacggctt ttcggccggc gtatcgcccc ccgaggacca	480
atacgacttt tctgtatttc attattttac ccattgtggc agtgctttga caactgctga	540
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa	569

<210> SEQ ID NO 102

<211> LENGTH: 1350

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 102

tttttttttt tttttttttt tttttttttt gaactaaaa tgaaaatata tttttgggct	60
acgtaatat cctatcagct cttttacagc tggaatgttg tatgtgctgc tcattattac	120
tgcgttcagc ggttttttat tcttgtcaat ttaatacatg atatttaaaa aaaaaaagta	180
tatttcaaaa ctttaggggt ttggaaaata atatgtacag tagatattac tctatgggca	240
gtaagtgtgc atatatgaaa gtcattgata tttacaatat ctggaaagtg attcaataac	300
tggatcttca gtgtgtcgat gtctatctgt tcaggcacag tctgtagaag aatcaggcag	360
ctttctttca tatatggata acttaagaac attatcaaag ttgaagatat tatcgccatg	420
ataggatcta tatattttgc agtatctttg tcagtaaaat atactaggag agcgcatatt	480
acaacaaaa tacaaccgtt tacatctctg gccattttcc aaaatccctg cttttgtttt	540
tgatggccga tcataggatg gatagttttg cttctggata atcgtcttgc gccttgcctg	600
aaagactggt caactactat ttacttaaaa actacatttc cgctttctgt tacataaaga	660
aaacttcctt ggtggaatgt atatccacca atcaacaggt agcatactcc gttgagtaat	720
aaaccacatg ctctcaaaac taaaacagat atggaatgat gcatctcgtc atgatggctg	780
atatgaacca atgtctgaca tgcttcaaca aaaatagaaa aacttaacga agctaagaac	840
acacaacata ttaacataaa tatgacatca gttctggccc agccaaatgt attttttagc	900
ttcttttctt ggttggacct ggtaacggac gctttcgtct tcttatggtc atggcacttg	960
gccgggttgg atgttaactc ttctcctata ctttcgcttt cgcttgggtgc ctttttcatt	1020
tcgaataact gtttcggagt atctttttcca tacttaatag ttaaaatata tctcccaat	1080
gccataatat tacacaaagt gtggtgaagag tccattaata gtgtcagagc atgagtgggg	1140
tgacttacaa ttagttctaa taagaaaaag gcgatgggtc agcctagtag cacgtacagc	1200
tgaaaagggt gcatccttct taccattctt ttcattgcca tgggtgaact attcagagca	1260
cacgtctgaa cgctaggaat atcttaattg aatattttcc actgaacact gcaactatac	1320
tgtagaaact gtcagggtgc gactgtcccc	1350

<210> SEQ ID NO 103

<211> LENGTH: 991

-continued

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 103

```

tttttttttt tttttttttt tttttttttt ttaattacaa atatttacta attttcttat    60
tattatcagt caaattacaa aacaaattct atttttgctc atcaatgggc ttaaagtgat    120
ttagtaaaatt tacgggtccaa tctccttcaa ccccttttgt aaattctctg ataaatctat    180
agttgcaaat cgaaattttt tgttgatatt caggtagcat tcccatattt aagggaggtt    240
cttcacctct agatctcatt ccagctaaac ctttcaaaga atggtaaacc atgggtattt    300
cgacgaatcg tttttgttct ttgccttctt cttcgttaaa tataacacca acctgatatg    360
gaaatgaaaa atatatgtca tctacactag ttgctatctg ctccttttga ctcatggaca    420
tcatagatat tgctttttgt agactaccga taatgtcatt tgttactaga ccgtctaatt    480
atttaatatc accttcagac aatttatgtg atactacctc cactgctttt ttagaagcac    540
ttacaaaatc tggaagatta aattcttgat ctaaataagg cctaatagata aaggtagcaa    600
gaataaaaatt tcttatagtt ttaaataaag aaggccaac aaatatggga gagtctggca    660
gtaatggagg taatttgttt gaaggagaac ttggatcatc tgaataccat cttctttgat    720
taaggcctga atttaaggat ttgttattta aaaaatatga aggctgcttg gtacaaaaac    780
ttgcatgttt acataagaaa tgatttgta ttgtactatt aaatttacac aaatttaaat    840
tactataatt tcgcacatct ctgaacaaaa cgtaaatatt cattttatca ttttaatata    900
aatcaacaaa gtcaaaagta ctaaaatatt ctaaaatttt agatttttta ggttctgtcc    960
tgtcacgggt ctgtcctgtc acctactccc c                                991

```

<210> SEQ ID NO 104

<211> LENGTH: 445

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 104

```

ggggagtatt cacttgatct tcaaggtaga ttaacgcaag tagaaatcta aaacatgtct    60
ggacgtggta agggaggcaa agttaaggga aaagcaaagt cccgatcaaa tcgtgctggt    120
ttacaatttc ctgtaggtcg tattcatcgt ttattgagaa aaggaaatta tgccgaaaga    180
gttgggtgctg gagctcctgt atacttgga gctgttatgg aatatttagc tgctgaagtt    240
ttggaattgg caggaatgac agctagagat aacaaaaaga cccgtataat tcttagacat    300
ttacaattgg ccataagaaa tgacgaggaa ttgaacaaat tactgtcagg agttaccatc    360
gccaagggtg gagtattgcc taatatataa gcagtacttt tacctaaaaa gacccaaaaa    420
aaaaaaaaaa aaaaaaaaaa aaaaaa                                445

```

<210> SEQ ID NO 105

<211> LENGTH: 2235

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 105

```

ggggcagtg ctttagaggcc acgaagcaat ttctaggata gacgaacgac gctcgcgacg    60
acgcgctg cgcacacga caaaaaata cacaatacga caccacgcgc cattttgcca    120
ttttctgtgt gtgcagtga gtgaagtgc actaaaatct tcaaaattca acccttctaa    180

```

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gaaggccgat	ttcatgtgtt	ctatatcgaa	gtaaaagagc	aatagcatgg	gagtggcaga	240
ggatttcgct	cccagcttca	cgcaaaagcc	tcaattgagg	caggaggacg	atggaaacaa	300
actcattttc	gaatgccagt	tactggctgc	tccgaaaccg	gaaatcgaat	ggtttcgaag	360
cgatatacca	ctttcagaag	acagtaggac	taatttttaa	attcaatcca	taggcaccaa	420
caaatTTTTA	gtagtactcg	aattagatga	tgttattgaa	accgacgtg	gcctttacaa	480
ggTcaaagcg	aaaaatacca	tgggggaaat	agcagcctcc	atcaatctca	acttcagccc	540
catggacgaa	ccaaaagaaa	aacaaataga	cggcctagca	cccacttttg	cgaagaacc	600
agctattcgc	caagaagatg	atggcaaaaa	attattattc	gaatgtagga	tacaggccga	660
tccccgtcca	acggctcagt	ggtccacaaa	tggcaacgct	gtagcgaag	gtccacgtca	720
caagttgagg	atagataaag	atggccattc	atattttgcg	acccttgaaa	taatcgatgt	780
cacggtagag	gatgtcggca	aatacaaggt	gaccgcaaaa	aatgacttgg	gagaaagtaa	840
cgccacaatc	agccttaact	ttgacagtgg	agatagcgct	gatggctttg	cgccttcttt	900
ccttgagaaa	cccaaaatca	tacctaatga	gagtggcact	cttattacta	tgaatgtaa	960
atgcaaaagct	aaacctaaac	ctgacgtcac	gtggttcgcg	ggaaccacag	cgtcaagga	1020
atcttccaaa	attaaaatcc	agatcgttga	tctcgaagaa	gacaaattcg	aactgtcctt	1080
agaaatcaag	gatccatcgg	cagctgatgg	gggtacttac	agatgccatg	tgaagaacga	1140
atacggagaa	agtaatgcaa	atctgaacct	aaatatcgaa	gcagaaccag	aaccagaagg	1200
agaaggacca	acgttcgctg	aaaaaccag	gataacctct	cacgatggag	gcaaactcgt	1260
tgctatggag	tgtaaagttc	gtgctaattc	taaaccact	atagtttggt	acagagaaaag	1320
caaagaagtc	acagaatcat	ccaaaattaa	gatcagtatt	aaacaaacag	aagaagatat	1380
atattacgct	aaattggaac	tcaatgatcc	ggggattgat	gactctggct	tgtacaaatg	1440
caatataagg	aacacacttg	gtgaactcaa	cgccaacctc	accttaacaa	tcgagattat	1500
tctgtttatc	aaagaaaaac	ccaaagttat	taaaatcatt	aagaagaaaa	ctgttattgt	1560
tgaatgtaaa	gttctcagca	agtttgcacc	tgattgtaca	tggtttaagg	aaagcgatgc	1620
cgttaaagaa	gattcaagac	atactgttca	cgttgaccaa	gttaaagacg	gcgaatttac	1680
tgtaaactc	gaaattaatg	aagttgagaa	aaaagacaaa	ggatatgtaca	aattggttgc	1740
taaaaacgaa	aagggtgagg	caacttcaca	agtcgttgaa	gtcactgagt	tacctccaga	1800
ggagaaaccc	aaaggagaca	agccgaaact	gaccaaacta	accaatatcg	ttactgacga	1860
aggaaaaatc	gttgatttta	taacttctct	caaaatcgaa	gacaaaacag	tcaaaatcac	1920
atggtacaag	aacaccactg	tgataaccga	atcttcagaa	atcaaaatct	cttttgatgg	1980
cactgtgacg	cgacttagca	ttagtaaatg	taaagtatca	cattccgcta	catacaagtg	2040
cgttgccaaa	aacgaatttg	gcgaagacga	aataagcgct	acacttaaag	taaacgaagc	2100
taaagaggaa	gatgaagaag	aagaagaatc	cgaagaggag	gttatcgaag	aaaagaaaga	2160
ggaaaagaaa	gtagaaaaga	aagaagaaaa	acaggaaaag	aaagcaaaaa	aaaaaaaaaa	2220
aaaaaaaaaa	aaaaa					2235

<210> SEQ ID NO 106

<211> LENGTH: 1148

<212> TYPE: DNA

<213> ORGANISM: Diabrotica virgifera virgifera

-continued

<400> SEQUENCE: 106

```

ggggagagta gatagtaagt aagtgaatgt acgttggtgaa tgacggaagc cggtttggtta    60
cagagaggag gatggagtcc aacacgataa cggtgacgag atttttcttg gcggaacaac    120
aaaaatttcc agaagccaca ggtgaattga cccagctgct gacttctatt caaacagctg    180
ttaaggttat cagttagcgc gttagaagag ctggtattac caaattgttt ggtaccgtag    240
gtgaaacaaa tgtacaggga gaagaagtta aaaagttgga cgtattggcc aacgaattat    300
ttatcaatat gcttaagtca tcttatacag tagcattgct tataatctgaa gaaaatgaaa    360
caattttggg ggtagagact gaacaccgag gaaagtatat agtagccttc gatccattag    420
atggttcctc gaatatcgac tgtctggtat cgatagggtc aattttcgcc atttacagaa    480
aatccgacaa cacagttcca gccctcgatg acacactaat gtccggaagg aatgtagtag    540
cagccggata tgcgctttat ggcagtgcga ctatgctggt catatcttct ggatctggtg    600
tgcattggtt catgctggat gccaccatag gagaatttgt tttgactgaa cacaacatgc    660
ggattccgaa aaaaaggaaa aatctactct ataaacgaag ggtactacca cgaatgggat    720
gatgccataa gagaatacgt cgatgccaa gaaagatcct ctaaggggaa agcctatggt    780
gccaggtaac taggttctat ggtcgcagat gttcacagaa ctattaataa tggaggaaac    840
tttttatacc ctgcaacgaa gtcttccctc aagggaagc ttagactgat gtacgaatgt    900
gttccgatgg ctttttctg ctgaccaagc ggaggattag ctactgatgg caagattaat    960
atattagata tcaaacctac taaccacat cagagaagtc ctattttctt ggggtctata   1020
gaagatgtag aggaggttca aagttatatc aataaacatt gtgaatgtaa aaaatagggt   1080
aagagatttg tttcaataaa gtttattatt agttatacaa aaaaaaaaaa aaaaaaaaaa   1140
aaaaaaaaa                                     1148

```

<210> SEQ ID NO 107

<211> LENGTH: 574

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 107

```

ggggagttat ttttgattat ttttacgtat attatacagt cttaaagttt ggcttcaccc    60
tgtagtagta gttttcccta attctgacct gtttttttta ttgtttctaa attcccaatt   120
ttgtgtcagt gacacttttc cacaatctt tttacataaa agaccttatt aacaagaatt   180
tatattaact ataaacgaaa ataagatttt tttctgatac aatgtttggt gttttgtttc   240
tttttgcaac acgttttatt ctttgctata acttaaaaat gggctattca ttagatacca   300
attttttcat ttaagtccct tttttatttt tcatatcaat gatttggtat tgcgaaaata   360
ttcttagaaa tgaattatat aataaaaaaa acaataaaac taatgttaac cgtcttgatt   420
ttcgcaaaaa tatgggttca tcattttatc tttcggaagg actaacgaa aaattataca   480
tctactttgc attcggagta ttgtaagaaa aacatgcatt cgttacagta gtaccagcta   540
tacaagagat tcattatgat tcagctctgc gggg                                     574

```

<210> SEQ ID NO 108

<211> LENGTH: 725

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

-continued

<400> SEQUENCE: 108

```
gggagtggagg cttattgtta acaaactggc aaaaaataa ttaaaactaa acaaatttga    60
tgaaaaatgt tcataaaagg tatatttcgt tgattgggaa gaatagtatg atatttcaaa    120
aacatcaagt ttacagaaaa gacaattaaa gattgagatg ggttacaaga ttggattact    180
taagcaatac aatattaaat atgcttttca tcagaataat taaacatac agtattaact    240
gacaatatgg gtgttacatc caattcatat accaccccca actcatattt ttcaccccca    300
ttttgagtta taatactttt ctctataaaa attttgtact atttcacaat tataagggtta    360
ttagggacaa taaaacgaaa cagttttaa gttttattag agtttaaata acaatgaatg    420
aaaaaaatcg cagtttatgt acaataacaa tataaaaaaa attaaaaatt tgggcccggc    480
taaaaaaaaa gggtctacaa gttacaaccg ctacattttt tttcttttcc aaaaagagag    540
agcaggccag ctttcttttt ttcacttatt cccactttct tcttgtaagc ttgttttaga    600
gtaacgtcac gtgctgatgg aagtttgctt tgaagaacgt ttatggtggt aaattcctgt    660
tctttgtatg acttatatag taggtgacta gggattgatg tacatctttt ttcccgatgt    720
ttatc                                           725
```

<210> SEQ ID NO 109

<211> LENGTH: 725

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 109

```
ggggagtgtg ccacgggagc ggattgaggg tgattgtact gtttgtgtag aacattagtt    60
taataaaatg gcagccgtag taaacttgta caattatttt tataacttag cagatcccag    120
agtgaaaaac tggtttatga tggaaaatcc cttcccaact ttaggaataa ttggagtata    180
cctattatta gtccctgcaa tcctgccaaa ctttatgaaa aataggaaac ccttcgaact    240
aacgaagata attagattat ataatatatt tcaagtagtg gctgtattg gtataatgta    300
cagtatcctg acgtcaggct ggattcaagg agaataaat attggttggt ctccaattga    360
ttactccaac aaaccaaact ccgtcaaaact cctgggtgca ttctactggc tctatttggt    420
aaaagggtga gaactgatcg agactatatt cttcgtctca cgaagaaaaa acaaccagat    480
aacaggcctc cacatctacc accatggatc tacgttcttt ttggcatgga ttgggtgcaa    540
attcattgga ggtggtatgg cttctattcc tcccttcggt aactcattca tacatgtact    600
aatgtacaca tattactact tgtcttcttt gggacctgaa tggcaaaaga agctgcaacc    660
atggaaacca aggcttacta tgttgcaaat gatacaattc accctcctca taattcactc    720
tctga                                           725
```

<210> SEQ ID NO 110

<211> LENGTH: 508

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: 439

<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 110

```
ggggagtgtt acgacgcgaa cggtgccaag cgctgctgta aagttgcgtg cttttctgaa    60
```

-continued

```

aaaactttcg atttgcgtgc cgcgaaaaag cgagttgtca cagacaattt tgttttgtgg 120
tgaatattcg gcggattgcg taatttgtcg attgggtttt ggtgtttttt tgtgtgtgcg 180
acagagtaac tattttattg gattgtgttt tgaagattac tcagctttat cggaacctct 240
gagaggaaag tctagtattc gagcaggtcg aatggagttc ttctacaccg aaaaaaacca 300
gtgaattgtg ttttaaagtg tgcgtttttg tcgatttcca atttctctcg cggcgtataa 360
tttctattgg ctacattatc tatacagttt gtgtttgtgc tttgtaccag atttccaatc 420
acttagccat gtttgagng gaataattaa aaggtgagtt tgaattttt ttacattatc 480
tcttctacaa aaggaacaat agaagctc 508

```

```

<210> SEQ ID NO 111
<211> LENGTH: 623
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

```

```

<400> SEQUENCE: 111

```

```

ggggatatca aacgccaaaa gacgtttata aacatattta atgcataaat acatcctact 60
aaactatatt ttccataaaa tctacaataa ataagttata taaactttac acgcccatct 120
gcttcttcca agatgacgtc accatctttt tcaactcaca aaatatcaca atctacaaat 180
caccaaacat ctccaaaata tcggttttat ccaaactatt tctgatattt catatcgtat 240
atctcagtta tcgcaagtgt tgagaacctc aatagcaaaa tagatttgcg ggccttattt 300
ttcacttcaa aatgtctgct aaccagtata ctattagaga gattgtggac tatcagtcta 360
cccataatgc aagtagtgcc gatgacgaaa atgacaccgc atcggacgaa gaacaagtac 420
ccattatgta ccaatacgaa atggtgggcc cattggaaag gacagtaaag cgacgaggcc 480
atcttcctaa agaagcgggt aaaattctaa aaaattgggt atacgaacac agattcaatg 540
catatcctac ggaaattgaa aaacagattt tgtcacaaga aacgaacctg acggttcttc 600
aaatcagcaa ttggtttata aac 623

```

```

<210> SEQ ID NO 112
<211> LENGTH: 625
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

```

```

<400> SEQUENCE: 112

```

```

gggtttgttt gaatttttcc gaaacaatgc atgttttctg tctaattgca ctcccctaca 60
tagttacagg ttattgaagc gctattatag tcgaggcaat aaagcagtaa aaagatcaaa 120
acccgccaaa tttttgcagt tggatgaatc tcaatgaaat attttgcatt cgattcgtaa 180
gagacttagg aaacttcgta aacaaaaatg atgatgaccg aatgtaaatt gcataattga 240
tttgcaaaaa tgtaaacata atgtgtataa gtcgtatttt ataatgaata acgtcataat 300
tgaggaggaca aaaactgaaa cgatttaca tataccgctc caagttgtaa atcctcatag 360
ttaacattgt atttgtgttt gactagatca ttaacgaata cggaaataat caaataaaca 420
actgttttcg aacatggtaa atgttatgtg taaaattatc attttactta aattttttta 480
aacctaattg gcatcagcgg tattttttaa tttataacgt cataattgga gtaaaaaaaa 540
tgcaacatgt taaatataca gcaccaggta gtacaaattt tgtctagacc ttagagacct 600
tatattatag acccttagcat agtta 625

```

-continued

<210> SEQ ID NO 113

<211> LENGTH: 664

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 113

```
gaggagtcca ctttgggatt gtattcctga atattaaccg gtagtgccag gtgacagtgt    60
ttaattaaat atccagaaaa aatgccaggc ccttcaagac ctctgtggca agtagccgga    120
aagcgtgata cagaacaaga acgcgaagct caagcatgga tcgaagctgt cacaggaatg    180
aggtttcctc caggagtctc atacgaagat tgtcttaggg acggtattct cctttgcaca    240
ttgatgaacc gtttggcacc tggaatcatc caaaaaatca acacatctgg tggagactat    300
aaaaatgatg ataacttgaa ccaattccaa aaagcttctg tgaaatacgg tgttcccgat    360
gtagatcttt tccaaacaac tgacctgtgg gacaggaaaa gcatcgtttt agtcacaact    420
accatttttg ctctaggtcg cacctgttac aaacaccctg aatggcgagg tcctttcttg    480
ggaccagac  catctgaaga aaacaggaga gacttcagcg acgaacaatt aagagctggt    540
gaagctatta ttggactcca agctggccaa aacagaggtg cactcaagc tgggcagaac    600
tttggtgctt ctagaaaaat cattttggga aaataaaca acattcgaag agacatattg    660
aatc                                             664
```

<210> SEQ ID NO 114

<211> LENGTH: 656

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 114

```
gggtaagaat gcagcagcta gcaataaggg cgaagtagtc tgcagaagca tttttctttc    60
tagagctcct taaaacatca ttcacgattc attaatacca gttttcattt ttttttaaatt    120
atgtagtcct tttattgaaa cattttcaaa tcaaaatttc tagaaaacgg tgtgttttac    180
tgacttaatc aagagtacct tctaatacta gaataccgca caatttaata atccagtgtt    240
agaaatgttt aaaaattaaa gacaaaaaaa ttatccgata aaattacagt tatcctacca    300
aaaaaggagc cctacgatcg gtactaggaa ttcacagtag ggcttttcat tcacagaagc    360
tcgaaacaaa tgacaatcga tgaaaagcct tattaatgga atcaatttat ctccgggaga    420
taaacaggca taccagtttt ccatttttca aaatagaagc gttctggagg tattaagat    480
aactagttaa aagacgcaa cgtccaagag ctctagttcc cttaggaagc aatttcgaac    540
tacttgaatt aggttaaaaa caggagagtt tctggacacc ctgtataaga aagacaccag    600
gaatatattc acgaatacga caaccagtgg agctaagagt tgaatctttt gtcacg    656
```

<210> SEQ ID NO 115

<211> LENGTH: 185

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 115

```
gggatgtcaa atcataaaaa tcatccttat catttagtag atattagacc atgaccttta    60
ttaggagcct ttagagcaat attaacaata ttaggaataa ttaaatgatt tcatttatat    120
aataataatt tactaataat tggattatta attacaagat taattatata tcaatgatga    180
```

-continued

cgaga 185

<210> SEQ ID NO 116
 <211> LENGTH: 661
 <212> TYPE: DNA
 <213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 116

```

ggggaattgt caacctggaa aacgacttgt cgaagtcgca tagtttttat aagttttaat    60
aaactaaatt aaatataaat acttcgagaa tgcaataatt attattcttt aactagaccc    120
acagcttatt aattagcaga agtagtagca gacttatact aactagcata aggagaaaca    180
tattaacata gcatggcaga cttcatagat tctgaagcag aagaaagtag tgaggaggag    240
gaattagatc atagggatcg taaaaagcc caaaaagcca aagttgtaga tagttcagat    300
gaagatgatg aagatgatga cgaaagactg agagaggaat taaaggattt gattgatgat    360
aatcctattg aagaaagtga tgctgagtct gatgcttcag gaagggaaaa acgtaagaaa    420
tctgacgacg aggatttgga tgatcgactg gaagatgaag attatgattt gcttgaagaa    480
aatttgggtg ttaaagttag aagaaggaaa ttcaagcgac tgcggcgttt tgaagatgaa    540
gaaagtgaag gagaagaaga acatgatcct gaacaagata gggaacaaat tgctatggat    600
atattttcag atgatgacga tgaaagacga tcagaacgaa gtcacaggcc tgcgcgtcgaa    660
c                                                                    661

```

<210> SEQ ID NO 117
 <211> LENGTH: 488
 <212> TYPE: DNA
 <213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 117

```

ggggccactt gattttttgt tttagaaaaa ggcacgaaaa tggctggaga ctcaattgat    60
gcttcaaagt taaccggtat gagcaaaatt ttcaatggct ctaccatgag aggaagggca    120
aatgttcgct tagccacata tgccagtgtt ggactcctaa tcgcctatct ctactgaaa    180
ccatcaaaac ccaaggcacc aaaaaattag tctagtagtc tattccgtaa tgttactcta    240
taactatgta catgtttaat aaaacttaaa atctcaatgc ttaataagtt tttttagata    300
caatgttttt tgtagacata tgtaatgact caataaaatt gatgttgtat acaagggcaa    360
gatgaaaagt tctttgcctg gtagtgaata gtgagttttt tattcaaaac atgcctttat    420
ttacagtgca atctcacttt attgtaatat tatttgatat atttttccag taaagagatt    480
ccaccatc                                                                    488

```

<210> SEQ ID NO 118
 <211> LENGTH: 616
 <212> TYPE: DNA
 <213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 118

```

ggggattgtc aaatagtgtg cagcgttaca cagcgaatat tttcctcatc agttcaatat    60
taacaataaa ttgttttgtt gaaattgaaa tcacaaatta ctttataaaa tggtaactct    120
agaagacggt gaaatgaaaa atgcagacag tctccagga ttagaagctg gtgatacaaa    180
gaaagatacc gacctacaaa gtgtaataga gattcgtgaa catgcaagac aaatagaaaa    240

```

-continued

atcagtcaca agtaaagaaa accgtttcat cttacgagtt ttacgttgct tgcccaacac	300
tagaaggaag cttaatggac tgggtgctgag aagcctcatt actcaaatat atcctgtagc	360
tgaacgtgat gccctcctta gtttcgtcga ggaagcttct ggagaactcg acgccacca	420
gtcacgagca agatcagctg ttaagtcgcc tgttcccagag gtggatacat atataaatct	480
tttaatacta gtacgtttaa ttgataccaa taagttagtt gaagcagagc gctgttctca	540
agctcttatg aataaaataa ctaacaaaaa cagacgtact atagatcata ttgctgccaa	600
gtgttatttc tatcac	616

<210> SEQ ID NO 119
 <211> LENGTH: 609
 <212> TYPE: DNA
 <213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 119

gggggacaag attttgcaat ggcggatgta gtagacgagg tgattatgga ctctgatgaa	60
aatgaggaaa tactatcaaa aagcccagaa gagatggctg aactcaaaaa ggaaaacggt	120
aaccagttat acaaaaccaa acagtacaga tctgcactcc ctctctatag cgaagccatc	180
aatctttgtc caaatgtagc cccttattat ggaaatagag ctgcctgcta catgatgctt	240
tacaggttta cagaagcttt ggaagatgtc aggaaaagtg tgcagctgga tccagaattc	300
gttaaaggat acatcagaat gttaaagtgt gctatagcaa tgggtgacac cactacagct	360
gattttgcca ttaagaagct tcaggacttg aaagttgacc acaaacatt tgcaaatgaa	420
ttaaaatcgg ttcagcaatt gaagcagtag gagtcagatg gaaccaaagc gtacgataaa	480
aaagattatc gtttggttgt tttctgtatg gacagatgtc tcgataatgc ccctacttgc	540
taccgataca aaattgccaa agcagaatgc ctcacatata tcggccgtta ccaagaagct	600
caggaaatt	609

<210> SEQ ID NO 120
 <211> LENGTH: 517
 <212> TYPE: DNA
 <213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 120

ggggtcttga aggtggctcg ttgtagcaga tttgttgaaa accatggaaa tcgttcaaga	60
attatccagc caatatgttc tgtatattcc tgtagcttta gtaatcgttg gagctatttt	120
ggtgttcact tttggtttta aatctgcaga acaaccaccc ttcgacaaat tatcatttga	180
cgatagaaaa tctgctggga aaaagcgtaa aactaaggaa aagaaaccta ctgctaattg	240
tcacatcagc aatgtagaaa aatctgataa atccccatca aaggactcca agaagtcccc	300
ccagaaagaa gctgttgaag caaaacaaga aaagaaggag aagaaactag acaaacaaaa	360
tgaaaagcct aaaaaacagg aatcaaaaaa gacagaggaa atcaaaaaata agaaaaattt	420
aaacaaagtg tcagagaagc cagtagattt tgatgatggc aactgggaga cagtacctct	480
taaatctgat aagaagaaga aagaccaatc gccagtt	517

<210> SEQ ID NO 121
 <211> LENGTH: 607
 <212> TYPE: DNA
 <213> ORGANISM: Diabrotica virgifera virgifera

-continued

<400> SEQUENCE: 121

```

ggggacagcg tgaatctgt gcgcggacaa aaaaaacttg ttatcgccga tttattataa    60
tttatattta tgaagtgact gtgtcggtag ttaatagctt tatgtatatt gtgtttgttt    120
tcatttaaat tttaaatttc tataccaaag atatgagccg gttgaacata ttcagttttt    180
tgaaaatgct tcaagcattg tgttgtgtac tgggagttac atcagcatct tcagaccag    240
ttatagtctc cagagaagaa tggggggccc gcgctcctaa aaacatagaa aatatggcga    300
accagtagcc ttacgtcgtt atccaccaca gttatctacc accagcttgt tacaatttaa    360
ccgattgttt caaagccatg cgttggatgc aagaccttca ccaagacacc aacggttggg    420
cggatattgg ctacaacttt ggtgttgccg gagatggtag agcctacgaa ggaaggggat    480
ggtccagagt tgggtgctcat gctccctatt acaacagcag aagtattgga atatgtataa    540
ttggagattg gacagttgaa cttccaccag aaaatcagct agcgacagtt catgagctaa    600
tacaaaaa                                     607

```

<210> SEQ ID NO 122

<211> LENGTH: 590

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 122

```

gggggttgcc caatttgttt caatattgtt ctgattttat ttaaaagcgg cacttaaaca    60
tagtatataa ccatggttga gaacagtaca ttaactatag atgaaaaatt tcacctata    120
tccagaaacc tgcagaaat attaggtgaa gatagaatta aagcagtatt gaaagaacgt    180
gatttgaaat tgtattgggg cacagctaca acgggtaaac ctcacattgc ctacttcgtt    240
ccaatgtcca aggtagcaga ctttctcaga gctggtgtag aagtactat tctttttgct    300
gatcttcagt cgtatttgga taatatgaag gcaccctggg aacttctagc gcttagagtt    360
cagtattacg aacattgcat taaagctatg cttcaatcta ttggagtcc tttggacaaa    420
cttaaatltg tgaagggaac agattatgaa ttgtctaaag aatacacact agatgtttac    480
aaaaatgact cagttgttac tgaacatgat gcaaagaagg ctggagctga agttgttaaa    540
caagtagaaa atcctttact aagtgggtct ctatatccta gtttgcaagc    590

```

<210> SEQ ID NO 123

<211> LENGTH: 103

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 123

```

gactcttacg aactcagata cttccagatt gacagtcaag aagacgatga tgaagaagat    60
aatgaataat ttattcagtt atttttttta taaatagat tat    103

```

<210> SEQ ID NO 124

<211> LENGTH: 381

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 124

```

gggaactata aaatgcggtt acaacgttgt tccagcttag cattctagta tagatttcca    60
tttcagcata tcaagaacga tcacaattta gtgaaagtgt acatgggaat aacaacaact    120

```

-continued

```

ctatattgaa atattgttta atatttaata tgctaagtaa tattcagtta gaatattatc 180
atggatcatg gatgggtgaa atatcacagt ttaacaaaa aaaaaaagaa tgtgtgtgat 240
ttgtacgcg cctaagaagt tatacttcta ttatgtgatt tcaatgaaat aaacatattt 300
taaacagttt atttgtattt tatttaaata ttaactaat ttaatacct atttcttacc 360
aaatttgttt attaaaatag c 381

```

```

<210> SEQ ID NO 125
<211> LENGTH: 627
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

```

```

<400> SEQUENCE: 125

```

```

ggggaacagt ttaattgcta gagttgtata gtcagtgtct ccagttgttt attatcaaac 60
aaaaatgtct ctgacaatga ttggtggtgt aaagatcccc atagtggggc taggaacatg 120
gcaggctacc aatgaagaag aattggaagg tgccgttgag gcagctctgg aaactggata 180
ccgccacata gatactgcat ctgcatacca aaacgagcat gtcacgga aagttctaaa 240
taaatgggtg gcgtctggca aacttaagag agaagatatt ttcattacta ccaagcttcc 300
aatgacacac atccatcccg atctcgtcga aacagctctt aaagaatcct tacagaagct 360
tcagctggac tatgttgatt tgtacttggt gcattctccc atatacatga aatttgttga 420
agctggaaag ccaatggaac ctctacctac tgaccatctg gctgtttgga agaaaatgga 480
agagcaagta gatgcgaaaa gaaccagaac catcgggtctc tccaacttca acgtaaacca 540
gatcgacaga atagtgaaga attgtagaat tcaaccagcc aacactcaag tggaactgca 600
cgtttactac cagcagaaaa aacttag 627

```

```

<210> SEQ ID NO 126
<211> LENGTH: 640
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

```

```

<400> SEQUENCE: 126

```

```

ggggattgta ttttagtatt ttacaattct ttgaattgca gattatttag cggtttagta 60
caaaaacctg aagtaaatcc tataacggaa agtgcttaaa ttttaattgt aaaatgtcca 120
ttctagctta caatggtggt gctatggtgg cgatgaaggg agaaaactgt gtagcaattg 180
cagcagatag gcggtttggt attcaagccc aaacagtagc tacaaatttc caaaaaatct 240
ttgaaatggg accacattta tatgtgggtc ttccaggatt agccacagat acccaaacag 300
ttatgaaaaa actccgttcc cgaaaaaact tgtacgaact taaggaaaat cgaaaaatat 360
ctccaaaagt atttgctctc atgatataca atatgttgta tgaaaaaaga tttgggccat 420
tttttgtaga acctgtagta gctggacttc tacctaatac ttatgaacct tttatctgta 480
atatggattt aattggttgt ataaaccaac cttcagactt tgtgtgtggt ggaacagcgt 540
cagcacagtt gtatggtatg tgtgaagcac tttgggggcc taacctagga cctgaggatc 600
tttttgaaac catctctcaa gctctcatca atgcctttga 640

```

```

<210> SEQ ID NO 127
<211> LENGTH: 591
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

```

-continued

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: 156, 241, 244

<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 127

```
gtacattaaa atcgctaaaa acataaaaa atacaatatg ggtacttgta tgtgataatg      60
ttacctgtta gttactaaat ttaaaacggt tgatattttg tatacttata tttagacatg    120
gcggtaaatg tttattccac gaacgttaca tctganaatc tatcccgta tgatatgcta     180
gcatgggtga acgaatgttt gcagagtagt tttgcaaaaa ttgaagaatt atgtacaggc     240
nccngcatat tgccagttta tggacatgct ttttcctgga tctgtgcaat taaagagagt     300
taaatttaga accaattttg aacatgagta catacaaaat ttcaagattc ttcaagctag     360
ttttaagaaa atgcaagtag ataagatcgt ccccatagat agactggtga aaggtagatt     420
ccaggataat tttgagttcc tacagtgggt caagaagttt tttgatgcca attacaaagg     480
gacggactac gatgcgctgg gagcacgtgc cggagagcaa ttggggcaag gaggatctaa     540
cgcccctaga ggtcaatctt tgatgttacg tcggccgaac gcgacgcctt c              591
```

<210> SEQ ID NO 128

<211> LENGTH: 614

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 128

```
gggggaggag gttaagttaa acttcgtttg gtttggtttg gttgaccgag tgattttcca     60
gggtggagtt tttttgtgat gctaatttat ttatggccat ttcgcgttct ctgataaatg    120
aactataaag tattaagca cataaattaa taatctttga ataacttaca ttgatattgc     180
gatcaacaag gtttttctaa acaaattttt agttaaaagt gcacaagttt ttatgcagggt    240
tgtcttgtaa ttgttttcaa ctgcttagag cttctatctc caccatgggc gatcagggtg    300
aaaattcgaa caataaagtg accgaaaatg atccacagcc caacagggac gaaatgataa     360
tggttcagca gaggcaaatt gaacaagagt atattgatgt cctcagaaga ctaaaagata     420
tagataatat tgatgaagcg cttaagaat tatatagtgt atttaatgat caaggtttct     480
cagattattt ggtggtctac ctcagattgt taaccagtgg ccagttacaa aaggaacacg     540
aattttacag ttgtttcata gaaggtgata gaacggtagc tgatttttgt caccaggaag     600
tagagcctat gtat                                     614
```

<210> SEQ ID NO 129

<211> LENGTH: 639

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 129

```
ggggagtcga aaaatatggc agcgtttcta aggcattggcg ttttcaaac aggacgagtt     60
gtctcttcaa aaaacgtact tttgaggtcc tttgccacga aggctgagaa gaggaaagga    120
atcgacagaa aagttggccc aaaaatagac tccacagctc aatcttttagc ttcaaaaggg    180
tttctgaggc aacaaagaga ttattctcca cctgaagatg ttaattccaa gttagaagca     240
atcttcagaa ccgtcgctcg tagttcagat atatctaccg aactcacaga tctgaatcaa     300
aagtttactt tattcatgca gtgtgaacag caactaggcc atagtattcc taattcgtaa     360
```

-continued

```

cttcacacac tgaaacatt gaaggacgtt caaatattct ataacatgcc cgtagatata 420
agaacgccac tggaaagaat gaaatccatg gacttgccgg aaaatttaca tgttcagtac 480
gaatataaac gatttaatgc tgatactgat acgatgtttg gaggaaaaac agcattccct 540
aagagttcta caattgttac aggattaaaa tacaagata agtacaagg acaaaagcaa 600
ccattacctg atttctagt tttttttcta gaaaataaa 639

```

```

<210> SEQ ID NO 130
<211> LENGTH: 651
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

```

```

<400> SEQUENCE: 130

```

```

ggggatgttt taaaaggcgc ttaagtta agattcacac attgcataaa ataattttat 60
aactaaacta aatcatgggg aagaataaga aagacaagaa aaagggaaaa ggggccgaga 120
aaacaacagc aaaaacagaa aagaaactgt caaacaaaat gaagaaagaa ctgcaagcta 180
aggagagga tgatatagaa tctattttat tacaattga gaaggaagag aagaaaaggt 240
tgactgttac tgaagtata atcagtcac cttcaagaag attaaatttc acctttatgg 300
cccatccaga aaaagaacag cttattttgt atgggggaga atttttcaat ggacaaaaga 360
cttttgtgta tgggtactta tttttctaca atataccaaa taacaaatgg acagtagtta 420
aggctcctaa tggccccc cctagatgtg gacatcaaat ggttgtctct tcagcaaata 480
aaggtaatt atgggtgttt ggaggagagt ttactacacc cacacaatca caattttatc 540
actacagaga tctttgggtc ttccatttag ctactaaaca gtgggaaaaa attactgttc 600
cgaatggacc atcagcgaga agcgggcaca gaatggtatt aataaagaag c 651

```

```

<210> SEQ ID NO 131
<211> LENGTH: 652
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

```

```

<400> SEQUENCE: 131

```

```

gggggacctt aatatccaga tattttaaat ccttgctgag caagacaatc ttcaacttca 60
taacattgaa tatttcttaa ttagttatct ggataactgc tgattcaata tctccagga 120
gtttcatagg acaacacttg tctcatgaa gtgtaaatca aaagtgatcg atatttaata 180
caccattcta cattcatgaa ccattctaca aaaatttgc caaattgtc ttctttctta 240
gatattctta tacattttgt tctcttaatg ttttgtgaaa gttcatatct cttagactta 300
cttctatgat tctatttggc tccccacgtt gggcgccaaa tgttactctt cgccgatgtt 360
accagttttt ctataaggta tgccaaggta attaactact tttattttct aacaaacgaa 420
agagaataat aataagaat caaaaaatc ggagaatcat acactattta ttcttattaa 480
ccaaaattat aaaatttata ttaattctaa ttgaagatat aaaaaacca aaagaaaaag 540
gtaaaaagct taaataaagt ttatgcttgc ctctaagaat attcttttca gcgtacacac 600
atattaaaat tcttaaaact atgtaaatatt atatttaggt actatttaca ag 652

```

```

<210> SEQ ID NO 132
<211> LENGTH: 658
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

```

-continued

<400> SEQUENCE: 132

```

ggggacatta ttattccaag tatctttaag cagtgcacac gagtggttagg cttcaaagat    60
gaagggtttt ctaagtatta gtattggact ttttgactt tgttcaatag aatcaaggtc    120
tctaaatagc aagcttttcta aaaagccaat atttaaagac ttttacggaa agctaaacat    180
agaagtaaga ggaaaccctg gagagccact gatattaact gacttgatta aagcagggaa    240
gctggatgaa gctcagaacc aatcactcgt gcaaggattg gacacagagg ttaaaagtta    300
ttccggctat ttcactgtag ataaaaagca tgattctaata atcttcttct ggtttttccc    360
ttcacaaaagt gatcccagtt cggtatccgt tgttctatgg ctccaaggag gaccaggatc    420
tacatccatg tttggacttt ttcaagaaaa tggacctctt acagtaaaag atggtgagct    480
gggtattaga ccaacgtctt ggaataggaa tcactcagtt atctacatcg atcagccagc    540
tggaactgga tggagtata ctaacggagg atacgccaag gatcaacata aagtagccac    600
tgatttgtac gaagccttgc agcaattttt caccctcttc tatcaatacc aggagaga    658

```

<210> SEQ ID NO 133

<211> LENGTH: 638

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 133

```

ggggatattg acattcgaca acttttttgg gaggacaggt gaatgttgta gcgtttttca    60
aagtgttaagg tgtttatttt caaaaagttt ataaaataag caatcactat gggtaattgt    120
tttgcaaatt tattcaaaag cctctctggc aaaaaggaaa tgaggatatt gatggttagga    180
ctcgatgcag ctggtaaaac cacaatttta tataaactta aattaggaga aattgtaaca    240
actattccaa caattggatt taatgtggag actgtagaat ataagaacat tagttttaca    300
gtatgggatg taggtggtca agataaaatt aggccattgt ggagacacta tttccaaaac    360
acacaaggcc taattttcgt agtagacagt aacgacaggg aacgtatcac tgaggctaaa    420
gatgaattaa tgcgtatgtt ggccgaagat gaacttagag atgccgtact tctcattttc    480
gccaacaaac aagatttgcc caatgcaatg aacgtgcag aatcaccca caaactcggt    540
ctccattcac tacgcaaccg caactggtac attcaagcta cctgtgcaac tagcggagat    600
ggtctctatg aaggtctgga ctggtgtgcc aatcaatt                                638

```

<210> SEQ ID NO 134

<211> LENGTH: 192

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 134

```

ggggaaaata cgtcaagctg tcattaatgt cgctatcctt tccttctttt tcctttttta    60
cttaacacac gtttgcatag gtaggtcaaa atgaccaaag gtacotcaag ttttggtaaa    120
cgtcgcaata agaccacac cctatgcagg aggtgcggtg gatcttcata ccacatccaa    180
aagtcacaat gc                                192

```

<210> SEQ ID NO 135

<211> LENGTH: 576

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

q 421

-continued

<210> SEQ ID NO 138

<211> LENGTH: 508

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 138

```
gggggttcacg aagacaaaaa tcgggtaccc ttcgtcaaag gggcaactga aaggtttgtc    60
tcaagccccg aagaagtatt cgaagctata gaagaaggaa aatctaatag gcacatcgct    120
gtaacaaata tgaacgaaca ttcgtctagg tctcattcag tatttttaaat aaatgttaaa    180
caagaaaatt tagaaaacca aaagaaacta tcagggaaac tttatttagt agatttggtc    240
ggttcgaaa aagtgtcgaa aacaggcgcc gaaggtactg ttttgacga agctaaaaat    300
attaacaagt ctctgtcggc tttaggaaac gtaattagt cattagcgga tggtaacaaa    360
actcacattc cttacagaga ctctaaacta accagaatcc ttcaggaatc gctcggagga    420
aacgccagga cgacgatcgt tatttggtgt tctcctgcta gctttaacga atctgaaact    480
aaatcgacgt tagaatttgg taaagagc                                     508
```

<210> SEQ ID NO 139

<211> LENGTH: 517

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 139

```
gggtcagccc gatattccca aatttccttg gtacaagtct ttaggggctt ctgaaaagta    60
cataacttct attattagag tacgattcgg gcacgcatgt tatccaaagc atttatttaa    120
aatacaggtt ttggataatg ataaatgtga gcattgtgaa gaggaagtg atttagatca    180
tatatttttt ggttgttcta aaaatacaat ttactcatct aaattaatga atgattttatt    240
aaaaatgtaa gtagcaactc cttggaatat actatattta ttatcacttg gttctgcaga    300
tgtataaaac tctttaatta actttttaaa agacagcaaa tcacattat aattccctta    360
aacattttta attaatgcct ttggtagtta gttgttttag ctgttaagct tagtggtact    420
taataccttt tagttgttat ctttgtttta aacctgtttt gtataacttg ataacttgta    480
ttccttatgt gtctggcagt atgacggtaa gtctaag                                     517
```

<210> SEQ ID NO 140

<211> LENGTH: 585

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 140

```
gggggtcggg aaaaagtatg tcaagtaaat gatttatcca atccaaaagt ccaatctgat    60
taaaactttt cctgtttggc tgagttgtga atctggtcga gcagggatta caaggaagaa    120
tagaacacta gttttattct cactatctcg ctactcttat ttcagatgta tcggtcgcca    180
tcgcatgata gaacgcacaa gagatgataa agtttcttcc tacctatagg cttagcgaat    240
acaagtgaac aaagccaaag ttaattaagt aatagatatg attatcagag acagagtacg    300
ttaaaataaa ttgccatgtt accggcggct cacagtgggt ccaaatgctg aaaacgtggt    360
catgagatgt catattctcc ctaaaattgg ataatactta atacaaaaaa agtgataata    420
tggtaaagaa tcagcttcta tggatgacg gtgtgttcgc ttctcaccac tggcaaagag    480
```

-continued

```

agtttcatct tcattggtaa gataaaatgg gaaatagtag taaccatgca ttaagatata 540
acgcagaatt tcgactacgt cttctgggtt ggcgatttaa acttt 585

```

```

<210> SEQ ID NO 141
<211> LENGTH: 383
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

```

```

<400> SEQUENCE: 141

```

```

gggtatatac ggatataaaa atttatattt ttaaatttaa gcggaagtgc ggacacaatt 60
ctaactttaa agtgaactcg tttaagatag tgtacacaca agtggtcaat tggtattata 120
acagtgtgac atgtttttga atttgtagcc tttgaatgga gactatggaa tgaagaccgt 180
gatgcttgca gagttgtcag ccattagatt aacacaaaaa tgccacagat gacaccacaca 240
aaaaaaaaaa tgtgtgtgta ctttgtacgc acgtaagaag ttatacttct attatatgat 300
ttcttaaaaa taaatatact ttaaacagtt tgttttaatt ttttttttta acaccaaact 360
aattttgtgc ttaccgcctc cag 383

```

```

<210> SEQ ID NO 142
<211> LENGTH: 616
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

```

```

<400> SEQUENCE: 142

```

```

ggggggcata attatatctt aagccaagaa gttaatttta attatgaaaa taattttagt 60
agttttggtg attgtagctg cagctacagc atctacggac gaagaaaaat ggagacaatt 120
taagattacc cacaacagag tatatacaa tattgaagag cataaacatc gatttgaaat 180
ctttaagaaa aatctgattc gtattaaaga gcaaaacgaa aaatacgaaa aaggggaatc 240
aacttttaac ttcggaatca ctcaatttgc agaccttacc gaagaagagt tccttagtgc 300
ttttaaaact gctggtagtt ctaagttaag caaaattaat agcaatgtct cttcttctaa 360
aagtagaagt aaaacctccg gtggatcaga tgatttgcca gaacaatatg actgggtccg 420
cactggtgca gtaacatctg taagagatgt tgcagattgt ggtgattgca cagctgaaag 480
cgtggttagcc gcagtagaag gcgctgagtt tataaaaact ggaaatctaa tacagcgaag 540
tcccaagcag ctagaagact gcattccttt taaccagat gaatggtgga tatgttatga 600
gaaggtcctt aattac 616

```

```

<210> SEQ ID NO 143
<211> LENGTH: 174
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

```

```

<400> SEQUENCE: 143

```

```

gggttgataa gaacatgttt agttgttaaa gtccttaact ttttttatta cacaacatag 60
gcgaatgaat ggaaagcaga atgttaagaa aatatagcct gaggctatag ttgggtttta 120
atttcaatat ttataaatg ctagaatatt cctcagggtg ttgtgaaagt tgag 174

```

```

<210> SEQ ID NO 144
<211> LENGTH: 619
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

```

-continued

<400> SEQUENCE: 144

```

ggggctacta cttcagttca gtgtgtaagt aagagagacg agaattcatg cttttcgtct    60
ctatgtatgt ttggaattgg aatttcatgt gggctgcgac acgacacgat attgctgtgg    120
tggtagggaa aggtgttgac gtttaaagtt cttacagcaa cagtgtggaa tttgtgatta    180
aacggcccaa tgggcgaact tttgtgaaat atcagaactg acaggcaata cttatcaaca    240
atgaagctca gcactcagga aaaacgggaa ttggataaat ttacaaaatt tttggcttta    300
aaatgtactc agatcatcgt acagtccaga cttggagaaa aagtaacaag caactgcaga    360
tcacaaaacca caagcacgga ttggttcaac ttgaacatca gtgatctccc ggaagtcctt    420
gcggaaacga aaagagttct caacggcgaa atcctatcct caaatctgcc cttatgtgtc    480
gaaatttctt tgcgtacggt cgagggtgac catatggtcc tcgaaaattg gtgtctgggc    540
atgttgcccc aacaacagtg tgatcctacc acaagaatag tgcatacaat ctataatcgt    600
atggggactc tgctaaaat                                     619

```

<210> SEQ ID NO 145

<211> LENGTH: 612

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 145

```

ggggaacatt ttgcgattta taatagtttt gtcagttttg tttattatag atttaaatag    60
attataaatg ggtacattgc ttacatttga ttattttcat taacatatgt attttctaatt    120
agtgtggcgc aattatataa ttatcaaaag tacgatttat ttggaaaata gtaaatccaa    180
acaccaaata gcaaagatgc ctcatgaaca tattaaatac acaaatcttg tatcttcggt    240
aaataattca gatgaagaag aagatgtgga aagtaagact tctcccatga gctacaaaga    300
acgcaggaga gaagctcata cacaggcga acaaaaaaga cgtgatgcaa ttaaaaaagg    360
atatgataca ttacaagaac tggttccaac ttgccaacag cctgatgttt ctgggtacaa    420
attgagtaaa gctactgtct tacaaaaatc catagactat attcagtatc tccaaatgca    480
aaagaagaag caagaggagg aacgaaatgc ttaagaaaa gaggtagtag cgtaagaat    540
aatgcagacc aactatgaac aaattgttaa ggcacaacaa tcacaaccgg gacacactgg    600
aactagaatt tc                                     612

```

<210> SEQ ID NO 146

<211> LENGTH: 434

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 146

```

gggtaataat aaaataaaat acactgcgaa tctcaacgca aagaaaataa acaacggctg    60
tgaactctga gcggcttgac gaaaacaagt agaatggtgg tgcgtggccg gattatctat    120
caccatcacc accaccacca tgtgattgtg cttgtgtctac gacgttgccg gttgcattca    180
aaaggcgcgt aggttcgtag gtattcgacg tattatattt aatatcttag accatggtct    240
aagtttaata taatattatc tccataattt tgtttttggt ttatatactt gtataatata    300
ccttttatgt caacgtaaag gtattaactt tttaggtttg agtacagaaa aatatacaaa    360
atagtaaaat ctcagggggg gccacgaccc ccccttgccc cctctctgcg ggcgcccattg    420

```

-continued

gatggaaaga acac 434

<210> SEQ ID NO 147
 <211> LENGTH: 590
 <212> TYPE: DNA
 <213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 147

```

gggaagcagt ggtatcaacg cagagtggc attacggccg ggatattgat acctacgaaa    60
gcctcctgaa ttgtaaaaat ggtcttcgag ggggctgcgc gtcgcatcta agctatttga    120
ttatctgatt ttgtgtacc cacttcatta tttaggattc tgggggctca acaatcctat    180
atgtataatg tagttatgga gcgctgaaaa ctacacctgc atattttagg ccaattgtgg    240
gatgcaacac tctttgtatg aggtatcaga taatcaaata gcttagatgt gacgagaaga    300
caattttcac gatttgggag cctttcgtag gtataaataa cccatatttc tagtataata    360
tcataataat agaaccagtg gaaattgcta cccacaaaagc aaaggcgctc gagtcgtaaa    420
aagtcgaaaa tttattataa cggaaacagc ggatattgat acctacgaaa ggtgccagaa    480
tggtaaaaat ggtcttcgag ggcgcgcgcg gtcctcgag cggtattga taccacgac    540
gaaaggcgct cgaatcctaa aaaatctacg acggcgacaca gtggtccaaa    590

```

<210> SEQ ID NO 148
 <211> LENGTH: 149
 <212> TYPE: DNA
 <213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 148

```

ggggtgcggc gcgctccatt tcaaaaatct cctattttca tccgaaaaat attttttata    60
gattcttttg gacattctaa ataaaataag tttcttgaca tttttctcaa aagttaatag    120
ttttcaagtt ataagcgatt gaaaatccg    149

```

<210> SEQ ID NO 149
 <211> LENGTH: 625
 <212> TYPE: DNA
 <213> ORGANISM: *Diabrotica virgifera virgifera*
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: 498, 499, 500
 <223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 149

```

ggggaagata aaataatttc ctgaaataaa gtattgccgt tgaaaaatat ctacaaaacc    60
actttggggg gtgttcaaaa tggacgtcat tcttcattat cgctaattgc cggtgaaaaa    120
tattgtctag agttaaaatg gaaacagtaa attcacagtt gttgacccaa gccataaaact    180
ttcatggtca acagctgcag aagttgtggg aaggagaatt tggagaaaat gatttgacaa    240
gaaaaaatgt caaagatttg aattacaatg tgtatagtea acgccagaag aacctatctt    300
ttcaagatag aggtaaacgg ttgaaactcc aacagttttt gataaagaag gctaatttta    360
tctatagttt ggaacccacg aagcaaaaaga acaatgagaa agcgattact gaagatatgt    420
atgctgttat gcctcctttt gaaacttaca ccagtgtaga caaacaaaaa agagtggcat    480
tcttcatgga gaatgtgnnn taggtaatct aatcctgggc accattgtga gcagacaaca    540
atcaggaatg atgttgaaag tggtgtgtac tactggaaat ggtaacactt gtttatatgc    600

```

-continued

tgctgatatc aacgtcaagg cattc 625

<210> SEQ ID NO 150
<211> LENGTH: 594
<212> TYPE: DNA
<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 150

ggggggtatg aggatgcagc acaatttggg gcaacagata caagcgagaa accagtccgg 60
tgtgagcgag gatgccctaa aagagttctc catgatgttc aagcacttcg acaaagaaaa 120
atccgaaaa ctcaaccatc aagagttcaa gagggtgcct cgagctcttg gatacgactt 180
acctatggtg gaagaaggcc aacctgatcc agagtttgat gctatactgg atgtagtgga 240
tccgaatagg gatggtcacg tttctctaca ggaatacatg gcctttatga taagcaaaga 300
aactgagaac gtccagagtt ccgagggaat agaaaaggcg ttcagggcaa taacggcagg 360
agatcgcca tatgtacca aagaagaatt atatgccaat cttaccaagg aaatggcgga 420
ctactgcgtg gcgaggatga agccttacgt agagccgaag acagaacggc ccatccaggg 480
cgctttggac tatatcgagt tcacacgcac actttttcaa aattagttag gttaggttcc 540
gcattagtcg cttactcttg ctaaacgtta gatagacagt ataattattat tatt 594

<210> SEQ ID NO 151
<211> LENGTH: 627
<212> TYPE: DNA
<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 151

gggggtaagt ttgtaatcga agtcgtttcg ttttcgtttt gtcgtttgta ctttattttg 60
cactttatgt gtgataattg ataataaaga caaattaata caaaatggaa acaatttttg 120
aacaacagcg tcggttaccat gaagaaaaag aacgtttaat tgatgccatg gtaaaagaaa 180
tgcttcacaa aaagacaact ttcagagaag caataaactc agaccaccga caaaagtacc 240
tgctggatag atatatggct tcaacagaaa gactaataga tctttatgat gatagagacg 300
gacagcgtaa ggctgaagta gccgctctta cgggccccaa cgagttccaa gaattctaca 360
gtagggttaa attaatcaaa gacttttaca gaaggcatcc aaacgaaatc agtggttccta 420
tgtcagtgga atttgatgag ttgccaag ccagggaaaa tcctaacgag gatatggcta 480
actttgtaga atttacagat gaggagggct acgggaagta tttggattta catgaatgtt 540
acgaaaagta tataaactta aaaggcatag aaaaggtaga ttacattacc tatttgggta 600
tgtttgacca actatacgat attccga 627

<210> SEQ ID NO 152
<211> LENGTH: 526
<212> TYPE: DNA
<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 152

ggggggcatt gtcttttata aatcgttatc taaaagtttt cagtatgaag gtcgctttac 60
ttttactagt ttttatctgc ttgttaaata ggacctatc cggaccaaatt attttttaat 120
tcaaagacgc caaacgaatc catgcccgtat gtcaagcaaa ctcggaaaca catgtcaacg 180
agtaccttga aaggcttcaa gaatttgga agattgaagt tccaaatatg gcgaagcata 240

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cactctgtat gaacattaat gccggactac aatacgaaaa cggatgatatt gcagttgaga	300
gattaagaag cgacttgga gaagtttcaa acaacgaaaa taaaatcaaa gaaattgttg	360
atacttgtgg tgttcgagcc cctggaagcc ctgaagatgc agctatggct ttgggcaaat	420
gtctatgcag tcaatggcct caacatgcag tatgtgtttg cagcacatag tagcagcgaa	480
aaatagtttt tatataaata tatatcaata aataaatttt atcttc	526

<210> SEQ ID NO 153
 <211> LENGTH: 601
 <212> TYPE: DNA
 <213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 153

acttttttagt cttacacttt tcaaacaata aaatatatcg ccatgtttat taaaatatat	60
gtataaaaca tatgatgtac aaacatgaaa agtagtcgga accggcaaaa aatttaaaac	120
ttttttgttt atttgtgaag cataacgtaa acaattaacg taaaagtct tatttttaaa	180
aattcttgta gttgatgcac taacaaaaaa tgacatgtga aattatcaac aaaaaaaaaa	240
aagaatctag aaacataaaa ttgtaatat tttcgatata aaaaaatttg ggaggtacac	300
ccaaattttt caaggtatac accaacaact ccaaaaaaca aaccaaataa gattttgttt	360
aaaaattatc atcaaaacttc ggagatatgt ttatatacac atttgtcaaa aaaaaaacg	420
ataaatcgat attttttgat atattttcgc ttaaacataa aatatttaca catatgattg	480
aagggtttca aaaaaacaaa atgagacttt ctaaatata atgaaaaaag tttatgccat	540
aattacaggg gaatagcgct actaaacgtt gcgtataaaa tacttgcagt acatataaaa	600
g	601

<210> SEQ ID NO 154
 <211> LENGTH: 95
 <212> TYPE: DNA
 <213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 154

aatgtgaaag ggcgacttg atgaaaagga acccccgtaa agtaacatgg actgtcttgt	60
acagacgtaa acataagaag ggtcaggagg aagaa	95

<210> SEQ ID NO 155
 <211> LENGTH: 635
 <212> TYPE: DNA
 <213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 155

ggggattctc gcgtcctttt ccccaagaga tcgtgacgaa aataactgtt tgttgaattt	60
ctccaattat ttgtgtaatt ttgccattaa tcgcgttttaaatggcaacc cgagtgtttg	120
tgggtgttct tacttacaaa attcgcgaac gtgacttaga aaagtcttc agaaagtatg	180
gaagaatcaa ggaggtttcc atgaagaatg gttatgcatt tgtggaattc gacgatcgca	240
gagacgccga cgacgcttgc tatgagctaa acggtaagga cttaatgggg gaaagaatta	300
ctgtagaaa agccccgtgt acgccccgcg gaagtgatca atggcgggga agcggtcgag	360
atagaggtta ttcaggttat agcggtcac gcggtagaaa cgataattct agagctcgtg	420
acaaatatgg gccccgcg cgtacagaat acagagttat tgttgaaaac ttgtctagcc	480

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gtgttagctg gcaagatttg aaggattaca tgcgtaaagc cggtagagga acctttgctg 540
atgctcataa actagttcca aacgaggagg tcgtcgaatt tgtttcatac agcgatatga 600
aaaatgctat tgaaaagctt gatgatactg aaatt 635

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<210> SEQ ID NO 156
<211> LENGTH: 599
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

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<400> SEQUENCE: 156

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```

gggggacctt ttctggttgc acctccaagg cttctaaaat ttgcaagcca taacggatgc 60
tgagactaaa aaagatgagg gaattttaca atttataatt cacgtctcat ctgctcagcg 120
cggtaaaagt ccaacgagaa tggttccctt agtactccaa tcagagtaaa catgttaatc 180
aaaaattaat aaccattttc aatttcgttg caacactaca gccgcacatc attctagtgc 240
aatcagaggc cgcacatcat tctagtccaa tcagagagtg cagcaagcac ctctaccggt 300
ttcgaaactt attagtctct catcaggagg cacatctgct gctctctctg acccaaccag 360
gacaaacctt ggcgtgcagg tacgcattgc aacgaacgaa atggcaggga tgctctagcg 420
gcaactgcta gcaagagact aagttttcaa actaatagca cataaaataa tatcaaaaaa 480
attactctac atcccaccag attgaaaaca atgagaacct tctctgatta cacatacgag 540
gcttctaaaa ttgcaagcc ataacggatg ctgagactaa agaagatgag ggaatttta 599

```

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<210> SEQ ID NO 157
<211> LENGTH: 167
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 85
<223> OTHER INFORMATION: n = A,T,C or G

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<400> SEQUENCE: 157

```

```

agagtacgga atcaagtaga tgaaaagagg cgaatatttc aagcaatatc tgcgaatgtt 60
agttctgaag gtcagagatt gttcntagct atagctaaaa caattagtga ggttaggtgg 120
aacgattcgg aaattgtggt ttttaatcga gatgttataa ttagtcc 167

```

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<210> SEQ ID NO 158
<211> LENGTH: 650
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

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```

<400> SEQUENCE: 158

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```

ggggaaatat gttagtatgt ggaaattact tgataaataa ataaaatatt gcaaaaagga 60
gcctaaaccg ccattaagaa agacaaaaaa atacacttta ttcaaataaa cttttttatc 120
ccacgcctag attttgtgtc acattggatc tactaaaaat cgattttcta taacaagaaa 180
tcgaacgtga ctgactcggc aacatttcgc gcctatgagt ataaaaatta ttgtttttga 240
tagtataaaa atgtcattgt cagtgtcgaa ttaccgacgc actgttgctt cactgttgaa 300
agttcgaga actttcgaaa aacaagaata ttgatgacgc gctactgttt actcttaata 360
ttaaatttgt aattctcttt tagcgttcct caataccttc ctctatgctt ggtgtccgct 420
caattttttg ttctagtatg ctggtcattt cttgttttac aatatcacat accattttct 480

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ctctatcaat aataactatt tgctttgtca cccatataat cttgtttaat ctcaatctga    540
tttttcctac aaaaatatgg tctccttggt gccaatcctt aaatagtgca tgtcttctca    600
gttgggtttg agttttggag atattattta caccaattgt aatttcaact                650

```

```

<210> SEQ ID NO 159
<211> LENGTH: 584
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

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<400> SEQUENCE: 159

```

```

ccactgaaaa ataaaaaaaa aaacttttag taaggggcta ttctggacta cggggcaatt    60
ctggacagtc aaaaaaatgc ctgtccagaa tggccccggt tgacaaatat acttataact    120
tttttttggc tagaacaaaa aacacaacct caaggggtcaa taataacaag ccatgtaaca    180
ttttgttaag gtgaaaaaca ttaccattac ttacttgtaa atgagtgcag cacagaaagc    240
ttgaccgcta ttttttttta acggttttct cacgaaattt tgtttgcgcg ccaaaggtg    300
aaaaatgccc gcgcggacct tccaacagtt atcaaccaac tggctgaatt tctcgcgaaa    360
agttgtgaat atcacgccac ccgcaagtgc aggttttcgg cgcggttgcc acgtttacct    420
gagaaaacgc gttgtccaga attaccccg atgtccggat taaccccggt atacggtaacg    480
tttttactta aaacttacgt aaaagtttct aaaaattgca tttttgcgtc atatcatttg    540
aattaaattt ttggcatttt ttgaaatgaa acattgttta gtaa                    584

```

```

<210> SEQ ID NO 160
<211> LENGTH: 508
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

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<400> SEQUENCE: 160

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```

ggggacattt gaaatttttt ttggagaaga ctggactttg agaaattcag gttagttag    60
gacaaatttt gcggacttac cttctagtga actagtcaaa ttgtcggtaa ggagtgttct    120
agggcggtac acagtgttct caaatgctga aaacgtggtc atgaggtaaa agagtgtggg    180
tacttatgta caattgtaca gctccagaa agaatcatgg ccgatgacaa acgctgtcgt    240
cggctgtaca cccacctaaa ctttagcaga gaggatttct ctcgttggtc atggttcgct    300
ccgggagctg tacacacgta acaagttata cttctttggc gtcattaaaa agtagttttt    360
gattatatta tgtaaataat tacaataaaa taataaaagt actggaaaac gatagtcaaa    420
gttcagttta aatttgaaaa attaaatatt taaatatttt tttatttatg tataaaattc    480
gttaatatac cagaaataaa acgaaaag                                508

```

```

<210> SEQ ID NO 161
<211> LENGTH: 644
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

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<400> SEQUENCE: 161

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gggttctgag aaatgttaat tggtttataa caattttttt aaacatttaa agattatgca    60
aaaaactgaa aaatttatat ttgtcgaca aaatattaaa taggcatcac acctttatca    120
tctttctaag ttgatcaat gtctcatgat tttttggtt gttattgcga ctgtaaatg    180
ttaattaaca attgaattgt tgctaaagta ttcgtttcat tttaccggc tctgaattt    240

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ataatctata ccaagaaaga ttttatttct ccaagctata tactgataaa taattactgg	300
ccccaaaaaa ttatttgaaa attcgagatt ttgttgggga aaccacatt ttccgaggaa	360
aattttcgtc ggagcaaate gggaaaaaca tgcctctatg tagaattaaa ttggggtgaa	420
tttttatttg agtggttttg gtgtaaagtt aaaatcttcg gagttataga gcaataattg	480
aaaaaaatac gatttgctcg cgcaattttg ttataaaaa agtagcacac tatctgcgga	540
cttttcaaac ctatattaat aatatatagg atcttataat tagattccag caataaaatg	600
gctggtaaat aaccttttct tgtacttaac taattagacc agcg	644

<210> SEQ ID NO 162
 <211> LENGTH: 659
 <212> TYPE: DNA
 <213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 162

ggggcgtgta tatgtatata tttttatatt catgtaacgc cttggaaatc tcaatattta	60
attttatttt ataatctctt ggtattaaaa tttttggtat cggaactaat aaaagatagc	120
ggcttatata taattttgtc acgtttttatc cttgatacat aacaagggtt ccaaaatctg	180
ccagtttata tcaactaggta aaaagtttta gttcgacggt ccttctcact tttgttgtaa	240
aagccgtgaa tacctgtggt ccagaggcgt gcggtccatg gaagcggggg aagcaccgct	300
tctctattat atacttcgat ataacaaaat atattattaa ctaatattta attatcaaaa	360
attttcccca atcccagtaa tctacatatt attacctagg caataggcat tgaaaaatat	420
taaaaattaa tcgcatagga aggaactcaa tatgcactat gcacacaatt caactattcg	480
gtccaccctt gacagaagcg catctcaaaa tcgccgcttg tcatgcagtt gtcctgtata	540
aaaattggtc agggttcaat aaccgcaccc actagtcgcg cgaatttttg tacctgtag	600
aagcgattgt tcgatcgctt tccaagagtg ggatcatctg actgttactg cttctaagg	659

<210> SEQ ID NO 163
 <211> LENGTH: 598
 <212> TYPE: DNA
 <213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 163

gggggaagtt gcgctgtgct gtgagttaca accacgaatc tctcgccag gatgctggca	60
atttggtttt tatttggttc tgtttcatcc tcaaatcaat ttgtcgttga taccgtgacg	120
gccaatgaag tctggcaagc tcctgggttc cataaagtgg gtcatactag aaaagtcagt	180
attccaaact gcgtagaatt cgtgataaca acaaacgctt gtcgcggtt ttgtgaaagt	240
tgggctatac cgtcattaat aaaaggatcc actatccaac cgataacatc cgttggccaa	300
tgctgcaata taatggagac agaaaatgtg tttagcaaagg ttatgtgcgt tgaaggatg	360
aaagtattca cgttcaaate ggccgtcaca tgttcttggt accactgtaa gaaagattag	420
agcgactgct ggaaaggacc aaggcgagtt tattcaaaat ttatatgtaa catactaaa	480
gttcattgat tatatttagg cgtaagtaaa aattacaata tactttctta attactgtat	540
atattgtact gactgactga ctgattgtag gaattatggt cattaaattt tgtttccc	598

<210> SEQ ID NO 164
 <211> LENGTH: 410

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<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 164

gggagacagg taatagcaga gataataga aaaagggtag aataagagaa taatatataa    60
aggtaaatgac acacagatag gagaagctat gctctaagtg aataaaatat atcttgaaaa    120
gctagaataa atggaatatg gagagaagta gaaagttgag agatatgtga agaaaattta    180
ttgaaaaagt tacttaaata cgaatgaaga acggtaggag attcatacag aaaacacaga    240
aacagcgtaa aaagactaat aagtgaaca cagagaataa taattaaatg acagtttgga    300
aaataataat acatagtctt gactatgaac tacaagattt aaagaaagga aaaagtcgag    360
gtaatagcac ctatacaaaa aattacagta attacaaata aaagcaacac                410

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<210> SEQ ID NO 165
<211> LENGTH: 646
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 165

aaaaaatctt tacctaaat aagagaatca aagaagattt cccagtaga aatcagtaca    60
tttatcgaag aagaaagatc cgctatatta aaggaaaatg atcatgtcgt tgatagttct    120
tgggtcgtaa tagaagagga agaacttagt tatataccag aagtaatacc acctgtcatt    180
gttgaaccag aaaaaatgga tgcagatact actgaaaaag atgaacctat tcaagttaaa    240
cctgaagata gtttacctga agatcaaatt gaacatacag agtctatcaa aaagccaaga    300
aatcgggtcta agtcaaaacg ccaaaaaacc cctaaagaac aggaattgtc tgaaactatt    360
gagcattcgc cacgtgtatt accagctata gctactgtcc aatctaacga acagtttgaa    420
gttaaatcaa ggtcccttag tagaacctac gcatcagttg tgaagtcgca tatagaagga    480
gttactcctg aatacattca gtatacccaa gttattactt ctatcgataa taaaccccag    540
accgttgaaa gcattactga ttcaacagtc gaagaaacta cagaagagat aatatcagaa    600
aaagtagtgg agcaaccac agtgcaagaa ttgcaacaa cagaga                    646

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<210> SEQ ID NO 166
<211> LENGTH: 277
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 166

gggggcctgg tacttactta tataatgtta agcttcttta aagtaacttt ttctacaacc    60
gtgttaaaaa tgcaattttt agcactccat acgagcgtta aaaatgctac ttaaggcac    120
tagtgcttta aaaaatttaa ggcagtcgag ttcattatga ccgtatacgc tgtgagctcg    180
tacgtagagg ggatgtttac aaattcgcga gcgccagtag tgacaagtcg gtaaacgttt    240
accggaaatt tgacataaat gtcaaagtgg ttaattc                        277

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<210> SEQ ID NO 167
<211> LENGTH: 659
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 167

gggagtgatg aagttttatt cagactgggtt attcatccta tatttttttt gtaataatta    60

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tggcgacatc aaaattaatg gtgtatctga agaaaaagta tcacaatcct gatgtagctt	120
atagagaaat aatcaacatc accacacaaat acagagggtt acatccagaa cagagtgtct	180
acaccttcaa cgatggcaca agaatggatc tcattaactt aactgggtaca attcctgtgc	240
gttacaaaag caatatattat aatattccaa tttgtatatg gttaatgac acgcatccag	300
agaatgctcc catttgctat gttaaaccga cttccgacat gtccataaaa gtttccatgt	360
ttgtagatca aaatggaaaa gtttatctgc catatttgca cgattgggtg ccgaatgaat	420
cagatttgct aggattaatc caagttatga ttgttacatt tggcgaacaa cctccagtgt	480
ttgctagggc caaagacaat gaatcgtatc cgtcaaattc attcatgcct caaccatctg	540
gtggttacat gcctccgtat cctacccct acccaccagc atcaggaggt ttcggcgggt	600
accctccata tcctccaacc agcaacaatt ctttccaagg atatccacc tacccttct	659

<210> SEQ ID NO 168

<211> LENGTH: 409

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 168

ggggagggta aggttaaact tatgtcaaat caaattttta atttgaacat tgggcctgtt	60
atatacacag cactcagaac atatgcaccc tatgtaactc ttctgtgtgc tgcctctgta	120
ggagtcata gttacaatct agaaagtgtg atctctaata gatatacacc atacaacaaa	180
tctattaaag aacaacgaga agataggcta ttagttgaag caaaacttaa agaactgat	240
aaagtagaga agttaaaata taaggctaatt attctagaca caaatttatc tccttcctta	300
acttgaacat tagaatggtg cattggtata cacttaaatg ttaataaact ttaataaatt	360
ggagtatgta ttgttttagt tctctatatt aataaaaagt tgtgatatt	409

<210> SEQ ID NO 169

<211> LENGTH: 253

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 169

ggggacaaaa tatggagaaa taaaatatcg gaaaagaaat aaaaggcaga atttacaaaa	60
cagtcacag accaataatg acatacgcgg cagaaatcg acccgacaca gagaggacca	120
aaagattgct cgaaacagag gagatgaaaa cctaataata atcgacaagc tcacccggaa	180
aagagaatcc aatcgtcttc agcaactagc ttacaattca aaccagtcac tcacaccaat	240
ctataggtcc ctc	253

<210> SEQ ID NO 170

<211> LENGTH: 633

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 170

ggggaaatag gaatatgaaa acatttcacc acatcaacac gtgaattaat attcgaaaat	60
ggagtagcaa aatacacaac aaaatataaa cttcgtaccg tgtgtaagat ggggttaaag	120
aggagtggcc aattcaagcc cagtaaaatt gcaactgtcg aaaaacgagc tggctcaaat	180
tattaatgac accaagatta aattacaaga atccaatgaa aatgaagatg agcctatgga	240

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agaaggtgaa acgtctcaaa cagatgagtt tgccttagag gattacgata aagaagacga 300
aatgaggac actgcaaagt ctttaggaat tggatcattg gcagaactcg ataatgatgc 360
tgcagacaat ttttctgagt cagacgattc tgaaaaagaa gatgataaaa tcaaaccatc 420
tgacaatctc atactagtag gacatgtaga aggggatgca agtctattgg aagtctacat 480
atacaatgaa caagaagagt cattgtatgt tcatcatgat attatgttat catcctttcc 540
tctgtgttta gaaccgctaa actatgaacc gaagatgcc aaaggaaatt attgtgcagt 600
gggatcaatg tcacctgtta tagaggctcg gga 633

```

```

<210> SEQ ID NO 171
<211> LENGTH: 640
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

```

```

<400> SEQUENCE: 171

```

```

gggccctgta tatacctcga tggcaataat ggacctgacg gatgtgctat tttttataga 60
aaggacaaat tcgaattact tgaggcacag accaaaattt tggagatatg gaaggttcaa 120
agtaatcagg tcgttctact gacaatctta aagatgaaag aaacaggcca aaaaatctgc 180
gtcaccacaa cccacctcaa ggccaaaaaa ggagctctac tatccactct tcgcaacgaa 240
caaggtaaa atctctctca gtttgtgaaa gcaaacagcc aggatcttcc tttgattcta 300
gccggagatt tcaacgcaga acctactgaa cctatctact caaccgtact cgacaatcct 360
ctgaagctgg gtagtgctta tgctgactgt gatattgac ctacgatttc ctcagctgaa 420
agggaaacct cgtacacgac gtggaagatc agagggtgag gagaggctcg ccataccata 480
gattacgtgt tttattccaa gaataagcta gaactagagg ccgtattaga tatgccgacg 540
ggagaggaaa ttggagagaa cagagtaccc agcttttctt acccatcgga tcacttttcc 600
ttagtgtgtg atttcaaaat aggccatagt taagtttagg 640

```

```

<210> SEQ ID NO 172
<211> LENGTH: 651
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

```

```

<400> SEQUENCE: 172

```

```

gggggacaaa ttgatgaaag aatgatggtt ggtgcttttt tcaagtctat accaatggca 60
gcttttgccg actgtagcga tctgaaataa gaaaaaaagt ttttttcgaa ccaccctatt 120
aagcagacaa attaataatt gtatcagaat catttattca ttgggagtta gtaaatatct 180
ctgctcataa tttaaaaata aatattttaa aaatatcccg ggaagtcttg aagaattctc 240
ggtaatcggg attttcattt tttactgatt tcccagagaaa tttgtcccg gaatgcagct 300
ctattttagt gtactctact ggatgattga gaaaaacaa cactaaaaag cttattgtaa 360
aaagttatga ccgagaaaaa aaggccgact taaaagtacc attgggaagc aactgtcaaa 420
aaaaatctaa atgtgctgag agactaaggg ttaattatga tatacagatg tcgttttcct 480
cctcacaact ttttctgttg tcccttgggt ctactagctg ataactttgt aggttccttt 540
aaattcatgt gtaactggag tagttgaatt tggtttcact tctctttagt tcatataggt 600
cttgatcatt atcatcatc aatgatgatc ttgatcatca atcagttttg a 651

```

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<210> SEQ ID NO 173
<211> LENGTH: 667
<212> TYPE: DNA
<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 173

```
ggggcctttt ccaaagtttc atataatttt taagatgagt actgttatta aaatcgtttt    60
aaaaatggaac ggaaaagaat ttaatttaga atcatcggaa gatgacactg tatctgattt    120
aaagaaaacc atagaaaatg taacctcagt aaaatgtgga agacaaaagt tgttaaattt    180
aaaaatacaa gggaaaacgc ctgaagatga ttgtactctt ggtcttttga aacttaaacc    240
caactttaaa ctcatgatga tgggttcact tgaagaagac atagcagaag caaatactgc    300
acctgaaaac cttcctgatg ttgtcaatga tttagatata gaggaagagg aagttgccat    360
tgaaaatcag gatgtatata ttgcaaaagt ggaaaaacgt atcaaagatt ataaaaataa    420
tatgttaaat gatctccggc ctgaaaaaaa gttgctagta ttagatatag attacacact    480
ttttgatcac agatctaccg cccaatctgg agcagaatta atgaggcctt atttacatga    540
gtttttaact acttcttatg aacactatga tattgttatt tggctctgta caggaatgaa    600
atggatcgag gagaaaaatga agctattagg tgtttctacg catcctgatt acaagattgc    660
cttttat                                         667
```

<210> SEQ ID NO 174
<211> LENGTH: 623
<212> TYPE: DNA
<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 174

```
ggggagtctt gtgaaaaaag tcacagcgct cactggcggt ttattaagat caaaatgcca    60
tcttcaccgg aggaaacaac ttttcctcaa agactgcagt caagcaacaa cttaggcgaa    120
caaaattcaa aagaccaaat aaaaaaaaaat gggtatttcg agcaagattt ggtatggagg    180
aatgtaatta tatatatagt actccattat ctgttaattt ttgcaatatg gagacttttg    240
accggtcaaa tgaagcttgg aacttttatt tttcattgta tttacgctac ggcttctgtc    300
cttggatatca cagctggaaa tcgtcgtctc tgggctcata gaacctacaa agcaaaactg    360
ccattgcgaa tatttttaat gttaatgcaa acaacgacca tccagaataa tatttacgtt    420
tgggccagag accatagact acatcacaaa tacacggaca ctgcagctga tcctcacaa    480
tcgaatatag gattcttctt ctctcacgtt ggatggctat taatgaagaa gaaccctgaa    540
gttaaaaaac aaaggaaaga atattgatat gagcgatgta gcagctgacc ctgtggttca    600
atttcagatc aagtattatg gaa                                         623
```

<210> SEQ ID NO 175
<211> LENGTH: 406
<212> TYPE: DNA
<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 175

```
gggatatgca gaagacataa ttcttatagg cagatacaag gaaagataaa aacaagcagt    60
aacaatcctg gcaaatcaag tatgggaaag aggtctaaag gttaacgaaa taaaaacaaa    120
atatctactc tgctctagaa gagaagataa aaagacgaga gaaatcaaga tagaaaacta    180
cacttttgaa agggttcaat aatttaaata tttgggagta attgtaaatg gcaaaaataa    240
```

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gaaaagtgaa gaagtaatgg agcgaatact agcaggcaac gaaaatactg gagatatcat 300
aggctaataga aggaccagca cttatccaga aatacaaaaac tgaaaatata cagatttgca 360
atcagaccag tatttacata cgcagctgag acaatgtgcc tcacag 406

<210> SEQ ID NO 176
<211> LENGTH: 660
<212> TYPE: DNA
<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 176

ggggggaaga atttgtaggt taagaataaa ctgcatgttt ttgttttaaat ttaaattttt 60
gaaagatcag taatacaaaa tggaaacaca ttcacttgaa agttcacaaa aaagaaataa 120
cagaaaaagg aagaagtctt ttctaaaaaa tgcaagaaaa tatgccaaaa aaggacattt 180
tggaagaggt tcccaattgg attctgatac atatcattat ttcgtaaaaa tattagaaac 240
atataaagaa ggttttgata cagatgaaga taaacaagtt tttgctaata atgtgtttgc 300
acaaaccgaa gatcaagaag tgaattgttc ttgtaaccaa gtaggatgca gagttgtgga 360
aatgctatta ccttttgcca atgatgacat attgaagaaa ttcatggttg cctttagtga 420
agatatgagg cctctaatac gtgatagatt tgcaagccat gtattagaat gtcttgtttc 480
ggaaagtgtt aaaaggactt taaataacaa agtgccagaa gaatcaagaa cagagtatca 540
gaaatttgct attaaagta gcaagttctt gttaaacaat ctaggaggatt atatttgga 600
tacttatggg aatcatgtta tacgaagtg tcttacacat ttaatacaga tgctgttgga 660

<210> SEQ ID NO 177
<211> LENGTH: 578
<212> TYPE: DNA
<213> ORGANISM: *Diabrotica virgifera virgifera*
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 284
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 177

ggggcatgct ttgagcgtac agttgaactt ctctacaaat atgtagtacc taaaccacgt 60
gctgactgca ctaaaggcga acaattgatt gttacatttg ctgctgggta cattgcagggt 120
gtattctgtg ctattgtatc acatcctgct gatactgtcg tcagtaaatt gaaccaagaa 180
aagggatcaa ctgctctcga ggctgctaag aaattgggaa tggtctggatt atggaaggga 240
ttgactccta ggattgtgat gattgggtaca ttaactgctt tgcnctgggt catctatgat 300
gccttcaagg ttgcatgag aatgccacga ccaccaccac cagaaatgcc agaattatta 360
aagaggaagt tggagggcaa atagagaatt aatttattaa cactaatatg taatttatga 420
ctttatttcc agaaaaacga aatcgcagta tttccattag ttcgttatag ttattgattg 480
tcatcaactt tgcaattttt gatgttttta agttcatacc agttatgtcc gatattttag 540
attgtaata gataatcatc aatatacaac tggaactc 578

<210> SEQ ID NO 178
<211> LENGTH: 678
<212> TYPE: DNA
<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 178

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```

ggggagaatc aaattagaat ataaatttca aatgttttca aattttcaaa tatgaattat    60
taaaataaat agaaatgatt ttgtttaata acttctttct tcgacacgta aataagttaa    120
taaaacaagc atactgtaca aatataagta gtttgtcaaa agttgaaaga attaaattcc    180
taaggaaaat ggcccgctct aacgcaaggg aaaacccggg gataatgaaa ctaaactcac    240
aagaattcca ctctatattc aacgaggaat tgcgaacttt agtatcctta tttaaagagt    300
atggctatga aattcgaatt gcaggtggag cagtaagaga tcttttaatg ggaatgcaac    360
ccaaagattt agattttgcc actacagcta ctccaacca gatgaaagaa atgttcatat    420
cggaataatgt tcgaatgata aatgccaatg gagaaaaaca tggcactatc acaccagaa    480
taaatgataa agaaaatttc gaggtaacta ctttaaggat agatgtggta actgacggta    540
ggcatgcaga agtacagttt acaacagatt ggctactaga tgcactgaga agagacttga    600
caatcaattc aatgttccta ggtctggatg gttctgttta tgattacttt tatggacatg    660
atgatcttca aaaacgaa                                     678

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```

<210> SEQ ID NO 179
<211> LENGTH: 647
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

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```

<400> SEQUENCE: 179

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```

ggggctctgt cattttaaaa tgggtagtgc aagaactctt tttggaattt taggctcaaa    60
acagatatta ctatgttcaa attcccagtt tactactaaa atttcaagaa catttcttca    120
tcaatgcttt agatgtcata aatctctact gctaaatacc tggtcagcta ataatttaac    180
tcaaaattct ttactccata aaagaacggt tcataagtca cacagtttca atgccgcaag    240
acgggattat tatgaattat taggagtagg taaaaatgct tcaaaactctg atattaagaa    300
agcttattac aaattggcca aaaagtatca tccagatgta aataagaatg atccagaagc    360
atctaaaaag tttcaagaag tttctgaagc ctatgaaatt cttggagatg aaaataaaag    420
aaagcaatat gacacttggg gtgcaacagc tgatcaaatg ggaggcatgg gtggtggagg    480
aggccattca aaaggccac aaggattcag tcagcaatgg caatatcaat caacaattga    540
tccagaagaa ttgtttagga aaattttcgg agatgctttt actcgaggct cttctcattt    600
tgaagatttt gcagaatcaa actatggatt tggcgaagct caagaga                    647

```

```

<210> SEQ ID NO 180
<211> LENGTH: 204
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

```

```

<400> SEQUENCE: 180

```

```

gggttgtagg ataaattgaa aaaaaatgta cccacgaata tattacaaca acattacatt    60
ttctcgagaa tgggcgggca tgatgacgta atcgatgatt tttattaaat gataatagga    120
ttcgtgtgat atctcactcg aaagtttatt caatgctcta ttcactaata taaacattta    180
tataattatt tataaagggt gccc                                     204

```

```

<210> SEQ ID NO 181
<211> LENGTH: 98
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

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```

<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 73
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 181

gtttggacag tctggagctg gaaacaactg ggccaaggga cattacacag aaggtgctga      60
attagttgat tcngtattag atgttgtaag gaaagaag                               98

<210> SEQ ID NO 182
<211> LENGTH: 174
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 182

gtaaaattaa ctacttctgt gaaaacattt atgaaattat gtaagtagtc gtttttatat      60
tatattggta ttaagattat aataatattt ataaattagt attaaaaata gatggatgca     120
acaaatgta ctctacagt gcgctggagt aagtgttagt gttaccccc cccc             174

<210> SEQ ID NO 183
<211> LENGTH: 577
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 183

ggggagtagc tgataagcat ggatcataca cctattcaac agttttatag ggatgccaac      60
gtattttatca ctggaggggac gggatttatg ggaaaaattc tcgtggaaaa gctgctgagg     120
tcaacggagg tggaacttt gtatttgctt gtacgagaaa agaaagggaa gcacaaggat      180
gacagaatca cggaatatt cgacgatgtg gtttttaaaa gacttaaatc agaaaaatcc       240
aaattcagac atcgagtaca agctatatcc ggagacttaa tgctaccgca tttgggatta       300
tcagagtcag atagacagct tttaatttca aaagttaacg taattatcca catgggagca       360
acaatcaaat tcaatgaaag catcatcagt gcattacatg ccaatgtata tagtaccaa       420
ttagttatag acttagccaa agaaatgaaa catataaaat cgattgttta tgtatccact       480
gcctattcaa attgcacacg aagcgaagta gaggaaaggc tgtatgatcc accgatatcc       540
tatgagaaat cagtagagtt aatagaaaag ttgtcaa                               577

<210> SEQ ID NO 184
<211> LENGTH: 473
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 184

gggattcctg aagttgattc cgttgtagaa cgatcagaca aaagtcgaag aacagccatg      60
ttgggtagtg tcggcgaaaa aagtgtatgt tcctagagaa aaactcgag atttttgtgc       120
ttgtgttgty caatttgta agtgtttgac ataatttga ttatgaccgc cgtagcggag       180
aacotcaact ggggcaccga gctctgggac cagtatgaca acttgtccct gcacacgttg       240
aaaggaatag actttttgga aaaatatgga cagtttgta gggatcgagc tagtatagaa       300
tgtgaatatg ctacaaaatt aaggagacta gtcaaaagt atcagcctaa gaaaaaggac       360
gaagatgatt accaatttac ttcctgtaag gcatttcgag ccttaatgaa cgaagtaaac       420
gactggcgag gccagcatga gttagttgct gaagatttac aagcgaatgt gat             473

```

-continued

<210> SEQ ID NO 185

<211> LENGTH: 683

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 185

```
gggggggattt tcaaaggtgt ttacaaattc aaattgttta ttacaagttt attacaatga      60
gagtgtatct ttgaaactgg aaatggcata gtccaagaag aaaaaggatt ttgaaaaaac      120
gccggtacaa aggaagaagc tcaagtcgct caagggtttt cctcatatac tcccccgaa      180
ggagtaaaaa tagaactccg gtacatcgca gacgaaaacg gttccagcc aatcggagac      240
cacctaccga ctccgccacc aatccctgag gctattttac gagcgctaag tgtactgaaa      300
cagttgggta atttgaatga agaccaagaa gaaaataaca acattagatg aagagagagt      360
gtgatcaaat cgttattttg gataagtcct ttcatttttc aaaatggtac cataactaact      420
atgaaatact tcaaagaatt aagatctttt taaaatacgt caacacttta gagtaggaaa      480
cagcggtgga acctcgcaaa atgtacacaa gttcgggttt atttttttgc aggaaaatca      540
aggggtgctt ataatgaaac taacattttc ttaaaaaatt tcgcccctga accccccttt      600
ttatcccttt aaagggggta tttgtggttt ttgcgaaaac aggcccttcc tgtatacgtt      660
ttgcaaagaa atgtacttaa tgg                                     683
```

<210> SEQ ID NO 186

<211> LENGTH: 446

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 186

```
gggttatttt agtatttgca cgaatctgcc gcacatgggt gcatgtgaag gtgagttgtg      60
cattttattac atggtggttg acatagctaa aatgtttaaa atgtttccta aaaaatgttt      120
ttgcgctctt ttcaatggcg gtattaactt ttttaaaaat taatacatatc aggggtgaaag      180
aattaaaaaa aaaacaacat atttttacat tctaggaaaa acacaacttc tggtaaaccg      240
attcttcggt ttcgacacct tgatcttaca cattaaataa agaacctata taccaaatct      300
ggtttgaata tgacgtctca ataaagaagt tatcgtgcta ttagtcacat atgtatagtc      360
agggccctcg ctacaatatg tgcaaagtgt gaaatgcaca cgggctccgt tcttttagggg      420
cgccacaacc gaggggtcaaa aagtac                                     446
```

<210> SEQ ID NO 187

<211> LENGTH: 148

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 187

```
ggggtgttct tcattcttgt tgctttactt aacacatctt caaattacaa agaccggatt      60
tctgtaactt ttgaaacgct catttttacc accgttaaaa atgggtttatt ccatttttcc      120
atgttgagat tgttgtttta tctacgct                                     148
```

<210> SEQ ID NO 188

<211> LENGTH: 517

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

-continued

<400> SEQUENCE: 188

```

ggggggtttcg tttcatcatc atttgttgta attttttagt taaagcacat taaaaaaaaa    60
atctgtttta aagccatggc tgatgaagaa tttgacgaaa atgatgtagc agatgatttc    120
gatgacgacg tagaggatga taatatcgaa gaactcgaac aacccgagga agatggagat    180
aacatcgata tccttgctcc aggacaagca ggaggtggtg taccaaaaaa caagaggata    240
acaactaaat atatgaccaa atatgagaga gccagagtat taggtactag agccttgcaa    300
atagccatgt gtgccccagt tatggttgaa ctataggtg aaactgatcc tctgcaaatt    360
gccatgaagg aattaaaaca gagaaagatt ccaattatta ttagaagata tttacctgac    420
cattcctatg aagattgggg aatagacgag ctcatatta tagatcacta gattgtaatt    480
tttatgtgga tattatttaa tacatagggt tttataa                                517

```

<210> SEQ ID NO 189

<211> LENGTH: 654

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 189

```

ggggacatac gtggaactta gctataagtt gtagttttgt agggtaaatt cgtaggtttt    60
agtgaagaa aatgtcgtcg aaaagaaaaa gtaagaaag cataattgct aggggtgaatt    120
tcccactata tactcttcag atgttaacgt caaggcatgt aatcgttggt ggtggaggag    180
ggacatccaa aactggtgta cacaatggtt ttgaaatatt tgagattttt catgacggca    240
cacgctttgc agcaaaagaa gtaaccgac acgaaactgg aggcaatggt gttatgaact    300
gttctgttta cagtgataga aaatattctc ttttggtagc tggacaagaa agtgagtgtc    360
aattgtacaa actgaatcct aaactagtcg aggaagtgga aaatcgggt aataaactc    420
atctcaggca acggaataca aaaaacaaag aagttacaga tgacaacaaa aacgtgacaa    480
aagagttata ttttgatggt aatgcaatag aaaatgttca aactgacttt aatgggagtg    540
aaccattatc gaggggtgga aaaattaatc atgatggtac attattagct acagggtgga    600
cagatggaga tgtacgaata tggaagtgtc ctatgatgca acctctatct attc        654

```

<210> SEQ ID NO 190

<211> LENGTH: 433

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 190

```

gggccacgct acaatagaag acgcggtgta cggcgggtta acgaactccc ttacattaag    60
agccaatata tggtagaggt acattttcag ggtacaaggt ttctccccat gtaataatct    120
gacgcgctcg agtaactgca aaaatccccg cttgggctcc cctactatat tgaatgtagc    180
aaatatattat tgaaatcttt tattttcaca aaatatttat ttagtattga tattttcaga    240
tagaaaaatgt tctgtcagac atactgcata ataataaaa attgaggtat aggctgttga    300
ttatgtactt tagaaagga ctacaatgtc aaaggtgttt tattgtttca tatagtcaaa    360
gggtccccaa atataaaaa accgcggagt gctattactt aaagggtac gtttctaagg    420
aaagggtgaa tta                                433

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<210> SEQ ID NO 191
<211> LENGTH: 316
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 191

tttaatactt cagaaagttg catttcagta tttctttaat ttaatttta taaaattaat      60
tcacattgta ttcatttaaa tccttagaag caaaaatcca ataatggccc taccaccatg      120
gttgaagtcc ccttttacag acttaacggg atctctagta aatcaccagt ggtacggaga      180
atgtgctgat atggaattaa aagttttaga ctgtctagat gcctatggat tggacagggg      240
cttaaaaaaa tgtgatgatc tgattgaaga cttcagagag tgtgctttaa aaacaaaaca      300
gttcaaaaga atgtac                                     316

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<210> SEQ ID NO 192
<211> LENGTH: 673
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 654
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 192

gggggagcga cgtggtggcg acgtcagctg attatttcta tttccctatt tctatttctt      60
acccgttttg tagtttataa atttataaaa acaacgaatt tagaatgtag ttttctgtag      120
gtaggaacca taaacataaa aatcatatta tttgattttg ctttttgat gtaaaccgtaa      180
aactgaaata cctctacaat aacgatctat ttatacataa atttatttta aaaatcaaat      240
atggaaaata atcgagaagc tagtgaaaaa actgttgaaa taaaagtaga aaacgaagac      300
acctgtgttg gtcccttgga tgctttcaaa attgaaatta cagaagaacc caagagagaa      360
cccagagaac ccgcatacga ggcatttggt tcttttagact caaataaatt tctgttaaac      420
actgaagtaa aacaagacga atataaattt gcaccatttc aagaaaagca aagaacagat      480
gaagaaaaat atattataca agttctaact actctatact gaaatcataa tgaagatgca      540
ctagaaataa acaaaccaat atttatatat taagcgcaaa aggccttgta ggcctagggc      600
taaaatgttt acattttctga ttacataaat aatataataa ataacttagt atancttaca      660
taacttataa aag                                     673

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<210> SEQ ID NO 193
<211> LENGTH: 614
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 193

ggggtcatca agttcttggt ttgtctcgag gagttgattc gttttgttgg cagtacattt      60
tataattatt ggagtcggaa tatttaatta atgtgattag aaagtgtata gttttagaac      120
tagccatcac ttacttaaat ttctttaata gactcattgt tttaatatag tttggtcagt      180
tagttaataa agtgtaatta aaaatgagtg accccacaaa tcctactgga ctacctagaa      240
gtttaaatta tgaagcatta aaggctcata taatatcgca caaaataaat tgcggcctat      300
ggttaattag ggtagtaggc attctctgct ccatagctta cttcattcca atttttggaa      360
atccttacia ctactattac aaagtactcc tagcaaatgc agctatcagc gcattgagat      420

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tacatcaaag gataggcaga gtgcaattca cgagacaatt tgctgcagaa ttactttcag	480
aagatagttg tcactatctt ttctattcgt tgatattttt atacgtatcg ccagtatcat	540
tggtactcgt accaattatc ctctctcgcg tactccattc agctagttag tcaactcacat	600
tgttagatac atta	614

<210> SEQ ID NO 194
 <211> LENGTH: 396
 <212> TYPE: DNA
 <213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 194

gggataatca ttagtttttt tattgaaagc tggaatgaag ggttgatga aaaaaaaaaac	60
tgtctttatt taatttataa agaattttat ttttaagtta aaaagcttaa atttttttta	120
aagacgagaa gaccctatag agttttataa aattattaat aagttttttt agtattaaat	180
ttatttatat aataaattta tttaattggg gtgattaaaa aataaattta acttttttta	240
tattattata ttaattaata attttttgat ccaatttttt tgattataag aataaattac	300
cttagggata acagcgtaat ttattggag agttcaaac ggtaataaag attgcgacct	360
cgatgttga ttaaagttta taattggtgt agcagc	396

<210> SEQ ID NO 195
 <211> LENGTH: 533
 <212> TYPE: DNA
 <213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 195

ggggagggtta taaaatattt gatttttgct ttttgcaacg gggatttttg atttattatt	60
tatttataat tcataggatt tatttgaggg aaaatttgaa aatttgacac agatttgggg	120
atgacctgtg tgtaagtgt tggtagagag taatcagttt ctatttatca tgggaaaagt	180
aaagaaacca aaagcgaag cgctagggtc gtttgaatcc aaaaataata gtgtccaat	240
aaaggaatcc atttcagcca actttgattt tagtataaaa caaggaaaat cagttgtggc	300
agatgatgta aaaagtgttc ttcatataa atccattaag tcccataatc caattaacag	360
gattataaag aaaaaagaaa aagtgaattt aaaacgaaag ttactgatga aaaaaattga	420
tttaggcaat gtactaaaga aagaacaaaa gatcagggtc aagagaaaaa atacatcact	480
tattggtgac actaatgcac tgcattgatgc tttaccttca ctggattcat tat	533

<210> SEQ ID NO 196
 <211> LENGTH: 655
 <212> TYPE: DNA
 <213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 196

ggggatttgt aattgagata tctgttggtt tgtgttggtt ttctatacac ttgagtctca	60
tatccagtat ccttctttta gactaaagca tcgaggaaag gcagggtgtt attatattcc	120
ttttccattg taaattttat tgtctctttt atttatttta ttgtctattc tattatctct	180
aacgcgagag ttttagtgtc accgttgcat gtggttgtct ttttgaagac agatcgcatg	240
ctatgatttt tttttgtgac ggatgttctt gagttggggt tgatttcattg tggtcgagtg	300
agctatcttt cagtggagtc gtcccaggaa cgcgactcat aaatgttggc agtatcattt	360

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taaagtcttc tactttggaa tgtgtcatat gtatctgaat tgccgatgtg aatgagtcgg	420
attaagtaaa ttattggaag aattttttac taagcaacaa catttttggt tatattagt	480
gtattttgta ttttgacagc ggcgcccgat ttgggcgtcg aaacgttagt aaaaatcatt	540
ttttaatgat attgtggttt atttccatt ctaaatagtt aaaaatgatt tctttgattt	600
gtgtctgatg aataattatt taggtatttt taaatgtac ttaaattata ttttt	655

<210> SEQ ID NO 197
 <211> LENGTH: 602
 <212> TYPE: DNA
 <213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 197

gggtattcgc tttaaactcc agttttttta aaaactaatc attctaagcc agtcaaactt	60
ctagaatcta ttaataatac ataaataaag aagaataaat agtccaatg actgaaaaca	120
ccgccaaactt acattattat gcttccaatt ggatttctct ttttttttc aaaaaatat	180
attgattttt taaccgtaac tttttaaatt tttatcttag aaagtctgtt aaataagaat	240
ttttaggttt ttacaagggt ttataatgct attaacatta aatcctttta aaattctcag	300
tcacaaaaag aggtggcatt gaaaggggtg gtaaggtgg ttttgcgtg atattacaag	360
ttttaattgt caatagctca ctcaattttt gtcgtaaaaa aatttttgca aactaaattc	420
ttgggaatta aataagttac aatttcatat ttaaataattt ttttttcgta tctctgatgc	480
tactctttct attctgaaga aaaggcattt tttacaacac tacaaaaact cgttattcgc	540
ttttaactca atttttttaa aagctgatca ttcgaagccg atcaaaacttc tagaacctat	600
ta	602

<210> SEQ ID NO 198
 <211> LENGTH: 557
 <212> TYPE: DNA
 <213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 198

gggacatggc ttgctgtatg ttgtacagag gggatgttgt accaaaggat gtaaatgctg	60
ctattgcaac cattaagacc aaacgtacca tccaattcgt agactggtgt ccaactgggt	120
tcaaagtagg tatcaactac caaccaccaa ctgttgtagc tggaggatgat ttggctaaag	180
tacaacgtgc cgtatgcatg ttgtccaaca ctacagctat tgctgaagcc tgggcaagat	240
tggaccacaa attcgatctt atgtatgcca agagagcttt cgtccactgg tatgtaggag	300
agggatgga agaaggtgaa ttctctgaag ctctgaaga tttggctgct ttggagaaag	360
attatgaaga agttggtatg gactcggag aaggtgaggg tgaaggagct gaagaatatt	420
aaatttgatt ccaaactga caaatcactt gtttttaaga caaaaaattc ctttcaattt	480
ttttacactt tttcattact tttctgtgaa acgattattt aaagtctgat ttaacttaat	540
acagaatttt ttacgag	557

<210> SEQ ID NO 199
 <211> LENGTH: 630
 <212> TYPE: DNA
 <213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 199

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gggagttact cggatttcgg tatcaataat gttattaaca gactcgttta atattttatc    60
agttttctcc tcgacaatga gcagctagta tggctcgttcg gaaatacttg tatataaaact    120
ttttgatatt aatggagttg tcctatttct acgcgacttt ctgaacgtgt tagagaatat    180
agttgatcta acatttggtg atagtatttt ttagagtgtt tattagtgtg ttcaagatgg    240
ttaactttac gaagagacag tgggtcaacgt tgatcgttat tgggtattgt gatttttgta    300
acgctgtttg tgtgtcgtcg caagctccat tttatccaca agttgccgaa agtaagcatt    360
gcacagcgac ggagtatgga ttggtgtttg gaatttttga atttgtgtg ttcttgatta    420
gtcctatata tggagcaaac ctgaatagaa ttggacctaa actcatgttt aatggtggag    480
gctacactat tgggtgtgtg gctatattgt ttggagctga gacaaaaact gagcatcgga    540
atctgaagct agcgggggtt aatgtaagtt ccaataaata attttagaca atagattgta    600
ttttagttga gtgattgctg aataaatagt                                     630

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<210> SEQ ID NO 200
<211> LENGTH: 615
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

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<400> SEQUENCE: 200

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ggggagtgaa aaccctcac cacaacgcac cgacaccgag tatgattcaa cttcaacaag    60
agtgcacca ttcgatatag aatcacatc tcatatcgat tttgccaccag taaataatca    120
gaatcagaac aactgtgata gtttagacgc gaaagaaatg agtgcacga aagaacaaca    180
aagtacattg gggggagcgg ataaagtga aaaacacaag aaaggccctc gacctccgcc    240
tccccctgga ttaaagatg atctaacaac aattgcacat gttctgtgg tgattttcgt    300
agggttattc ttgtatttat gttttgcacg gccgtttgaa ttcttcacgt ggcatccttt    360
gttgatgtct gtagggtaga tgcttatgat gatagaaggc gttctcttca tatccaaga    420
aaacccgata ggaagaagac taaacttggg ccgcctttta aaagtctgtt tccattggat    480
agctttaaca ataagttcta ttttagttac gatcgggttc gtaatagtag ttataagcaa    540
aaacaaccac ggcaaggaac attttaaatc cttacatgcg attttcggtc tcataggttt    600
attagggtgt atacc                                             615

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<210> SEQ ID NO 201
<211> LENGTH: 587
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

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<400> SEQUENCE: 201

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ggggatttta ttttttgtaa agtttagtac atgtacatta tatttaaaaa cagtattgtt    60
taaaataaaa ataaattctt gacgattgtc agacgtagaa aatgttacia agtgtaaaaa    120
agtagcagac tattatcaga accattgatg atgatgaaga agttgaagat ttatcagaaa    180
acagtgatga ggaaatagag tttcaacat ccaacaaaa aactcgaagt aaggaggatt    240
ttgatacgga atttaatttt gtcagttccg tagaagaata taataaagat gtttggaatg    300
atttgactaa atacgttaaa aggaaagcaa aacaaaaaac tgatgacaaa attaaaaaag    360
tcagaggcac acaagctgat gaggatcaaa caaacactga aaatggtaca aatgatcttg    420
tcgattccga tatatctctt tcagaagatg aactaaaaa tgataggatt aaacttaaag    480

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aaaagaaaaa gaaaaaagta aaagctgaca atgatacaga agaatttttt gaagagggtg 540

aattaaattc tggagaaact gttagttttt atcagatgaa tctgtca 587

<210> SEQ ID NO 202

<211> LENGTH: 559

<212> TYPE: DNA

<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 202

ggggacactt cctttcggtc cggctctgca tatcaaaggt gcgaatttag tcattaaatt 60

gccaaatttt ccatttgtat tctctaaatc attcgttttg taagaagatg gcagacttag 120

atgatttctt tgccaaaaa gaccgcgaga agtccaaaag tacaaaaaa tatgtacca 180

ctgaagaagt tgccaagaag ctagaagaca ctgcaaaaa gactgacaaa ttaaagaaag 240

aacgtgttaa tgaggcgcaa gatagtatag ttactgaaca agaccaagac gaatggaagg 300

acttcgagga agaaaagaaa gactacacag ggttaaagat aggaaactta gccatcggtc 360

aaaattcgga aagcagtact acgggagcta aggaaagtac cgaacagcaa caagaagatg 420

agcctggaca agatgtagac aagaaatctg gaccttgga acgcacgcac gtcggggaag 480

cagcggaaagt ggagaaagtt gaatataaac cggaaccgat acttcctaata gtatctaaga 540

ctggcactta tatacccc 559

<210> SEQ ID NO 203

<211> LENGTH: 631

<212> TYPE: DNA

<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 203

gggggattga cgtgaagtta gcagctgcac gcagtgacag ctcagtggtt accgtcagaa 60

aatttttaaat taaaagaaat aaaattttaga atatgttgaa attgttcaa gaaatatctt 120

caagtttggg gaaatctctt accaaaagg gacttcaaac tacttccact ttacaacatg 180

atagcttatt tgtacatcga gatactcctg aagataatcc agatattgtc tttgaattca 240

ccccgaaaa taaaagagg gctgaagcta ttctagccat atatccagaa ggccacaaga 300

gggctgcaat gattccatta cttgatttag ctcaaagaca gtatggatgg ttaccaattt 360

ctgctatgca taaagtggct gaaattttta acttgccaag aatgaggggtg tatgaagtag 420

ctactttcta cactatgttt atgaggaaac ccacaggtaa atatcatgtt caaatttgta 480

ctacaactcc ttgctgggta agaggatcag atgagattct ggaagctatt aagaaaaatc 540

ttaagtaga agttggagag acaagcaaag acatgttatg gaccttatct ggggttgaat 600

gtctgggagc atgtgttaat gccccatgg t 631

<210> SEQ ID NO 204

<211> LENGTH: 93

<212> TYPE: DNA

<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 204

taggattttt cgtaaaacta atccacatcc ccatcaacaa cattatagtg ggatcataaa 60

tatatttttc atatttatgt cagttcatatc aat 93

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<210> SEQ ID NO 205
<211> LENGTH: 614
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 205

gggaataaaa aatttatttt atttatattt ttatttattt taaaataata aaatattttt    60
tagtaaaagt aaagaaaaat tttatttaaat gatagttaat tagtattgtg agagaatatt    120
ttatttttat aaaagaaaaa tttatttttt gtaccttggtg taccagggat tattaattaa    180
taattatata tttattattt tcgaatttaa aagagctaaa aaattaaaaat tttatttgta    240
aaataaatat tttaaataat ttttttgtaa tgaaatgtta ttcgttttta aatataatcta    300
attttttaag aaataaatta aatttattta ttaacaatat atttataatt aaatattttt    360
atattattaa tattaatat ttttagggat gagcttaaaa ataaaatttt attaaaattt    420
aatttttaaa taaaaattag gataaaaaat tttcatattt taaaatatgt tattatttat    480
ttttatata tattattttt attttttata aattttttat taaaatataa atttaattaa    540
tttaatttta gtaatgatga taatattagt attaaaaaat tgtatattta gtaaaaaat    600
ataggtttaa taaa                                         614

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<210> SEQ ID NO 206
<211> LENGTH: 621
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 206

ggggcttctc tgtgcatgtt tcaccatttt taataattta aaaacccgct attcgtaatt    60
ttgttggttg tctttacgga ttacttacaa ttttggaat aaaatgactc ccggccgatc    120
atcaacgact acaaaagtgt ttgtaggaag tttgcctcca gacgctaccc cagaggattt    180
gaagaaactt ttcgagccct acgggaacat tgcagaatgc gacatcgcg acaaatgtgg    240
attctccac ttggaggatg gcgaattggc aatgaaggcc attgacgaac taaatgggat    300
ggaatttatg ggttccaaaa tttcagtgga aaaggggcga gttaagccgc gaaggagtgg    360
cggtaggacc agagggtgaa gagaacgagg agggccgtat tcaagagtta tggtaggatcc    420
aacggatacg gcgcttctgc cgggttacgg cgcgacgcgc gtggctacgg cgcgcctat    480
ggagatcgcg cagccgcgga tccgtacgct gcagctgac catcacagagg ggcttcagcc    540
ggtggtggct atcaggatag aggtgataga ggatacggtg ggcgacctgc tgagggttat    600
ggaaactcat acgtgctgc a                                         621

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<210> SEQ ID NO 207
<211> LENGTH: 624
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 207

gggggagtg gtggtgagtg tcagttaaac gttaacgtta aacaagtatt ttattacatg    60
gtaacacacg tgttgtagga attcccttta aaaacgatgg atgtccttag tcgtcctgcg    120
gaagaatttg aaaatgacca aacagtggaa actatgtggg ctataaaagc cttcgaacat    180
gccgaagttt actttaacat tttatgttca gttgatccaa aattgctcaa actaacacca    240
gtagacgatt taatctataa agtccttaga gaagaattcc caaaactaga agtcgaagta    300

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ataatagaaa atgaattgaa gagcacaaaa gaaaaaagca agtggagacc tttttgtgaa 360
cgatttaaga ccattgcaga agactatagt tatggtactt tactgagagc agatgccaaa 420
gatgattata aagaggagaa caccatatta gttactagga ttcaatttta tgccatcgaa 480
ctggccagga atagggaggg agtcaatgac attctaagga aaaagtcttg gcctgaagcc 540
aaggaagaga aagacgatta ggaagtattt aataaatctc agttttttta tacatttttag 600
ttattttataa gttttttgta agtc 624

<210> SEQ ID NO 208
<211> LENGTH: 574
<212> TYPE: DNA
<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 208

ggggagcctt ttttttttgg tttcgacatg tgcgatgtcg agatcccttg tatatcgggg 60
gcccctttta attgatacgt cggtagctac gcctctgctc ataccagacg gaaaagttga 120
tttaagcgct ccgtacctat cttgttttaa aggggtgtgca acaaagtctc gaagccacgg 180
taatccggaa atcacatata tcgaagaact tacgaaattt ggcaactatt acaacagaca 240
atttgttatt tcaagtataa tgcaacatcg gaatcattaa tttgttgctg ttcgtttagt 300
agttttttat aaaaatgggt ttgggaagaa gaaatggttag tagctgttgt agaaaatggc 360
ttataggaac ttgtttgtat atatttgttt tattactatt aatattttta atagtatttg 420
ttgtagtccc agtcgttttt aaatatagtg ttggaatcca aagaagtata atatttccgt 480
catgggtaat cgaccggaaa aactattcaa acatcgacca atttgggatc aaaggggtga 540
aaaacttcta cgcgaaacttg caagaagatg acaa 574

<210> SEQ ID NO 209
<211> LENGTH: 600
<212> TYPE: DNA
<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 209

gggggagatg atgagcaacc aaaacaaaac attaacattt taatttaaca cccccatttg 60
attactaata acatttttaa aacggctctt aagacacgat gaattacgta tatctttgta 120
ttcttattgt aatattagtg ttagttaaga aaagtgaagc agtaagatgc tatcaatgctg 180
gatcagatga agatggcaaa tatgaagaca actgtggtgc ctatcaaaaa tttgacaaat 240
tgaatcacat tgccattgaa tgtaatagtg aggaaagtca tatgcctggt tctttttgta 300
tgaaatttac tcaacaaagt cctagagggt ttatttggga tggcagatgg agacaagtaa 360
taagaagatg tgcactgtga gctgacacgg gagtaacagg agtatgtaac tggggggtgt 420
atgaaaatgg catttactgg gaagaatggt attgttcaga agatgaatgt aatagtgcac 480
atatgactaa aatatcaata ttttcagtta ttagttttat cattttacca attgtgaggt 540
atatttggaa ctaaaagata tattatctta ttagttttgt gactaatgaa agtagtcaga 600

<210> SEQ ID NO 210
<211> LENGTH: 574
<212> TYPE: DNA
<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 210

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gggatcccg tatatacacg acacgatttc taagtttacg ctcaatacac gcgtgaatcg      60
agtcacactc catttgagta tgaccctttt ctagataata ttgaaatatt tctacacctg    120
atgttcttga taagtaagaa agagcattcg aaagcgtaac atttcgagtt tggtagcagc    180
atccgtcgct gaagcaaaca acggatttag tagcaggaga taaatttctt ttgatataat    240
ctatgataat ggaagtgaac tcgtttgctt caaccccacc tgaaccctca tgccatacat    300
agcaatggcc ttgtccagtg gataaattat agaagctata gttgtgaaca tttagcttca    360
ttttataata tgcagctgat acttgtaatc ttggtgctgt taatattgcc tgtgcatcca    420
tagtcaaaac aagtttactg ttgtccttac tagcctcttc ttttagtttt tctttttcag    480
cacgagctaa attttttttc tccaaatgct gctgaaactg ttcatcattt attttgccga    540
cagaataccc agtgcaagtg tcgcactgat cttt                                574

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<210> SEQ ID NO 211
<211> LENGTH: 227
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

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<400> SEQUENCE: 211

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gggacttaga ttttattcat catctcgta aactgtacaa tgagaaacgg tcagatctgg      60
aggagcaaca gttgcatttg aacgttggtc tgaataagat cgccgaaact gtagaacagg    120
ttgaagaaat gcagaagagt ttggccgtca aatctcagga gccacaggcc aaaaatgaag    180
ctgccaacgc taaactcagg cagatggtga aagatcaaca agaagcc                    227

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<210> SEQ ID NO 212
<211> LENGTH: 631
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

```

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<400> SEQUENCE: 212

```

```

ggggattatt tctgatttct gtttctgct ttgttgctta tacatattgt aaaaatacag      60
ctaaaaactt ttaaaaatga gcgaagccaa ggaagcaatg gaagttgaag tggaaacagc    120
cccggtggct gaaaattcaa aatcttccat ggaggtaacc acagatacag gaaaaaatgt    180
aatggccccg ggagctgttg gatcaatcac ttgttccctt catcctcttg taataatgaa    240
tgtatcagaa cattggacta gggaaaggcg ccaagaagga gctgtgcaac aagtcattgg    300
agctttgatc ggcaaacaaa agggtagaaa tattgaagta atgaactcat ttgagctagt    360
atttacactt ataggagggt atatagttat tgataaggat tattacaaca tgaaagaaga    420
gcaatttaaa caagtcttca gtgatttaga tttcattggc tggtagacaa caggtagacgc    480
cccaagtgaat atggatatca aggtccacaa gcaaatattgt gaaatcaatg agtctcccat    540
tttattgaag ctcaaccctt atgataaaaa tattgaacat ttaccagtaa acttatagga    600
atctgtgata gacttagtaa atggtgaagc c                                631

```

```

<210> SEQ ID NO 213
<211> LENGTH: 611
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

```

```

<400> SEQUENCE: 213

```

```

ggggaagaga tgacaatatg gcgtcaaggt attagttgct aggacgtttt atttttcatt      60

```

-continued

```

cgagagtttt acagtaataa atgagaaaagt tgtaccgaaa ttattgtgat ttcgacgtaa 120
tattttctcag tctaactttg gattatgaac attatcacga aagttgatgg agaacatagg 180
cagagacaag aggactatgg agcatctaga atagcagtag agccaattca acacaagcat 240
ggatgacatg gataacatga ggaagaggac tttgttcagc agtggacctt tgaggctgga 300
tgataatgga ctccatcaat gaggatgtaa aggatatcac tttcatgtac tggagtacaa 360
tgtaacattg tgtaggcata atattttact ctttttattt gacaaatatt taccaactcc 420
cttcatggg ggtagactaa tatttgacca cttctgaaaa tctcatttta tgttttttgc 480
atcaactgta ggcaatttgc tatacaattg caatattgtt tgaacgtcaa tattttgtta 540
aagtaaatta ttatctggtt ttgagtggta tactttttta atgaattcca aaaattactt 600
tattagccta a 611

```

```

<210> SEQ ID NO 214
<211> LENGTH: 569
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

```

```

<400> SEQUENCE: 214

```

```

ggggatttca tttttcattt gtttgtaaac aaatttatgt aaaattgaca gtttgtgcaa 60
aagattatta tattcttttg tttttgttgg gctgaaaatg ttaaaaaatg ttgtattaaa 120
taataaatga atgacattat acctttcttg caaggatttc gtagattgtt tggaacaatg 180
tcccgatcta aagttagata gtttgtaaac ccaaaagaag actatagaga atctagtcaa 240
attgtgattc cagtaccaga tataatacaa catttaaatg atactgttgt caaaatagaa 300
agtgggtgta agccagcaga agagaatgct ggagatggaa tttatttagg tactgctggg 360
atagcatata tgttctacca ccttagcaag gttccaacac tttcatcaa gcaatctcag 420
tatttaagac aagctgtaac ttacctaata cggcaataa cagtagcaag ctgcaacaaa 480
acagatagta tcccctcttt catattagga aatgctggaa tttatgctgt agcagccaca 540
gttttcaaca gtttaggaga tctgaatca 569

```

```

<210> SEQ ID NO 215
<211> LENGTH: 630
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

```

```

<400> SEQUENCE: 215

```

```

gggataatat agagataatt tcttcaccca gtgtgtactc tatactcagg tttttgactt 60
tatcaataat ttcattcatg atgaggtgaa actgtagcag gcttgacgta tgcctctttc 120
cacttgatc gccagcttct tattaataat ttcggcctgc atattatttc tctgtatat 180
gttttcggta gtcttgataa tatctgatgg tatgttttga ttacgtgaca ggtgaattac 240
gtcattcagc tctacgcggt cgaatgactt ttgtagatct atgaagcaac agtaaggcgg 300
gacgttgat tcaagtccgg atttaccact aggcgcgacta ggccgcggcc tagtgccgca 360
agcaaaaggg ggccgcgagc ctttgtaaaa aaaactttat tggtaaaaaa attgtcacia 420
cattgtcaaa aatagcaata acgataagaa actccttcca aaaagagtaa acgttacaag 480
acgggctgcc aaatggcatg ctgtaaaagc tattttactt aactactggg agctactacg 540
atgcaattaa aaaaaatc agccgataca ggggaaacaa atgtgagccg agctgaagct 600

```

-continued

aatggaatca gtaaacaatt tttaaaatta 630

<210> SEQ ID NO 216
 <211> LENGTH: 624
 <212> TYPE: DNA
 <213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 216

```

ggggacagca atcgagctg ttttaaaga aaaaaattg tccccctct tcgactgtgc    60
ctaccaaggt ttcgcctctg gtaacttggt caaagatgct gctgtggtaa gaaaattcgc    120
cgccgaaggc taggagtctt tctgtgccc gagttttgcc aagaacttcg gtctctacaa    180
tgaacgtggt gaaacctaa cagtagcggg tagcaaacca gaccttatgg cacctgtaaa    240
atcgagctt actctcatcg tcagaggaat gtactcaaac ccacctagtc acggagccag    300
gatagtatct tttgtgctca ataaccaga tttggcaaag cagtggcaag ataatatcac    360
tacgatgtct tcaagaataa ttgaaatgag gacctgttg agaaacgcat tagaggagtt    420
gggcactcca ggagactgga gccatttaac taaacacatc ggaatgttct cttacacagg    480
tctaaatgaa atccagtcag agcacttggt gaagaaacat catgtctacc tgctgcgttc    540
tggaagaatt agtataagtg gtttgaacaa tgacaacgtg aactatgttg ctaaagccat    600
ccatgaaaca gtaaccaccc tacc                                     624

```

<210> SEQ ID NO 217
 <211> LENGTH: 362
 <212> TYPE: DNA
 <213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 217

```

ggggacagtc gacatctgac agtttctaca gtatagttac agtggtcagt ggaaaatatt    60
caattaagac tgcgattata cgacacactt tcaactgtcaa ggccgtcttt cttgcatccc    120
taaaacgtac atttgcgaca aaaaaattga ctgctgggac ggcagcgatg aaaaaactg    180
ctactacgaa catatctgcc aagaggggga ataccattgt aataatggtt attgtataaa    240
atcggagcaa ttgtgtgatg gctttccgga ttgttctgat aactcagacg aaccatctgg    300
gtgttttaga tattatttgt caacaactac tgatgttaca agtccgaaa atgattatga    360
gc                                     362

```

<210> SEQ ID NO 218
 <211> LENGTH: 644
 <212> TYPE: DNA
 <213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 218

```

ggggttcgtg gggtagaatt tcagactttt gacaaattaa aattttgaac aatttatatt    60
attaatttca atcacattgc agttttaaaa agaattaaaa atggtatccc taaatcccg    120
aagaattctc aagcaagaag ccgaggaaga aagggcagag attgcccgcac tcagtagttt    180
tgtaggtgct atagctatag gagatttggt tagaagcacc ttgggaccaa aaggaatgga    240
taaaatttta gtatccagtg gtagatctgc aggatcagtt gaagtacta acgacggagc    300
aactatccta aaatcggtgg gtgttgataa tctgtctgct aaaattttgg tggatatgtc    360
aaaagtcag gatgatgaag taggagatgg caccacatca gtgacagtat tagcatctga    420

```

-continued

```

actacttaaa gaagcagaaa aacttgtaga acagaaaatt caccacaaaa caatcattgc 480
cggttggagg aaagcagtag atattgccag aaaagctctt ctagaaactg ccaaagacaa 540
cagctctgat tcggaaaagt tcagagaaga tctgatgaac attgccagaa ctacactcag 600
ctcaaagatt ctttcacaac ataaagaata ttttgccaaa ctgg 644

```

```

<210> SEQ ID NO 219
<211> LENGTH: 637
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

```

```

<400> SEQUENCE: 219

```

```

ggggagtgc agatgacaat aagaagaat gaatgaaggc caaaatagct tttcatttta 60
atattatgtt caaaaataaa ttactttaga caatccataa aattaaggca actccgtaat 120
tatgacagaa acattagcag ccgaagaaaa acctttaaca aacaatggac gacgagcttt 180
tagtcccgtt ccaactaaaa gaacatctgg aggactgatg aaactatcca gttatgtgct 240
agctcttcga ccatggcttc ttagtgcaag ttaattcca actctattag gatcgacaat 300
agcttataaa tatccagggt cttcgggatt taattatata actctatttt ttacgatatt 360
aacaattata tcagtgcagt gggctggtaa ttagtggaat acatactttg actatgtaaa 420
gggcatagac aatcgaaaat cagacgatag aattcttgta gatcatatat tatcgaggga 480
tgaagttgta tcgttgggtg ctatcttata tttcgaggga tgtattggat ttattatatt 540
agcgaacata tctccagcaa aaatggaaca tttagcttta gtgtattttg ggggcttata 600
gtcaagtttt ttatacacccg ggggcattgg ttttaaa 637

```

```

<210> SEQ ID NO 220
<211> LENGTH: 271
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

```

```

<400> SEQUENCE: 220

```

```

ggggactcca acgaaattaa tacgtacttt aaacgggttta tttatatttt atttaatat 60
aaactaatat taatacttac tactttccaa aaatttttat taaaacaata caaaaaatta 120
aaaaaataaa agaataaaac acacacaaac acattgaaaa atgccacaaa taaatgattt 180
ctgaacaata attgttggca aaaatctaac caaatacgca ttttctgaaa aaaaattata 240
taacaaatat acttacaatc ataaatgta c 271

```

```

<210> SEQ ID NO 221
<211> LENGTH: 80
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

```

```

<400> SEQUENCE: 221

```

```

taaagctttg gataaaagac aagccgtact ttgtgtgctc gctgaaaact gtgacgagcc 60
tatgtataag aaactagtct 80

```

```

<210> SEQ ID NO 222
<211> LENGTH: 657
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

```

```

<400> SEQUENCE: 222

```

-continued

```

gggggctctt taaattgtgg ttatgttgat ttatttataa agaaataaat ttattttaaa    60
tatgtttaaag aattggaatg atttagatgt agaacttcac tcagaggtaa aatgtggaat    120
tgaatcacta aaatttccta ctatgacacc agtgcaagcg tacactatac ctcagctttt    180
aaagaagaaa gatgttgacg ctgaagcagt tactgggttct ggaagactc tggcattcct    240
aataccaata ttacaaataa tgaagcaaag agaaactgaa gaaaaatggg ggaacatca    300
agtaggggca gttgtcttat ctccaacaag agaattagcc ttgcaaaca gagatgtact    360
tgataaactg ttagtcgatg ttaaaaaat atccaatatt ttattggttg gaggaatatg    420
tgttgaagaa gatgtaaata atttcaaac acatggagga aatattataa tttgtactcc    480
tggcagacta gaagatttgt taactaggaa atatgattta aaccttcaa aatcattaaa    540
gagtttgtaa atccttattt tagatgagcg tgatagactt ttagatttag gctttcaaaa    600
gtccattgac acaattttaa gttatttgcc taggcaacga aggacaggct tattctc     657

```

```

<210> SEQ ID NO 223
<211> LENGTH: 541
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

```

```

<400> SEQUENCE: 223

```

```

atatataact cggattacca cagtcaaagt gcataaaact taacaatacg caaaaaccgt    60
agcagtcctg ttatttcttt cctgcgccct tggetggagc cttcttggcc ttcttaggtt    120
ttgatttctt atctttcaag atttgtgccc ttctccttcc ttgcaatttt ctggatctaa    180
tcacgacgtt gtcggcactc acggtaatac cacgtttctt ggccaaaagt tcttcctgt    240
ttaactgtct cttttgatcc ttcaaaatgg cttcacgttt gagtacagca gcatatggat    300
tcaacttaag catggcctta gcgttggtca atggattgag acgacgtaca cgacgtacaa    360
ccttcttttg aggagcacgt aatacagctt tgatttcac agccttcaac aatctagata    420
gatcagtggt ggccatttta ggctggggtg gattgtaacc cttcttttcc aatgatgctg    480
ttttccatgt gccgaacaat ttatctaacc gttggaaaagc tgattcagtc caaataacaa    540
a                                                                    541

```

```

<210> SEQ ID NO 224
<211> LENGTH: 650
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

```

```

<400> SEQUENCE: 224

```

```

ggggacattt acgactgatg tgttgatata ttcactgagg gttacctata atggatatca    60
tagagaaaac cttatcgat aataacaaac taatagaacc ccacctgat aacattgtgg    120
tccaaaatga agataacgaa gaagttcact atgtaaatat tcatgaggtg cacgtcaaca    180
aagtcacoga gaaaaaactg ggcaccaatc atttcgttct acttaattat gagcttaaac    240
ctataactga ccgtcttggt cttcttgagg accacagtat tttgttcgta acattcctca    300
ataatattgg atccaaagaa catttgcaat ttttcgttaa gtattttcct tttactgaat    360
ctcaagcaca attcgtgat ggcacggag catttgaaaa agaagcactg gtttataaat    420
tgttcaaaga gttttataag caaggtatca ctcaagccag taatgttgtc cctactgct    480
atgtagtagc tcccaaaaaa tattttatat taaatgatct tactctcgag agttatcaaa    540

```

-continued

```

ttttaataa acatatttgc ttagaatacg atgtcgttgt agttgtttta caagcttttag 600
cccagttaca ttccggtagt atagcgtacg aagaaaaatt aaagaagaat 650

```

```

<210> SEQ ID NO 225
<211> LENGTH: 655
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

```

```

<400> SEQUENCE: 225

```

```

gggcattgag ctctgcata acaaaaacac tggaaagaat gataaaactt aggctcgaaa 60
gttggttaga aaaaaaaca taaattatca caaacacaat ttggatttcg aaaaaaatca 120
ttctactgtg gaagctgtga gtcatttggt aacagatata aatttagcgt ttacgaaaaa 180
ttcttcagta atcgctcttt tattagatgt tgaagcagca tacgacaacg ttaattttaa 240
tatactatat aacaaaatga tacaaaatagg tctgccagaa tgcttctgtc aaaaaataat 300
aaaattgtat gactgtagaa aaatttatat atcggtaaat aataacacat ttggtccaag 360
agtagcgatg ggtggtttac ctcaaggagg aatattaagc cctttgttat atttaattta 420
cacttctgat atagaaaaaa atttaaaactc aacaaaaatt ttacaatttg cagatgatgt 480
agttatttat caagaaaaca ttaaaataga aaatgcagtc aaatccattg aagaaggaga 540
caaacatatt aaaatatgga gtgaattaca tggactaaat atatctgatt caaaaacca 600
attatgtatt ttacaagaa aacgaaaaga aatacccaat cacatcttaa taaac 655

```

```

<210> SEQ ID NO 226
<211> LENGTH: 521
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

```

```

<400> SEQUENCE: 226

```

```

gggggaaacg atgacagttt tgaaagaagt aaaaaagcaa agagaacaca acagaaaaat 60
gaagcagaca aagatacaaa tgcagtcatg attagaatga tgaagaact tatggagaaa 120
aatgaagaaa tgatgaatga aataaaacag gtcagggaagg aacaagccga aaacaataag 180
caattaatgg aaatgaggca agagaatcag aacttgaaaa gagaagtaaa gcaactacag 240
gaaagaatcg aatacataga aaaatacagt aagaagaaaa gcctgataat atcaggatta 300
aaaatggaca caaacgacga tagaaacatt agagaagaaa tggaaaattt cctagtcaga 360
gaactgcaag ttaaagttaa attaaggaac gccacaaaaa ttggagagaa tctctgtgtt 420
atagaaacgg aaacaacgac tgaaaaaatg gagatattga aaaacaagag aaagttaaaa 480
aaccacaacg aacgcattta cataaacagt gacctaacga c 521

```

```

<210> SEQ ID NO 227
<211> LENGTH: 627
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

```

```

<400> SEQUENCE: 227

```

```

ggggagttcg ttctgtacg tctgtctgtt cgttcgtgcg tgaccatttt tgatttctac 60
aattattgcc accgccatca ggagagtagc taaactcgga taacttaaat agtgttgtgc 120
ggattgtgat ttctgacatg ggagataaca agaataacga ttctcgaaga aaggtaaaga 180
aagtaaggaa agcgggaagat ttagacgatt taaaacagga attagacatc gactatcata 240

```

-continued

```

agatctcacc agaagaacta tatcaaaggt ttcaaacaca ccagaaaaac ggtcttagtc 300
atgcaaaaagc gaaagaaaat ttggacaggg acggacccaa tgccttcaca ccacaaaaaa 360
caactcccga atgggtgaaa ttctgtaaaa atctcttcgg gggtttcgca ctcttacttt 420
ggattgggtgc aatcatttgt ttcctgcct actccataca ggctagtact gtagaagaac 480
cagcagatga taatctatat cttggcatcg tattagctgc cgttggtatc gttacaggta 540
tattttctta ttatcaagaa agcaaaagtt caaaaattat ggaatcttcc aagaacatgg 600
tgccccagtt cgcgaccgtt cttaggg 627

```

```

<210> SEQ ID NO 228
<211> LENGTH: 643
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

```

```

<400> SEQUENCE: 228

```

```

aggggtgaca acagaaaaat atagaaaatc atcctctgtg tttccgtttt gaacttaact 60
tgtatttagt ttaaaaaata atcatgtcta gaggaagcag tgcaggtttt gaccgacaca 120
taacaatttt ctgccccgaa ggcgcactct atcaagtaga gtatgctttt aaagccatta 180
accaagccgg cccacttcg gtagcagtc caggagtaga tgcgcggcg tgtgtgaccc 240
agagaaagat cccggataag ctgattgatc ccaacacaat tacacatctg ttccagttaa 300
cagaacacac tggatgtgtg atgactggca tgattgctga cagcaagtcc cagggtgcaga 360
gagctagata tgaggctgcc gagttcaaat ataagtttgg atatgagatg ccaatcgatg 420
ccttggttag gagagtatcg gatatttccc aggtttatac gcagaatgct gagatgagac 480
ctttgggttg ctccatgctt ctgataggat atgaccaaga aatgggacca tgtgtccaca 540
aagctgaccc tgcgtgctat tactgtggct acagagcagt aagtgtagga tccaaacaaa 600
ctgaagccaa cagctaccta gagaagaagc taaagaagaa aac 643

```

```

<210> SEQ ID NO 229
<211> LENGTH: 639
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

```

```

<400> SEQUENCE: 229

```

```

gataacgatc acaaggcaat aaataatcat tagcaatttc aactgttaca ttttcattat 60
cattagcaaa aaccagggtca agtaaaactc cgttacaatt tgtgatgtga ttaagctgaa 120
ataggttgta aaatgcaaaa gtatcaacta aagtatcagt agcagtggtta ctattattac 180
taaagacacc tcttttatca tgggtaccatt cgctatttgg cagattgtag tctcctgtta 240
gaatgaactt gtgttcagga aaattgttac agacagattc tataactaata caatgattct 300
cataggatat taaggctgaa ttaggaggaa gatagactgt accaaatata taacattcat 360
tcagagtgc aacttcaaca aacagttcct ccaacttaca cgaacataag gcaatacaat 420
taaaattgaa aatgttatcc attaatatat tataacaccc tgtaaattta gataataagt 480
attcttagat attaatttaa aattgttatt gtaataccat acaaaaaaaaa acaaatagtc 540
tggctaattg gctatgtcaa agccattaat aaaaaaaatc cttatgggag tttttagcgt 600
ggcgtgccc attttcttca aaataatttt caatcggaac 639

```

-continued

<210> SEQ ID NO 230
<211> LENGTH: 238
<212> TYPE: DNA
<213> ORGANISM: *Diabrotica virgifera virgifera*
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 139
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 230

```
gggtattaac ttttattatt aatttgtata tcgtcgtaat taaatatttt tttagaatta      60
aaatatttaa aatttttata aaaaaattaa tcagatcaag gtgcagtgag agccaaattc      120
aataggaatt taccagccna ggctatggga catcgatttc gtattatgct gtacccatct      180
aagatatagt tgtttttata aatataaata agaaataaaa aatacgtttt ccaaccgc      238
```

<210> SEQ ID NO 231
<211> LENGTH: 116
<212> TYPE: DNA
<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 231

```
gaaagttgtg tcttgaaaag tagaaatgac gtctaaagta tctcgtgata ctctatacga      60
gtgtgtgaat ggagtcttgg aaaatgccaa ggagaagaaa aggaactttt tggaaa      116
```

<210> SEQ ID NO 232
<211> LENGTH: 491
<212> TYPE: DNA
<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 232

```
cttatgtatt tagttatggt agtgtagtca tcttaacacc ccttcacccc tccctaacga      60
atctacgacc tagctccgcg acaacaaatg agctgccgtc ccgcaacgag gctttatgtg      120
tctgcttctt cttcttttag cccattctta cccccagta tctctataga tagtctttcc      180
ttgttcccat atgagcagac atgtaaaacg catcaaactt tgggactcac ccatttcctt      240
acgccccgct caaatcgta gatttttgaa atatacactc ctttccatgt acttaactta      300
ccttatctta atctgacaat ttcgagtttt ttttaaggat agagtttttt tttcgagccc      360
cccttaacga actccccgtg gttaagagcc aatatatggt agaggtagat ctgcagggtg      420
ccaggtttct ccccatatga taatctgacg cgctcgagta actgcaaaaa tccccgcttg      480
ggctccccta c                                     491
```

<210> SEQ ID NO 233
<211> LENGTH: 645
<212> TYPE: DNA
<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 233

```
ggggatgttg tgatggattt tttgatgtgt caattttata aatttaaaat ttaattaa      60
atcaaaaggg attttatttt atgtctgata gttactggta tattaaaact ataaaaata      120
ttttaagttt gaaatgaata atgtatttat gttctatatt aaaaggaaga caaaaacact      180
tacagagaag tttttactca gtgaaaaaat taattaaaga tgaagataac ttaggccgaa      240
gactttatca acaaattaa gtcaaaggtc ctataactgt agctgattat atgaaggag      300
tacttactaa ttctacaatg ggatattaca tgcataaaga tgtttttgga gtctcgggtg      360
```

-continued

```

attttatcac atctccagaa atcactcaga tgtttggaga aattgtagct gtttggttaa 420
taaagttagtg acaaaaaatg ggggtctcaa agccgctaca gatagttgaa ctgggaccag 480
gaagaggaac tttggccagt gatatcctga gagtgtttaa tcattttaaa gtactagagc 540
aaacacgctt acagcttggt gagattagta caacgttaag tgaaattcaa gctaaaaagt 600
tgtgtaatca aaataatgta atcgatgaga atcagcctat ctaca 645

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<210> SEQ ID NO 234
<211> LENGTH: 662
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

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<400> SEQUENCE: 234

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ggggataata agttcgattt ttacgaaaa tgacaagtat cgagactgtg gggaccattg 60
tcttgaaatt gctgaagttg gtgatcaatt tgatatgtct catcttgtac cgaaccggat 120
atcaaggcta cttcttggga gtaggaggaa cctggaatct aaacgaagaa aaaaatcccg 180
atgcagaaat tgtggcttcc ggcgtattcg taggatttat gatttacaca ttctctcgc 240
tgatcagcct ttgcttcgct agtgagatc acaaaacgac attcactgat attctgatga 300
atatagtagg gatTTTTatg tggatagctg ctggagctac agctcttcat tattggett 360
ggtacttgtc cgaatacaaa tacacgacaa tagattctga acgacaagtt ggtttggcgt 420
taggagcgat gtgtataata aatggagcgg tctatcttgt agacggagta ctttccgcaa 480
tctttatcct caaagccaaa atgcaataac tttcatcgta atataaatat atttatttag 540
gttatatact ttactttaag cagctcaagt ataccgtgac atccactca tacatcaatg 600
tctataattg ttcatgaca aatcatttaa tagtatttta aagcattcat tegtccaaca 660
cc 662

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<210> SEQ ID NO 235
<211> LENGTH: 677
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

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<400> SEQUENCE: 235

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ggggagggtg gtgtggtttt gtcaacaaat aggttgatct atttttgtgt tctttaataa 60
taattgagaa ataattcgat aaaatgggta aaaaggcaga agtaggtact cccaagtacc 120
tgcaaaataa aatgaaagcc aaaggtctgc aaaagcttcg atggtattgt caaatgtgtc 180
agaaacagtg cagagatgaa aatggtttca agtgccatac aacctctgaa tctcaccaaa 240
gacaactact gttgtttgca gacaactcca aaaagtatat agatgacttc tcatttgatt 300
tcgcaagggt atatatggag atccttcgaa gacaatttgg taaaaaaga gtcaatgcta 360
acagagtcta tcaagaatac atacatgaca gggatcatgt ccacatgaat ggtactagat 420
gggtgacact tactggattt gttaaatggt taggtaaaac tggacaagct gttgttgacg 480
aaacagagaa aggttggtac atcacttaca tagatagaag tcccgagacg gtagaaaagg 540
cagaatcgaa aaagaaaaa gagaaaatgg ataagaacga tgaagagaag caaatagagt 600
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atacagaatt agtgagg 677

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<210> SEQ ID NO 236
<211> LENGTH: 600
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 236
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aaacctgat ggaggtccgt agcgattctg acgtgcaaat cgatcgtcgg aactgggtat    120
aggggcgaaa gactaatcga accatctagt agctggttcc ctccgaagtt tccttcagga    180
tagctggcgc tcgttcctga cgagtttcat ccggtaaagc gaatgattag aggcattggg    240
gtcgaaacga cctcaaccta ttctcaaact ttaaatgggt gagatcttcg gcttgctcga    300
acttatgaag ccgtgagaaa cgaatcagag tgccaagtgg gccatttttg gtaagcagaa    360
ctggcgctgt gggatgaacc aaacgttgag ttaaagcgcc aaaatcgacg cttatgggat    420
accatgaaag gcgttggtaa cttaagacag caggacgggt gccatggaag tcggaatccg    480
ccaaggagtg tgtaacaact cacctgccga agttactagc cctgaaaatg gatggcgcta    540
aagcgtcgtg cttatactca accgtcagcg gcattgtcgg ttcgttaata gcgactatga    600

<210> SEQ ID NO 237
<211> LENGTH: 3928
<212> TYPE: DNA
<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 237
tgcagcgtga cccggctcgtg cccctctcta gagataatga gcattgcatg tctaagttat    60
aaaaaattac cacatatctt ttttgtcaca cttgtttgaa gtgcagtta tctatcttta    120
tacatatatt taaactttac tctacgaata atataatcta tagtactaca ataatatcag    180
tgtttttagag aatcatataa atgaacagtt agacatggtc taaaggacaa ttgagtatct    240
tgacaacagg actctacagt tttatctttt tagtgtgcat gtgttctcct ttttttttgc    300
aaatagcttc acctatataa tacttcatcc attttattag tacatccatt tagggtttag    360
ggttaatggt ttttatagac taattttttt agtacatcta ttttattcta ttttagcctc    420
taaatataaga aaactaaaac tctatctttg tttttttatt taataattta gatataaaat    480
agaataaaat aaagtgacta aaaattaaac aaataccctt taagaaatta aaaaaactaa    540
ggaaacattt ttcttgtttc gagtagataa tgccagcctg ttaaagcccg tcgacgagtc    600
taacggacac caaccagcga accagcagcg tcgcgtcggg ccaagcgaag cagacggcac    660
ggcatctctg tcgctgcctc tggacccctc tcgagagttc cgctccaccg ttggaacttg    720
tccgctgtcg gcatccagaa attgcgtggc ggagcggcag acgtgagccg gcacggcagg    780
cggcctcctc ctctctctac ggcacgggca gctacggggg attcctttcc caccgctcct    840
tcgctttccc ttctcgccc gccgtaataa atagacaccc cctccacacc ctctttcccc    900
aacctcgtgt tgttcggagc gcacacacac acaaccagat ctccccaaa tccaccgctc    960
ggcacctcgg cttcaaggta cgccgctcgt cctccccccc cccctctctc accttctcta    1020
gatcggcgtt ccggtccatg catggttagg gcccggtagt tctactcttg ttcattgttg    1080
tgtttagatcc gtgtttgtgt tagatccgtg ctgctagcgt tcgtacacgg atgcgacctg    1140
tacgtcagac acgttctgat tgctaacttg ccagtgttcc tctttgggga atcctgggat    1200
ggctctagcc gttccgcaga cgggatcgat ttcattgattt tttttgttc gttgcatagg    1260

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gtttggtttg cccttttctt ttatttcaat atatgccgtg cacttggttg tggggtcatc	1320
ttttcatgct tttttttgtc ttggttggtga tgatgtgggc tgggtgggag gtcgttctag	1380
atcggagtag aattctgttt caaactacct ggtggattta ttaatttttg atctgtatgt	1440
gtgtgccata catattcata gttacgaatt gaagatgatg gatggaaaata tcgatctagg	1500
ataggtatac atgttgatgc ggggttttact gatgcataata cagagatgct ttttgttcgc	1560
ttggttggtga tgatgtgggtg tgggtgggag gtcgttcatt cgttctagat cggagtagaa	1620
tactgtttca aactacctgg tgtatttatt aattttggaa ctgtatgtgt gtgtcataca	1680
tcttcatagt tacgagttta agatggatgg aaatatcgat ctaggatagg tatacatgtt	1740
gatgtggggt ttactgatgc atatacatga tggcatatgc agcatctatt catatgctct	1800
aaacctgagt acctatctat tataataaac aagtatgttt tataattatt ttgatcttga	1860
tatacttgga tgatggcata tgcagcagct atatgtggat ttttttagcc ctgccttcat	1920
acgtatttta tttgcttggt actgtttctt ttgtcgatgc tcacctggt gtttggtggt	1980
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gttcgatatc aacaagtttg tacaaaaaag caggggggctt tctgattttt gacagcttct	2100
atagaagttt atcaagatgt tgatgccaaa aaagaataga gtatgtattt acgaatacct	2160
cttcaaaagag ggagtcattg tagctaaaaa agattacat gccccaaaac acctcgaact	2220
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accacaataa atttattgat aagttaattt ttataaattg atcagccaat aaaaagtgtg	2640
gttaaaaaaa aaaaaaaaaa aaaaaaaaaa aaacagcttt cttgtacaaa gtggtcgata	2700
tcaggccgc cttgtttctc ctctgtctct tgatctgact aatcttggtt tatgattcgt	2760
tgagtaattt tggggaagc ttcgtccaca gtttttttgc gatgaacagt gccgcagtgg	2820
cgtgatctt gtatgtatc ctgcaatcgt ggtgaactta tttcttttat atcctttact	2880
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tggtccatcc gacagctcgg ctgaacacat catacgatct atggagcaaa aatctatctt	3000
ccctgttctt taatgaagga cgtcattttc attagtatga tctaggaatg ttgcaacttg	3060
caaggaggcg tttctttctt tgaatttaac taactcgttg agtggccctg tttctcggac	3120
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tggtgccccg ccacgtccga atccttgctt gaactcaaca tctccagttc ctggaccaac	3420
atcagcttcc ttgtcagctc cagggcctcc aggagtcctt ctgtatcctg cagggtcttc	3480
tgaaggttta gatgtctcag atctgagagc agctgggtcta ggacgggttg tttctgtcct	3540

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tgctgggagt	ttcaaggtag	atgggacaat	ttctccaggt	aagtgtgaaga	atgtgcggag	3600
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ttctagttag	aggtgtttt	gggcatggta	atctttttta	gctaccatga	ctccctcttt	3780
gaagaggtag	tcgtaaatat	atactctatt	cttttttggc	atcaacatct	tgataaaact	3840
ctatagaagc	tgtaaaaaat	cagaagcccc	cctgcttttt	tgtacaaact	tgttgatggg	3900
gttaggccgc	caccgcgggtg	gagctcga				3928

<210> SEQ ID NO 238

<211> LENGTH: 4181

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 238

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atacatatat	ttaaacttta	ctctacgaat	aatataatct	atagtactac	aataatatca	180
gtgttttaga	gaatcatata	aatgaacagt	tagacatggt	ctaaaggaca	attgagtatt	240
ttgacaacag	gactctacag	ttttatcttt	ttagtgtgca	tgtgttctcc	tttttttttg	300
caaatagctt	cacctatata	atacttcac	cattttatta	gtacatccat	ttaggggttta	360
gggttaaatg	ttttataga	ctaatttttt	tagtacatct	attttattct	atttttagcct	420
ctaaattaag	aaaactaaaa	ctctatttta	gtttttttat	ttaataattt	agatataaaa	480
tagaataaaa	taaagtact	aaaaattaaa	caaataccct	ttaagaaatt	aaaaaaacta	540
aggaaacatt	tttcttggtt	cgagtagata	atgccagcct	gttaaacgcc	gtcgacgagt	600
ctaaccgaca	ccaaccagcg	aaccagcagc	gtcgcgtcgg	gccaaagcaa	gcagacggca	660
cggcatctct	gtcgtgcct	ctggaccct	ctcgagagtt	cgcctccacc	gttggacttg	720
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ggtttggttt	gcccttttcc	tttatttcaa	tatatgccgt	gcacttggtt	gtcgggtcat	1320
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gatcggagta	gaattctgtt	tcaaactacc	tggtggattt	attaattttg	gatctgtatg	1440
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gatagggtata	catgttgatg	cgggttttac	tgatgcata	acagagatgc	tttttgttcg	1560
cttggttggtg	atgatgtggt	gtggttgggc	ggcgtttcat	tcgttctaga	tcggagtaga	1620

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taaccttgag tacctatcta ttataataaa caagtatgtt ttataattat tttgatcttg	1860
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tacgctattt atttgcttgg tactgtttct tttgtcgatg ctcaccctgt tgtttgggtg	1980
tacttctgca gaccggtctc tacgtacagt ccggactggc gccttggcgc ggtaccacat	2040
ggttcgatat caacaagttt gtacaaaaaa gcagggggct ttttcacaat gcaggcacca	2100
acgacaaagc caaaaagaga tccaatccac tctgtccaag tttttggcag aaagaaatca	2160
gtacacagccg tagcttattg caaaagaggt agaggagtct tgagggtaaa tggcagacct	2220
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aaaaaaaaa cagctttctt gtacaaagtg gtcgatatca ggtccgcctt gtttctctc	2700
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caatcgttgt gaacttatat cttttatata ctttactccc atgaaaaggc tagtaatctt	2880
tctcgatgta acatcgtcca gcaactgtat taccgtgtgg tccatccgac agtctggctg	2940
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cattttcatt agtatgatct aggaatgttg caacttgcaa ggaggcgttt ctttctttga	3060
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gcttgactat gcgattgctt tcctggaccc gtgcagctgc ccacgacca ctttgtacaa	3240
gaaagctgtt tttttttttt tttttttttt ttttttttgc gggaaaaaat tgtgtttatt	3300
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tcttttttgc tttgtcgttg gtgcctgcat tgtgaaaaag cccctgctt ttttgtacaa	3840
acttgttgat ggggttaggc cgccaccgcg gtggagctcg aattccggtc cgggtcacct	3900

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ttgtccacca agatggaact gcggccgctc attaattaag tcaggcgcgc ctctagttga	3960
agacacgttc atgtcttcat cgtaagaaga cactcagtag tcttcggcca gaatggccat	4020
ctggattcag caggcctaga aggccattta aatcctgagg atctggtctt cctaaggacc	4080
cgggatatcg gaccgattaa actttaattc ggccgaagc ttgaagttcc tattccgaag	4140
ttctattctt ccagaaagta taggaacttc gcctgcctgc a	4181

<210> SEQ ID NO 239

<211> LENGTH: 5247

<212> TYPE: DNA

<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 239

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atacatatat ttaaacttta ctctacgaat aatataatct atagtactac aataatatca	180
gtgtttttaga gaatcatata aatgaacagt tagacatggt ctaaggaca attgagtatt	240
ttgacaacag gactctacag ttttatcttt ttagtgtgca tgtgttctcc tttttttttg	300
caaatagctt cacctatata atacttcac ctttttatta gtacatccat ttagggttta	360
gggttaaatgg tttttataga ctaatTTTT tagtacatct attttattct attttagcct	420
ctaaattaag aaaactaaaa ctctatttta gtttttttat ttaataattt agatataaaa	480
tagaataaaa taaagtgact aaaaattaaa caaataccct ttaagaaatt aaaaaacta	540
aggaaacatt tttcttggtt cgagtagata atgccagcct gttaaagcgc gtcgacgagt	600
ctaacggaca ccaaccagcg aaccagcagc gtcgcgtcgg gccaaagcga gcagacggca	660
cggcatctct gtcgctgcct ctggaccctc ctcgagagtt ccgctccacc gttggacttg	720
ctcgcgtgtc ggcatccaga aattgcgtgg cggagcggca gacgtgagcc ggcacggcag	780
gcggcctcct cctcctctca cggcacgggc agctacgggg gattccttcc ccaccgctcc	840
ttcgctttcc cttcctcgcc cgccgtaata aatagacacc ccctccacac cctctttccc	900
caacctcgty ttgttcggag cgcacacaca cacaaccaga tctcccccaa atccaccctg	960
cggcacctcc gtttcaaggt acgcgcgtcg tctccccccc cccctctctc taccttctct	1020
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ggtttggttt gcccttttcc tttatttcaa tatatgccgt gcatttgttt gtcgggtcat	1320
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tacttctgca gaccggtctc tacgtacagt ccggactggc gccttggcgc ggtaccacat	2040
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ccaccagttc cagaatggag tgacacttat agcgtagaag gaactatcca tttgccttat	2220
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gattactaca atgggacggc taagacatac caacttgag gaaatggaaa tgggtgccaa	2340
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<210> SEQ ID NO 240

<211> LENGTH: 4939

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 240

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<210> SEQ ID NO 241

<211> LENGTH: 4661

<212> TYPE: DNA

<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 241

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<210> SEQ ID NO 242

<211> LENGTH: 5116

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 242

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<210> SEQ ID NO 243

<211> LENGTH: 4995

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 243

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<210> SEQ ID NO 244

<211> LENGTH: 7112

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 244

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<210> SEQ ID NO 245

<211> LENGTH: 4076

<212> TYPE: DNA

<213> ORGANISM: Diabrotica virgifera virgifera

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<400> SEQUENCE: 245

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<210> SEQ ID NO 246

<211> LENGTH: 4415

<212> TYPE: DNA

<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 246

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<210> SEQ ID NO 247

<211> LENGTH: 3389

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 247

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<210> SEQ ID NO 248

<211> LENGTH: 3349

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 248

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<210> SEQ ID NO 249

<211> LENGTH: 3953

<212> TYPE: DNA

<213> ORGANISM: *Diabrotica virgifera virgifera*

<400> SEQUENCE: 249

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<210> SEQ ID NO 250

<211> LENGTH: 3433

<212> TYPE: DNA

<213> ORGANISM: Diabrotica virgifera virgifera

<400> SEQUENCE: 250

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<212> TYPE: DNA

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That which is claimed:

1. An isolated polynucleotide comprising a nucleotide sequence comprising:

(a) the nucleotide sequence comprising any one of nucleotides 1-380 of SEQ ID NO: 45; SEQ ID NO: 45; SEQ ID NO: 13; SEQ ID NO: 15; nucleotides 1-266 of SEQ ID NO:50; SEQ ID NO:50; SEQ ID NO: 18; SEQ ID NO: 29; nucleotides 1-675 of SEQ ID NO:37, SEQ ID NO: 37; SEQ ID NO:16; SEQ ID NO:32; SEQ ID NO:25; nucleotides 1-132 of SEQ ID NO: 40; or any one of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 17,

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- (b) the nucleotide sequence comprising at least 90% sequence identity to any one of nucleotides 1-380 of SEQ ID NO: 45; SEQ ID NO: 45; SEQ ID NO: 13; SEQ ID NO: 15; nucleotides 1-266 of SEQ ID NO:50; SEQ ID NO:50; SEQ ID NO: 18; SEQ ID NO: 29; nucleotides 1-675 of SEQ ID NO:37, SEQ ID NO: 37; SEQ ID NO:16; SEQ ID NO:32; SEQ ID NO:25; nucleotides 1-132 of SEQ ID NO: 40; or any one of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 17, 19, 20, 21, 22, 23, 24, 26, 27, 28, 30, 31, 33, 34, 35, 36, 38, 39, 41, 42, 43, 44, 46, 47, 48, 49, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, or a complement thereof; wherein said polynucleotide encodes a silencing element having insecticidal activity against a Coleoptera plant pest; or
- (c) the nucleotide sequence comprising at least 19 consecutive nucleotides of any one of nucleotides 1-380 of SEQ ID NO: 45; SEQ ID NO: 45; SEQ ID NO: 13; SEQ ID NO: 15; nucleotides 1-266 of SEQ ID NO:50; SEQ ID NO:50; SEQ ID NO: 18; SEQ ID NO: 29; nucleotides 1-675 of SEQ ID NO:37, SEQ ID NO: 37; SEQ ID NO:16; SEQ ID NO:32; SEQ ID NO:25; nucleotides 1-132 of SEQ ID NO: 40; or any one of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 17, 19, 20, 21, 22, 23, 24, 26, 27, 28, 30, 31, 33, 34, 35, 36, 38, 39, 41, 42, 43, 44, 46, 47, 48, 49, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, or a complement thereof; wherein said polynucleotide encodes a silencing element having insecticidal activity against a Coleoptera plant pest.
2. The isolated polynucleotide of claim 1, wherein said Coleoptera plant pest is a *Diabrotica* plant pest.
3. An expression cassette comprising the polynucleotide of claim 1.
4. The expression cassette of claim 3, wherein said polynucleotide is operably linked to a heterologous promoter.
5. The expression cassette of claim 3, wherein said polynucleotide is expressed as a double stranded RNA.
6. The expression cassette of claim 3, wherein said polynucleotide comprise a silencing element which is expressed as a hairpin RNA.
7. The expression cassette of claim 6, wherein the silencing element comprises, in the following order, a first segment, a second segment, and a third segment, wherein
- a) said first segment comprises at least about 19 nucleotides having at least 90% sequence complementarity to a target sequence set forth in any one of nucleotides 1-380 of SEQ ID NO: 45; SEQ ID NO: 45; SEQ ID NO: 13; SEQ ID NO: 15; nucleotides 1-266 of SEQ ID NO:50; SEQ ID NO:50; SEQ ID NO: 18; SEQ ID NO: 29; nucleotides 1-675 of SEQ ID NO:37, SEQ ID NO: 37; SEQ ID NO:16; SEQ ID NO:32; SEQ ID NO:25; nucleotides 1-132 of SEQ ID NO: 40; or any one of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 17, 19, 20, 21, 22, 23, 24, 26, 27, 28, 30, 31, 33, 34, 35, 36, 38, 39, 41, 42, 43, 44, 46, 47, 48, 49, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, or 236;
 - b) said second segment comprises a loop of sufficient length to allow the silencing element to be transcribed as a hairpin RNA; and,
 - c) said third segment comprises at least about 19 nucleotides having at least 85% complementarity to the first segment.
8. The expression cassette of claim 3, wherein said polynucleotide is flanked by a first operably linked convergent promoter at one terminus of the polynucleotide and a second operably linked convergent promoter at the opposing terminus of the polynucleotide, wherein the first and the second convergent promoters are capable of driving expression of the polynucleotide.
9. A host cell comprising a heterologous expression cassette of claim 3.
10. A plant cell having stably incorporated into its genome a heterologous polynucleotide comprising a silencing element, wherein said silencing element comprises
- a) a fragment of at least 19 consecutive nucleotides of any one of nucleotides 1-380 of SEQ ID NO: 45; SEQ ID NO: 45; SEQ ID NO: 13; SEQ ID NO: 15; nucleotides

1-266 of SEQ ID NO:50; SEQ ID NO:50; SEQ ID NO:18; SEQ ID NO:29; nucleotides 1-675 of SEQ ID NO:37; SEQ ID NO:37; SEQ ID NO:16; SEQ ID NO:32; SEQ ID NO:25; nucleotides 1-132 of SEQ ID NO:40; or any one of SEQ ID NO:1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 17, 19, 20, 21, 22, 23, 24, 26, 27, 28, 30, 31, 33, 34, 35, 36, 38, 39, 41, 42, 43, 44, 46, 47, 48, 49, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, or a complement thereof; or,

- b) the nucleotide sequence comprising at least 90% sequence identity to any one of nucleotides 1-380 of SEQ ID NO:45; SEQ ID NO:45; SEQ ID NO:13; SEQ ID NO:15; nucleotides 1-266 of SEQ ID NO:50; SEQ ID NO:50; SEQ ID NO:18; SEQ ID NO:29; nucleotides 1-675 of SEQ ID NO:37; SEQ ID NO:37; SEQ ID NO:16; SEQ ID NO:32; SEQ ID NO:25; nucleotides 1-132 of SEQ ID NO:40; or any one of SEQ ID NO:1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 17, 19, 20, 21, 22, 23, 24, 26, 27, 28, 30, 31, 33, 34, 35, 36, 38, 39, 41, 42, 43, 44, 46, 47, 48, 49, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, or a complement thereof;

wherein said silencing element, when ingested by a Coleoptera plant pest, reduces the level of a target sequence in said Coleoptera plant pest and thereby controls the Coleoptera plant pest.

11. The plant cell of claim **10**, wherein the Coleoptera plant pest is a *Diabrotica* plant pest.

12. The plant cell of claim **10**, wherein said silencing element comprises

- a) a polynucleotide comprising the sequence set forth in any one of nucleotides 1-380 of SEQ ID NO:45; SEQ ID NO:45; SEQ ID NO:13; SEQ ID NO:15; nucleotides 1-266 of SEQ ID NO:50; SEQ ID NO:50; SEQ ID NO:18; SEQ ID NO:29; nucleotides 1-675 of SEQ ID

NO:37; SEQ ID NO:37; SEQ ID NO:16; SEQ ID NO:32; SEQ ID NO:25; nucleotides 1-132 of SEQ ID NO:40; or any one of SEQ ID NO:1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 17, 19, 20, 21, 22, 23, 24, 26, 27, 28, 30, 31, 33, 34, 35, 36, 38, 39, 41, 42, 43, 44, 46, 47, 48, 49, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, or a complement thereof;

- b) a polynucleotide comprising at least 130 consecutive nucleotides of the sequence set forth in any one of nucleotides 1-380 of SEQ ID NO:45; SEQ ID NO:45; SEQ ID NO:13; SEQ ID NO:15; nucleotides 1-266 of SEQ ID NO:50; SEQ ID NO:50; SEQ ID NO:18; SEQ ID NO:29; nucleotides 1-675 of SEQ ID NO:37; SEQ ID NO:37; SEQ ID NO:16; SEQ ID NO:32; SEQ ID NO:25; nucleotides 1-132 of SEQ ID NO:40; or any one of SEQ ID NO:1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 17, 19, 20, 21, 22, 23, 24, 26, 27, 28, 30, 31, 33, 34, 35, 36, 38, 39, 41, 42, 43, 44, 46, 47, 48, 49, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, or a complement thereof;

13. The plant cell of claim **10**, wherein said plant cell comprises the expression cassette of claim **8**.

14. The plant cell of claim **10**, wherein said silencing element expresses a double stranded RNA.

15. The plant cell of claim **10**, wherein said silencing element expresses a hairpin RNA.

16. The plant cell of claim **15**, wherein said polynucleotide comprising the silencing element comprises, in the following order, a first segment, a second segment, and a third segment, wherein

- a) said first segment comprises at least about 19 nucleotides having at least 90% sequence complementarity to a target sequence set forth in any one of nucleotides 1-380 of SEQ ID NO:45; SEQ ID NO:45; SEQ ID NO:13; SEQ ID NO:15; nucleotides 1-266 of SEQ ID NO:50; SEQ

- ID NO:50; SEQ ID NO: 18; SEQ ID NO: 29; nucleotides 1-675 of SEQ ID NO:37; SEQ ID NO: 37; SEQ ID NO:16; SEQ ID NO:32; SEQ ID NO:25; nucleotides 1-132 of SEQ ID NO: 40; or any one of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 17, 19, 20, 21, 22, 23, 24, 26, 27, 28, 30, 31, 33, 34, 35, 36, 38, 39, 41, 42, 43, 44, 46, 47, 48, 49, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, or 236;
- b) said second segment comprises a loop of sufficient length to allow the silencing element to be transcribed as a hairpin RNA; and,
- c) said third segment comprises at least about 19 nucleotides having at least 85% complementarity to the first segment.
17. The plant cell of claim 10, wherein said silencing element is operably linked to a heterologous promoter.
18. The plant cell of claim 10, wherein said plant cell is from a monocot.
19. The plant cell of claim 18, wherein said monocot is maize, barley, millet, wheat or rice.
20. The plant cell of claim 10, wherein said plant cell is from a dicot.
21. The plant cell of claim 20, wherein said plant is soybean, canola, alfalfa, sunflower, safflower, tobacco, *Arabidopsis*, or cotton.
22. A plant or plant part comprising a plant cell of claim 10.
23. A transgenic seed from the plant of claim 22.
24. A method for controlling a Coleoptera plant pest comprising feeding to a Coleoptera plant pest a composition comprising a silencing element, wherein said silencing element, when ingested by said Coleoptera plant pest, reduces the level of a target Coleoptera plant pest sequence and thereby controls the Coleoptera plant pest, wherein said target Coleoptera plant pest sequence comprise a nucleotide sequence comprising at least 90% sequence identity to any one of nucleotides 1-380 of SEQ ID NO: 45; SEQ ID NO: 45; SEQ ID NO: 13; SEQ ID NO: 15; nucleotides 1-266 of SEQ ID NO:50; SEQ ID NO:50; SEQ ID NO:18; SEQ ID NO: 29; nucleotides 1-675 of SEQ ID NO:37; SEQ ID NO: 37; SEQ ID NO:16; SEQ ID NO:32; SEQ ID NO:25; nucleotides 1-132 of SEQ ID NO: 40; or any one of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 17, 19, 20, 21, 22, 23, 24, 26, 27, 28, 30, 31, 33, 34, 35, 36, 38, 39, 41, 42, 43, 44, 46, 47, 48, 49, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, or a complement thereof; or,
- b) a nucleotide sequence comprising at least 90% sequence identity to any one of nucleotides 1-380 of SEQ ID NO: 45; SEQ ID NO: 45; SEQ ID NO: 13; SEQ ID NO: 15; nucleotides 1-266 of SEQ ID NO:50; SEQ ID NO:50; SEQ ID NO:18; SEQ ID NO: 29; nucleotides 1-675 of SEQ ID NO:37; SEQ ID NO: 37; SEQ ID NO:16; SEQ ID NO:32; SEQ ID NO:25; nucleotides 1-132 of SEQ ID NO: 40; or any one of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 17, 19, 20, 21, 22, 23, 24, 26, 27, 28, 30, 31, 33, 34, 35, 36, 38, 39, 41, 42, 43, 44, 46, 47, 48, 49, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216,
- 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, or 236.
25. The method of claim 24, wherein said Coleoptera plant pest comprises a *Diabrotica* plant pest.
26. The method of claim 24, wherein said silencing element comprises

217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, or a complement thereof.

27. The method of claim 25, wherein said *Diabrotica* plant pest comprises *D. virgifera virgifera*, *D. speciosa*, *D. barberi*, or *D. undecimpunctata howardi*.

28. The method of claim 24, wherein said composition comprises a plant or plant part having stably incorporated into its genome a polynucleotide comprising said silencing element.

29. The method of claim 26, wherein said silencing element comprises

a) a polynucleotide comprising the sense or antisense sequence of the sequence set forth in any one of nucleotides 1-380 of SEQ ID NO: 45; SEQ ID NO: 45; SEQ ID NO: 13; SEQ ID NO: 15; nucleotides 1-266 of SEQ ID NO:50; SEQ ID NO:50; SEQ ID NO: 18; SEQ ID NO: 29; nucleotides 1-675 of SEQ ID NO:37, SEQ ID NO: 37; SEQ ID NO:16; SEQ ID NO:32; SEQ ID NO:25; nucleotides 1-132 of SEQ ID NO: 40; or any one of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 17, 19, 20, 21, 22, 23, 24, 26, 27, 28, 30, 31, 33, 34, 35, 36, 38, 39, 41, 42, 43, 44, 46, 47, 48, 49, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, or a complement thereof;

b) a polynucleotide comprising the sense or antisense sequence of a sequence having at least 95% sequence identity to the sequence set forth in any one of nucleotides 1-380 of SEQ ID NO: 45; SEQ ID NO: 45; SEQ ID NO: 13; SEQ ID NO: 15; nucleotides 1-266 of SEQ ID NO:50; SEQ ID NO:50; SEQ ID NO: 18; SEQ ID NO: 29; nucleotides 1-675 of SEQ ID NO:37, SEQ ID NO: 37; SEQ ID NO:16; SEQ ID NO:32; SEQ ID NO:25; nucleotides 1-132 of SEQ ID NO: 40; or any one of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 17, 19, 20, 21, 22, 23, 24, 26, 27, 28, 30, 31, 33, 34, 35, 36, 38, 39, 41, 42, 43, 44, 46, 47, 48, 49, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199,

200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, or a complement thereof;

c) a polynucleotide comprising the sense or antisense sequence of a sequence having at least 130 contiguous nucleotides of any one of nucleotides 1-380 of SEQ ID NO: 45; SEQ ID NO: 45; SEQ ID NO: 13; SEQ ID NO: 15; nucleotides 1-266 of SEQ ID NO:50; SEQ ID NO:50; SEQ ID NO: 18; SEQ ID NO: 29; nucleotides 1-675 of SEQ ID NO:37, SEQ ID NO: 37; SEQ ID NO:16; SEQ ID NO:32; SEQ ID NO:25; nucleotides 1-132 of SEQ ID NO: 40; or any one of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 17, 19, 20, 21, 22, 23, 24, 26, 27, 28, 30, 31, 33, 34, 35, 36, 38, 39, 41, 42, 43, 44, 46, 47, 48, 49, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, or a complement thereof.

30. The method of claim 24, wherein said silencing element expresses a double stranded RNA.

31. The method of claim 24, wherein said silencing element comprises a hairpin RNA.

32. The method of claim 31, wherein said polynucleotide comprising the silencing element comprises, in the following order, a first segment, a second segment, and a third segment, wherein

- a) said first segment comprises at least about 19 nucleotides having at least 90% sequence complementarity to the target polynucleotide;
- b) said second segment comprises a loop of sufficient length to allow the silencing element to be transcribed as a hairpin RNA; and,
- c) said third segment comprises at least about 19 nucleotides having at least 85% complementarity to the first segment.

33. The method of claim 28, wherein said silencing element is operably linked to a heterologous promoter.

34. The method of claim 28, wherein said silencing element is flanked by a first operably linked convergent promoter at one terminus of the silencing element and a second operably linked convergent promoter at the opposing terminus of the polynucleotide, wherein the first and the second convergent promoters are capable of driving expression of the silencing element.

35. The method of claim **28**, wherein said plant is a monocot.

36. The method of claim **35**, wherein said monocot is maize, barley, millet, wheat or rice.

37. The method of claim **28**, wherein said plant is a dicot.

38. The method of claim **37**, wherein said plant is soybean, canola, alfalfa, sunflower, safflower, tobacco, *Arabidopsis*, or cotton.

* * * * *