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(54) **Methods for genetic control of insect infestations in plants and compositions thereof**

Verfahren zur genetischen Kontrolle von Insektenplagen bei Pflanzen und Zusammensetzungen dafür
Procédés pour le contrôle génétique d'infestation d'insectes dans des plantes et compositions
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Description

BACKGROUND OF THE INVENTION**1. Field of the Invention**

[0001] The present invention relates generally to genetic control of pest infestations. More specifically, the present invention relates to recombinant DNA technologies for post-transcriptionally repressing or inhibiting expression of target coding sequences in the cell of a pest to provide a pest-protective effect.

2. Description of Related Art

[0002] The environment in which humans live is replete with pest infestation. Pests including insects, arachnids, crustaceans, fungi, bacteria, viruses, nematodes, flatworms, roundworms, pinworms, hookworms, tapeworms, trypanosomes, schistosomes, botflies, fleas, ticks, mites, and lice are pervasive in the human environment. A multitude of means have been utilized for attempting to control infestations by these pests. Compositions for controlling infestations by microscopic pests such as bacteria, fungi, and viruses have been provided in the form of antibiotic compositions, antiviral compositions, and antifungal compositions. Compositions for controlling infestations by larger pests such as nematodes, flatworm, roundworms, pinworms, heartworms, tapeworms, trypanosomes and schistosomes have typically been in the form of chemical compositions that can be applied to surfaces on which pests are present or administered to infested animals in the form of pellets, powders, tablets, pastes, or capsules. There is a great need in the art for improvement of these methods and particularly for methods that would benefit the environment relative to the prior techniques. Commercial crops are often the targets of insect attack. Substantial progress has been made in the last a few decades towards developing more efficient methods and compositions for controlling insect infestations in plants. Chemical pesticides have been very effective in eradicating pest infestations. However, there are several disadvantages to using chemical pesticidal agents. Chemical pesticidal agents are not selective. Applications of chemical pesticides intended to control invertebrate pests, such as coleopteran insects including corn rootworm species that are harmful to various crops and other plants, exert their effects on non-target fauna as well, often effectively sterilizing a field for a period of time over which the pesticidal agents have been applied. Chemical pesticidal agents persist in the environment and generally are slow to be metabolized, if at all. They accumulate in the food chain, and particularly in the higher predator species. Accumulations of these chemical pesticidal agents results in the development of resistance to the agents and in species higher up the evolutionary ladder, can act as mutagens and/or carcinogens to cause irreversible and deleterious genetic modifications. Thus there has been a particularly long felt need for environmentally friendly methods for controlling or eradicating insect infestation on or in plants, *i.e.*, methods that are selective, environmentally inert, non-persistent, and biodegradable, and that fit well into pest resistance management schemes.

[0003] Compositions that include *Bacillus thuringiensis* (Bt) bacteria have been commercially available and used as environmentally safe and acceptable insecticides for more than thirty years. The insecticidal effect of Bt bacteria do not persist in the environment, are highly selective as to the target species affected, exert their effects only upon ingestion by a target pest, and have been shown to be harmless to plants and other non-targeted organisms, including humans. Transgenic plants containing one or more genes encoding insecticidal Bt protein are also available in the art and are remarkably efficient in controlling insect pest infestation. A substantial result of the use of recombinant plants expressing Bt insecticidal proteins is a marked decrease in the amount of chemical pesticidal agents that are applied to the environment to control pest infestation in crop fields in areas in which such transgenic crops are used. The decrease in application of chemical pesticidal agents has resulted in cleaner soils and cleaner waters running off of the soils into the surrounding streams, rivers, ponds and lakes. In addition to these environmental benefits, there has been a noticeable increase in the numbers of beneficial insects in crop fields in which transgenic insect resistant crops are grown because of the decrease in the use of chemical insecticidal agents.

[0004] Antisense methods and compositions have been reported in the art and are believed to exert their effects through the synthesis of a single-stranded RNA molecule that in theory hybridizes *in vivo* to a substantially complementary sense strand RNA molecule. Antisense technology has been difficult to employ in many systems for three principle reasons. First, the antisense sequence expressed in the transformed cell is unstable. Second, the instability of the antisense sequence expressed in the transformed cell concomitantly creates difficulty in delivery of the sequence to a host, cell type, or biological system remote from the transgenic cell. Third, the difficulties encountered with instability and delivery of the antisense sequence create difficulties in attempting to provide a dose within the recombinant cell expressing the antisense sequence that can effectively modulate the level of expression of the target sense nucleotide sequence.

[0005] There have been few improvements in technologies for modulating the level of gene expression within a cell, tissue, or organism, and in particular, a lack of developed technologies for delaying, repressing or otherwise reducing

the expression of specific genes using recombinant DNA technology. Furthermore, as a consequence of the unpredictability of these approaches, no commercially viable means for modulating the level of expression of a specific gene in a eukaryotic or prokaryotic organism is available.

[0006] Double stranded RNA mediated inhibition of specific genes in various pests has been previously demonstrated. dsRNA mediated approaches to genetic control have been tested in the fruit fly *Drosophila melanogaster* (Kennerdell and Carthew, 1998; Kennerdell and Carthew, 2000). Kennerdell and Carthew (1998) describe a method for delivery of dsRNA involved generating transgenic insects that express double stranded RNA molecules or injecting dsRNA solutions into the insect body or within the egg sac prior to or during embryonic development.

[0007] Research investigators have previously demonstrated that double stranded RNA mediated gene suppression can be achieved in nematodes either by feeding or by soaking the nematodes in solutions containing double stranded or small interfering RNA molecules and by injection of the dsRNA molecules. Rajagopal *et. al.* (2002) described failed attempts to suppress an endogenous gene in larvae of the insect pest *Spodoptera litura* by feeding or by soaking neonate larvae in solutions containing dsRNA specific for the target gene, but were successful in suppression after larvae were injected with dsRNA into the hemolymph of 5th instar larvae using a microapplicator. Recently, Yadav *et al.* (2006) reported that host-generated dsRNA produced in a plant can protect such plants from infection by nematodes. Similarly, U.S. Patent App. Pub. No. 2003/0150017 prophetically described a preferred locus for inhibition of the lepidopteran larvae *Helicoverpa armigera* using dsRNA delivered to the larvae by ingestion of a plant transformed to produce the dsRNA. WO 2005/110068 teaches providing, in the diet of corn rootworm (CRW), CRW-specific dsRNA directed to essential CRW genes. The dsRNA is provided in the CRW diet *in-vitro* and *in-planta*, with the result that CRW larvae are stunted or killed after feeding on the diet, and this effect was demonstrated for several different genes.

[0008] Therefore, there has existed a need for identifying efficacious nucleotide sequences for use in improved methods of modulating gene expression by repressing, delaying or otherwise reducing gene expression within a particular coleopteran pest for the purpose of controlling pest infestation or to introduce novel phenotypic traits.

SUMMARY OF THE INVENTION

[0009] The invention provides

(1) a polynucleotide selected from:

- (a) a polynucleotide comprising the nucleic acid sequence of SEQ ID NO:704;
 - (b) a polynucleotide that hybridizes to the nucleic acid sequence of SEQ ID NO:704 under wash conditions of 5X SSC, 50% formamide and 42°C for 10 minutes;
 - (c) a polynucleotide having at least 70% sequence identity to the nucleic acid sequence of SEQ ID NO:704;
 - (d) a fragment of at least 21 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:704; and
 - (e) a complement of the sequence of (a), (b), (c) or (d), wherein said polynucleotide is operably linked to a heterologous promoter; and
- wherein ingestion by a coleopteran plant pest of a double stranded ribonucleotide sequence comprising at least one strand that is complementary to said polynucleotide or said fragment inhibits the growth of said pest;

(2) a double stranded ribonucleotide sequence produced from the expression of a polynucleotide according to (1) above, wherein ingestion of said ribonucleotide sequence by a coleopteran plant pest inhibits the growth of said pest;

(3) a cell transformed with the polynucleotide of (1) above;

(4) a plant transformed with the polynucleotide of (1) above, or a seed thereof comprising the polynucleotide;

(5) a commodity product produced from a plant according to (4) above, wherein said commodity product comprises a detectable amount of a ribonucleotide expressed from the polynucleotide of (1) above;

(6) a method for controlling coleopteran pest infestation comprising providing in the diet of a coleopteran pest an agent comprising a first polynucleotide sequence that functions upon ingestion by the pest to inhibit a biological function within said pest, wherein said polynucleotide sequence exhibits from about 95 to about 100% nucleotide sequence identity along at least from about 19 to about 25 contiguous nucleotides to a coding sequence derived from said pest and is hybridized to a second polynucleotide sequence that is complementary to said first polynucleotide sequence, and wherein said coding sequence derived from said pest is SEQ ID NO:704 or the complement thereof;

(7) a method for controlling a coleopteran pest infestation comprising providing in the diet of a coleopteran pest a plant cell expressing a polynucleotide sequence according to (1) above, wherein the polynucleotide is expressed to produce a double stranded ribonucleic acid that functions upon ingestion by the pest to inhibit the expression of a target sequence within said pest and results in decreased feeding on said diet relative to a diet lacking the plant cell;

(8) a method for improving the yield of a crop produced from a crop plant subjected to insect pest infestation, said

method comprising the steps of,

- a) introducing a polynucleotide according to (1) above into said crop plant,
- b) cultivating the crop plant to allow the expression of said polynucleotide, wherein expression of the polynucleotide inhibits feeding by insects pests and loss of yield due to pest infestation;

(9) A method for improving the drought tolerance of a crop produced from a crop plant subjected to insect pest infestation, said method comprising the steps of

- a) introducing a polynucleotide according to (1) above into said crop plant,
- b) cultivating the crop plant to allow the expression of said polynucleotide, wherein expression of the polynucleotide inhibits feeding by insects pests and loss of drought tolerance due to pest infestation;

(10) a method of producing a commodity product, food or feed comprising obtaining a plant according to (4) above or a part thereof, and preparing a commodity product, food or feed from the plant or part thereof.

[0010] The method of (6) above comprises modulating or inhibiting expression of one or more target genes in a coleopteran pest that causes cessation of feeding, growth, development, reproduction and/or infectivity and eventually result in the death of the insect. The method comprises introduction of partial or fully, stabilized double-stranded RNA (dsRNA), including its modified forms such as small interfering RNA (siRNA) sequences, into the cells or into the extracellular environment, such as the midgut, within a coleopteran pest body wherein the dsRNA enters the cells and inhibits expression of at least one or more target genes and wherein the inhibition exerts a deleterious effect upon the coleopteran pest. The methods and associated compositions may be used for limiting or eliminating coleopteran pest infestation in or on any pest host, pest symbiont, or environment in which a pest is present by providing one or more compositions comprising the dsRNA molecules described herein in the diet of the pest. The method will find particular benefit for protecting plants from insect attack. In one embodiment, the pest is defined as comprising a digestive system pH within the range of from 4.5 to 9.5, from 5 to 9, from 6 to 8, and from about pH 7.0.

[0011] The nucleic acid of (1) above is homologous to at least a portion of one or more native nucleic acid sequences in a *Diabrotica virgifera* (Western Corn Rootworm (WCR, *Diabrotica virgifera* or *Diabrotica virgifera virgifera*), Southern Corn Rootworm (SCR, *Diabrotica undecimpunctata howardi*), Mexican Corn Rootworm (MCR, *Diabrotica virgifera zea*), Brazilian Corn Rootworm (BZR, *Diabrotica balteata*, *Diabrotica viridula*, *Diabrotica speciosa*), Northern Corn rootworm (NCR, *Diabrotica barberi*), *Diabrotica undecimpunctata*)).

[0012] The method of (6) above comprises the step of providing in the diet of the pest a gene suppressive amount of at least one dsRNA molecule transcribed from a nucleotide sequence as described herein, at least one segment of which is complementary to an mRNA sequence within the cells of the pest. The method may further comprise observing the death, inhibition, stunting, or cessation of feeding of the pest. A dsRNA molecule, including its modified form such as an siRNA molecule, fed to a pest in accordance with the invention may be at least from 80, 81, 82, 83, 84, 85, 86, 87, 88 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100% identical to a RNA molecule transcribed from a nucleotide sequence of SEQ ID NO:704.

[0013] According to aspect (1) of the present invention, an isolated and purified nucleotide sequences as set forth in SEQ ID NO:704 is provided. The aspect (2) of the present invention includes a stabilized dsRNA molecule and miRNAs for inhibition of expression of a target gene in a coleopteran pest expressed from this sequence and fragments thereof. A stabilized dsRNA, including a miRNA or siRNA molecule can comprise at least two coding sequences that are arranged in a sense and an antisense orientation relative to at least one promoter, wherein the nucleotide sequence that comprises a sense strand and an antisense strand are linked or connected by a spacer sequence of at least from about five to about one thousand nucleotides, wherein the sense strand and the antisense strand may be a different length, and wherein each of the two coding sequences shares at least 80% sequence identity, at least 90%, at least 95%, at least 98%, or 100% sequence identity, to any one or more nucleotide sequence(s) set forth in set forth in SEQ ID NO:704.

[0014] Further provided by the invention is a fragment or concatemer of a nucleic acid sequence of SEQ ID NO:704.

[0015] The fragment may be defined as causing a the death, inhibition, stunting, or cessation of feeding of a pest when expressed as a dsRNA and provided to the pest. The fragment may, for example, comprise at least 19, 21, 23, 25, 40, 60, 80, 100, 125 or more contiguous nucleotides of SEQ ID NO:704, or a complement thereof. One beneficial DNA segment for use in the present invention is at least from 19 to 23, or 23 to 100 nucleotides up to 2000 nucleotides or more in length. Particularly useful will be dsRNA sequences including 23 to 300 nucleotides homologous to a pest target sequence. The invention also provides a ribonucleic acid expressed from any of such sequences including a dsRNA. A sequence selected for use in expression of a gene suppression agent can be constructed from a single sequence derived from one or more target pests and intended for use in expression of an RNA that functions in the suppression of a single gene or gene family in the one or more target pests, or that the DNA sequence can be constructed as a chimera from

a plurality of DNA sequences.

[0016] Aspect (2) of the invention includes recombinant DNA constructs comprising a nucleic acid molecule encoding a dsRNA molecule described herein. The dsRNA may be formed by transcription of one strand of the dsRNA molecule from a nucleotide sequence which is at least from about 80% to about 100% identical to a nucleotide sequence of SEQ ID NO:704. Such recombinant DNA constructs may be defined as producing dsRNA molecules capable of inhibiting the expression of endogenous target gene(s) in a pest cell upon ingestion. The construct may comprise a nucleotide sequence of the invention operably linked to a promoter sequence that functions in the host cell. Such a promoter may be tissue-specific and may, for example, be specific to a tissue type which is the subject of pest attack. In the case of rootworms, for example, it may be desired to use a promoter providing root-preferred expression.

[0017] Nucleic acid constructs in accordance with the invention may comprise at least one non-naturally occurring nucleotide sequence that can be transcribed into a single stranded RNA capable of forming a dsRNA molecule *in vivo* through hybridization. Such dsRNA sequences self assemble and can be provided in the diet of a coleopteran pest to achieve the desired inhibition.

[0018] A recombinant DNA construct may comprise two different non-naturally occurring sequences which, when expressed *in vivo* as dsRNA sequences and provided in the diet of a coleopteran pest, inhibit the expression of at least two different target genes in the cell of the coleopteran pest. In certain embodiments, at least 3, 4, 5, 6, 8 or 10 or more different dsRNAs are produced in a cell or plant comprising the cell that have a pest-inhibitory effect. The dsRNAs may be expressed from multiple constructs introduced in different transformation events or could be introduced on a single nucleic acid molecule. The dsRNAs may be expressed using a single promoter or multiple promoters. In one embodiment of the invention, single dsRNAs are produced that comprise nucleic acids homologous to multiple loci within a pest.

[0019] Aspect (3) of the invention provides a recombinant host cell having in its genome at least one recombinant DNA sequence as defined above that is transcribed to produce at least one dsRNA molecule that functions when ingested by a coleopteran pest to inhibit the expression of a target gene in the pest. The dsRNA molecule may be encoded by any of the nucleic acids described herein and as set forth in the sequence listing.

[0020] Aspect (4) of the invention provides a transformed plant cell having in its genome at least one recombinant DNA sequence described herein. Transgenic plants comprising such a transformed plant cell are also provided, including progeny plants of any generation, seeds, and plant products, each comprising the recombinant DNA.

[0021] The methods and compositions of the present invention may be applied to any monocot and dicot plant, depending on the coleopteran pest control desired. Specifically, the plants are intended to include, without limitation, alfalfa, aneth, apple, apricot, artichoke, arugula, asparagus, avocado, banana, barley, beans, beet, blackberry, blueberry, broccoli, brusselsprouts, cabbage, canola, cantaloupe, carrot, cassava, cauliflower, celery, cherry, cilantro, citrus, clementine, coffee, corn, cotton, cucumber, Douglas fir, eggplant, endive, escarole, eucalyptus, fennel, figs, gourd, grape, grapefruit, honey dew, jicama, kiwifruit, lettuce, leeks, lemon, lime, Loblolly pine, mango, melon, mushroom, nut, oat, okra, onion, orange, an ornamental plant, papaya, parsley, pea, peach, peanut, pear, pepper, persimmon, pine, pineapple, plantain, plum, pomegranate, poplar, potato, pumpkin, quince, radiata pine, radicchio, radish, raspberry, rice, rye, sorghum, Southern pine, soybean, spinach, squash, strawberry, sugarbeet, sugarcane, sunflower, sweet potato, sweetgum, tangerine, tea, tobacco, tomato, turf, a vine, watermelon, wheat, yams, and zucchini plants. Thus, a plant transformed with a recombinant DNA sequence as set forth in SEQ ID NO:704, or concatemer, fragment, or complement thereof, that is transcribed to produce at least one dsRNA molecule that functions when ingested by a coleopteran pest to inhibit the expression of a target gene in the pest is also provided by the invention.

[0022] The method of aspect (7) includes a combination of nucleotides for controlling coleopteran pest infestations. One means provides a dsRNA method as described herein for protecting plants from insect infestation along with one or more insecticidal agents that exhibit features different from those exhibited by the dsRNA methods and compositions. For example, one or more Bt proteins may be provided in the diet of insect pests in combination with one or more dsRNAs as described herein. A composition formulated for topical application or derived using a transgenic approach that combines dsRNA methods and compositions with Bt may be used to provide synergies that were not known previously in the art for controlling insect infestation. One synergy is the reduction in the level of expression required for either the dsRNA(s) or the Bt protein(s). When combined together, a lower effective dose of each pest control agent could be used. It is believed that the Bt insecticidal proteins create entry pores through which the dsRNA molecules are able to penetrate more effectively into spaces remote from the gut of the insect pest, or more efficiently into the cells in the proximity of lesions created by the Bt proteins, thus requiring less of either the Bt or the dsRNA to achieve the desired insecticidal result or the desired inhibition or suppression of a targeted biological function in the target pest.

[0023] A *Bacillus thuringiensis* insecticidal protein can be any of a number of insecticidal proteins including but not limited to a Cry1, a Cry3, a TIC851, a CryET70, a Cry22, a TIC901, a TIC1201, a TIC407, a TIC417, a binary insecticidal protein CryET33 and CryET34, a binary insecticidal protein CryET80 and CryET76, a binary insecticidal protein TIC 100 and TIC101, a binary insecticidal protein PS149B1, a VIP insecticidal protein, a TIC900 or related protein, or combinations of the insecticidal proteins ET29 or ET37 with insecticidal proteins TIC810 or TIC812, and insecticidal chimeras of any of the preceding insecticidal proteins.

[0024] A ribonucleic acid that is provided in a diet can be provided in an artificial diet formulated to meet particular nutritional requirements for maintaining a pest on such diet. The diet may be supplemented with a pest controlling amount of an RNA that has been purified from a separate expression system to determine a pest controlling amount of RNA composition or to determine extent of suppressive activity upon ingestion of the supplemented diet by the pest. The diet can also be a recombinant cell transformed with a DNA sequence constructed for expression of the agent, the RNA, or the gene suppression agent. Upon ingestion of one or more such transformed cells by the pest, a desired phenotypic result is observed, indicating that the agent has functioned to inhibit the expression of a target nucleotide sequence that is within the cells of the pest.

[0025] A gene targeted for suppression can encode an essential protein, the predicted function of which is selected from the group consisting of muscle formation, juvenile hormone formation, juvenile hormone regulation, ion regulation and transport, protein synthesis and transport, digestive enzyme synthesis, maintenance of cell membrane potential, amino acid biosynthesis, amino acid degradation, sperm formation, pheromone synthesis, pheromone sensing, antennae formation, wing formation, leg formation, development and differentiation, egg formation, larval maturation, digestive enzyme formation, haemolymph synthesis, haemolymph maintenance, neurotransmission, cell division, energy metabolism, respiration, an unknown function, and apoptosis.

[0026] Aspect (8) of the present invention also provides methods for improving the yield of a crop produced from a crop plant subjected to insect pest infestation, said method comprising the steps of a) introducing a polynucleotide comprising a sequence of SEQ ID NO:704 or a complement or concatemer or fragment thereof into said crop plant; and b) cultivating the crop plant to allow the expression of said polynucleotide, wherein expression of the polynucleotide inhibits feeding by insect pests and loss of yield due to pest infestation.

[0027] In certain embodiments, the expression of the polynucleotide produces an RNA molecule that suppresses at least a first target gene in an insect pest that has ingested a portion of said crop plant, wherein the target gene performs at least one essential function selected from the group consisting of feeding by the pest, viability of the pest, pest cell apoptosis, differentiation and development of the pest or any pest cell, sexual reproduction by the pest, muscle formation, muscle twitching, muscle contraction, juvenile hormone formation and/or reduction, juvenile hormone regulation, ion regulation and transport, maintenance of cell membrane potential, amino acid biosynthesis, amino acid degradation, sperm formation, pheromone synthesis, pheromone sensing, antennae formation, wing formation, leg formation, egg formation, larval maturation, digestive enzyme formation, haemolymph synthesis, haemolymph maintenance, neurotransmission, larval stage transition, pupation, emergence from pupation, cell division, energy metabolism, respiration, cytoskeletal structure synthesis and maintenance, nucleotide metabolism, nitrogen metabolism, water use, water retention, and sensory perception.

[0028] In other embodiments, the insect pest is a corn rootworm pest selected from the group consisting of *Diabrotica undecimpunctata howardi* (Southern Corn Rootworm (SCR)), *Diabrotica virgifera virgifera* (Western Corn Rootworm (WCR)), *Diabrotica barberi* (Northern Corn Rootworm (NCR)), *Diabrotica virgifera zea* (Mexican Corn Rootworm (MCR)), *Diabrotica balteata* (Brazilian Corn Rootworm (BZR)), *Diabrotica viridula* (Brazilian Corn Rootworm (BZR)), and *Diabrotica speciosa* (Brazilian Corn Rootworm (BZR)).

[0029] Aspect (9) of the invention provides for a method for improving the drought tolerance of a crop produced from a crop plant subjected to insect pest infestation, said method comprising the steps of a) introducing a polynucleotide sequence of SEQ ID NO:704, or a fragment thereof, into said crop plant; and b) cultivating the crop plant to allow the expression of said polynucleotide, wherein expression of the polynucleotide inhibits feeding by insect pests and loss of drought tolerance due to pest infestation, are also provided.

[0030] Aspect (5) of the invention provides agronomically and commercially important products and/or compositions of matter including animal feed, commodities, products and by-products that are intended for use as food for human consumption or for use in compositions and commodities that are intended for human consumption including corn flour, corn meal, corn syrup, corn oil, corn starch, popcorn, corn cakes and cereals. Such compositions may be defined as containing detectable amounts of a nucleotide sequence set forth herein, and thus are also diagnostic for any transgenic event containing such nucleotide sequences. These products are useful at least because they are likely to be derived from crops propagated with fewer pesticides and organophosphates as a result of their incorporation of the nucleotides of the present invention for controlling the infestation of coleopteran pests in plants. Such commodities and commodity products can be produced from seed produced from a transgenic plant, wherein the transgenic plant expresses RNA from one or more contiguous nucleotides of the present invention or nucleotides of one or more coleopteran pests and the complements thereof. Such commodities and commodity products may also be useful in controlling coleopteran pests of such commodity and commodity products, such as for example, control of flour weevils, because of the presence in the commodity or commodity product of the pest gene suppressive RNA expressed from a gene sequence as set forth in the present invention. Aspect (10) of the invention provides for a method of producing such a commodity product from a plant transformed with a polynucleotide comprising a sequence of SEQ ID NO:704, or a concatemer or fragment or complement thereof, and preparing a commodity product from the plant or part thereof. Aspect (10) of the invention provides for a method of producing such food or feed from a plant transformed with a polynucleotide of SEQ ID NO:704 or

a fragment or complement thereof, and preparing food or feed from said plant or part thereof.

BRIEF DESCRIPTION OF THE FIGURES

[0031]

FIG. 1: Bioassay of F1 corn plant events transformed with pMON98503 (SEQ ID NO:820) and challenged with Western Corn Rootworm (WCR).

FIG. 2: Bioassay of F1 corn plant events transformed with pMON98504 comprising concatemer C1 (SEQ ID NO:821) and challenged with Western Corn Rootworm (WCR).

FIG. 3: Selection of Dv49 and Dv248 fragments and schematic design of Dv49-Dv248 concatemer C38.

FIG. 4: dsRNAs F1- F13 synthesized based on concatemer C38.

FIG. 5: DV49-DV248 concatemer 38 dose response (Fragments F1- F6).

FIG. 6: DV49-DV248 concatemer 38 dose response (Fragments F7- F10).

FIG. 7: DV49-DV248 concatemer 38 dose response (Fragments F11- F13).

DETAILED DESCRIPTION OF THE INVENTION

[0032] The following is a detailed description of the invention provided to aid those skilled in the art in practicing the present invention.

[0033] The present invention provides methods and compositions for genetic control of pest infestations. For example, the present invention provides recombinant DNA technologies to post-transcriptionally repress or inhibit expression of a target coding sequence in the cell of a pest to provide a pest-protective effect by feeding to the pest one or more double stranded or small interfering ribonucleic acid (RNA) molecules transcribed from all or a portion of a target coding sequence, thereby controlling the infestation. Therefore, the present invention relates to sequence-specific inhibition of expression of coding sequences using double-stranded RNA (dsRNA), including small interfering RNA (siRNA), to achieve the intended levels of pest control.

[0034] Isolated and substantially purified nucleic acid molecules including non-naturally occurring nucleotide sequences and recombinant DNA constructs for transcribing dsRNA molecules of the present invention are provided that suppress or inhibit the expression of an endogenous coding sequence or a target coding sequence in the pest when introduced thereto. Transgenic plants that (a) contain nucleotide sequences encoding the isolated and substantially purified nucleic acid molecules and the non-naturally occurring recombinant DNA constructs for transcribing the dsRNA molecules for controlling plant pest infestations, and (b) display resistance and/or enhanced tolerance to the insect infestations, are also provided. Compositions containing the dsRNA nucleotide sequences of the present invention for use in topical applications onto plants or onto animals or into the environment of an animal to achieve the elimination or reduction of pest infestation are also described.

[0035] The inventors have herein discovered that, contrary to the teachings in the prior art, feeding a composition containing double stranded RNA molecules consisting of sequences found within one or more expressed nucleotide sequences of a coleopteran species to the species from which the nucleotide sequences were obtained results in the inhibition of one or more biological functions within the coleopteran species. Particularly, the inventors have discovered that feeding the double stranded RNA molecules described herein to crop pest species such as corn rootworms results in the death or inhibition of development and differentiation of insect pests that ingest these compositions.

[0036] The inventors have identified the nucleotide sequences described herein as providing plant protective effects against coleopteran pest species. Amino acid sequences encoded by the cDNA sequences have been deduced and compared to known amino acid sequences. Many of the sequences are predicted to encode proteins that have some annotation information associated with them. The annotation information that is associated with a particular nucleotide sequence and protein sequence encoded therefrom is based on homology or similarity between the amino acid sequences deduced through translation of the coding sequences described herein as set forth and amino acid sequences that are known in the art in publicly available databases.

[0037] cDNA sequences encoding proteins or parts of proteins essential for survival, such as amino acid sequences involved in various metabolic or catabolic biochemical pathways, cell division, reproduction, energy metabolism, digestion, neurological function and the like were selected for use in preparing double stranded RNA molecules that were provided in the diet of coleopteran pests. As described herein, ingestion by a target pest of compositions containing one or more dsRNAs, at least one segment of which corresponds to at least a substantially identical segment of RNA produced in the cells of the target pest, resulted in death, stunting, or other inhibition of the target pest. These results indicated that a nucleotide sequence, either DNA or RNA, derived from a coleopteran pest can be used to construct plant cells resistant to infestation by the pest. The pest host, for example, can be transformed to contain one or more of the nucleotide sequences derived from the coleopteran pest. The nucleotide sequence transformed into the pest host or symbiont may

encode one or more RNAs that form into a dsRNA sequence in the cells or biological fluids within the transformed host or symbiont, thus making the dsRNA available in the diet of the pest if/when the pest feeds upon the transgenic host or symbiont, resulting in the suppression of expression of one or more genes in the cells of the pest and ultimately the death, stunting, or other inhibition of the pest

[0038] The present invention relates generally to genetic control of coleopteran pest infestations in host organisms. More particularly, the present invention includes the methods for delivery of pest control agents to a coleopteran pest. Such pest control agents cause, directly or indirectly, an impairment in the ability of the pest to maintain itself, grow or otherwise infest a target host or symbiont. The present invention provides methods for employing stabilized dsRNA molecules in the diet of the pest as a means for suppression of targeted genes in the pest, thus achieving desired control of pest infestations in, or about the host or symbiont targeted by the pest.

[0039] In accomplishing the foregoing, the present invention provides a method of inhibiting expression of a target gene in a coleopteran pest, including for example, corn rootworms or other coleopteran insect species, resulting in the cessation of feeding, growth, development, reproduction, infectivity, and eventually may result in the death of the pest. The method comprises in one embodiment introducing partial or fully stabilized double-stranded RNA (dsRNA) nucleotide molecules into a nutritional composition that the pest relies on as a food source, and making the nutritional composition available to the pest for feeding. Ingestion of the nutritional composition containing the double stranded or siRNA molecules results in the uptake of the molecules by the cells of the pest, resulting in the inhibition of expression of at least one target gene in the cells of the pest. Inhibition of the target gene exerts a deleterious effect upon the pest.

[0040] In certain embodiments, dsRNA molecules provided by the invention comprise nucleotide sequences complementary to a sequence as set forth in SEQ ID NO:704, the inhibition of which in a pest organism results in the reduction or removal of a protein or nucleotide sequence agent that is essential for the pests' growth and development or other biological function. The nucleotide sequence selected may exhibit from 80% to at least 100% sequence identity to one of the nucleotide sequences as set forth in SEQ ID NO:704, as set forth in the sequence listing, including the complement thereof. Such inhibition can be described as specific in that a nucleotide sequence from a portion of the target gene is chosen from which the inhibitory dsRNA or siRNA is transcribed. The method is effective in inhibiting the expression of at least one target gene and can be used to inhibit many different types of target genes in the pest.

[0041] The sequences identified as having a pest protective effect may be readily expressed as dsRNA molecules through the creation of appropriate expression constructs. For example, such sequences can be expressed as a hairpin and stem and loop structure by taking a first segment corresponding to a sequence of SEQ ID NO:704 or a fragment thereof, linking this sequence to a second segment spacer region that is not homologous or complementary to the first segment, and linking this to a third segment that transcribes an RNA, wherein at least a portion of the third segment is substantially complementary to the first segment. Such a construct forms a stem and loop structure by hybridization of the first segment with the third segment and a loop structure forms comprising the second segment (WO94/01550, WO98/05770, US 2002/0048814A1, and US 2003/0018993A1).

A. Nucleic Acid Compositions and Constructs

[0042] The invention provides recombinant DNA constructs for use in achieving stable transformation of particular host or symbiont pest targets. Transformed host or symbiont pest targets may express pesticidally effective levels of preferred dsRNA or siRNA molecules from the recombinant DNA constructs, and provide the molecules in the diet of the pest. Pairs of isolated and purified nucleotide sequences may be provided from cDNA library and/or genomic library information. The pairs of nucleotide sequences may be derived from any preferred coleopteran pest for use as thermal amplification primers to generate DNA templates for the preparation of dsRNA and siRNA molecules of the present invention.

[0043] As used herein, the term "nucleic acid" refers to a single or double-stranded polymer of deoxyribonucleotide or ribonucleotide bases read from the 5' to the 3' end. The "nucleic acid" may also optionally contain non-naturally occurring or altered nucleotide bases that permit correct read through by a polymerase and do not reduce expression, of a polypeptide encoded by that nucleic acid. The term "nucleotide sequence" or "nucleic acid sequence" refers to both the sense and antisense strands of a nucleic acid as either individual single strands or in the duplex. The term "ribonucleic acid" (RNA) is inclusive of RNAi (inhibitory RNA), dsRNA (double stranded RNA), siRNA (small interfering RNA), mRNA (messenger RNA), miRNA (micro-RNA), tRNA (transfer RNA, whether charged or discharged with a corresponding acylated amino acid), and cRNA (complementary RNA) and the term "deoxyribonucleic acid" (DNA) is inclusive of cDNA and genomic DNA and DNA-RNA hybrids. The words "nucleic acid segment", "nucleotide sequence segment", or more generally "segment" will be understood by those in the art as a functional term that includes both genomic sequences, ribosomal RNA sequences, transfer RNA sequences, messenger RNA sequences, operon sequences and smaller engineered nucleotide sequences that express or may be adapted to express, proteins, polypeptides or peptides.

[0044] Provided according to the invention are nucleotide sequences, the expression of which results in an RNA sequence which is substantially homologous to an RNA molecule of a targeted gene in an insect that comprises an RNA

sequence encoded by a nucleotide sequence within the genome of the insect. Thus, after ingestion of the stabilized RNA sequence down-regulation of the nucleotide sequence of the target gene in the cells of the insect may be obtained resulting in a deleterious effect on the maintenance, viability, proliferation, reproduction and infestation of the insect.

[0045] As used herein, the term "substantially homologous" or "substantial homology", with reference to a nucleic acid sequence, includes a nucleotide sequence that hybridizes under stringent conditions to the coding sequence as set forth in SEQ ID NO:704 as set forth in the sequence listing, or the complements thereof. Sequences that hybridize under stringent conditions to SEQ ID NO:704 as set forth in the sequence listing, or the complements thereof, are those that allow an antiparallel alignment to take place between the two sequences, and the two sequences are then able, under stringent conditions, to form hydrogen bonds with corresponding bases on the opposite strand to form a duplex molecule that is sufficiently stable under the stringent conditions to be detectable using methods well known in the art. Substantially homologous sequences have preferably from 70% to 80% sequence identity, or more preferably from 80% to 85% sequence identity, or most preferable from 90% to 95% sequence identity, to 99% sequence identity, to the referent nucleotide sequences as set forth in SEQ ID NO:704 as set forth in the sequence listing, or the complements thereof.

[0046] As used herein, the term "sequence identity", "sequence similarity" or "homology" is used to describe sequence relationships between two or more nucleotide sequences. The percentage of "sequence identity" between two sequences is determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the 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. A sequence that is identical at every position in comparison to a reference sequence is said to be identical to the reference sequence and vice-versa. A first nucleotide sequence when observed in the 5' to 3' direction is said to be a "complement" of, or complementary to, a second or reference nucleotide sequence observed in the 3' to 5' direction if the first nucleotide sequence exhibits complete complementarity with the second or reference sequence. As used herein, nucleic acid sequence molecules are said to exhibit "complete complementarity" when every nucleotide of one of the sequences read 5' to 3' is complementary to every nucleotide of the other sequence when read 3' to 5'. A nucleotide sequence that is complementary to a reference nucleotide sequence will exhibit a sequence identical to the reverse complement sequence of the reference nucleotide sequence. These terms and descriptions are well defined in the art and are easily understood by those of ordinary skill in the art.

[0047] As used herein, a "comparison window" refers to a conceptual segment of at least 6 contiguous positions, usually 50 to 100, more usually 100 to 150, in which a sequence is compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. The comparison window may comprise additions or deletions (*i.e.* gaps) of 20% or less as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. Those skilled in the art should refer to the detailed methods used for sequence alignment in the Wisconsin Genetics Software Package Release 7.0, Genetics Computer Group, 575 Science Drive Madison, Wis., USA) or refer to Ausubel *et al.* (1998) for a detailed discussion of sequence analysis.

[0048] The present invention provides DNA sequences capable of being expressed as an RNA in a cell or microorganism to inhibit target gene expression in a cell, tissue or organ of an insect. The sequences comprises a DNA molecule coding for one or more different nucleotide sequences, wherein each of the different nucleotide sequences comprises a sense nucleotide sequence and an antisense nucleotide sequence connected by a spacer sequence coding for a dsRNA molecule of the present invention. The spacer sequence constitutes part of the sense nucleotide sequence or the antisense nucleotide sequence and forms within the dsRNA molecule between the sense and antisense sequences. The sense nucleotide sequence or the antisense nucleotide sequence is substantially identical to the nucleotide sequence of the target gene or a derivative thereof or a complementary sequence thereto. The dsDNA molecule may be placed operably under the control of a promoter sequence that functions in the cell, tissue or organ of the host expressing the dsDNA to produce dsRNA molecules. In one embodiment, the DNA sequence may be derived from a nucleotide sequence as set forth in SEQ ID NO:704 in the sequence listing.

[0049] The invention also provides a DNA sequence for expression in a cell of a plant that, upon expression of the DNA to RNA and ingestion by a target pest achieves suppression of a target gene in a cell, tissue or organ of an insect pest. The dsRNA at least comprises one or multiple structural gene sequences, wherein each of the structural gene sequences comprises a sense nucleotide sequence and an antisense nucleotide sequence connected by a spacer sequence that forms a loop within the complementary and antisense sequences. The sense nucleotide sequence or the antisense nucleotide sequence is substantially identical to the nucleotide sequence of the target gene, derivative thereof, or sequence complementary thereto. The one or more structural gene sequences is placed operably under the control of one or more promoter sequences, at least one of which is operable in the cell, tissue or organ of a prokaryotic or eukaryotic organism, particularly a plant.

[0050] A gene sequence or fragment for pest control according to the invention may be cloned between two tissue specific promoters, such as two root specific promoters which are operable in a transgenic plant cell and therein expressed to produce mRNA in the transgenic plant cell that form dsRNA molecules thereto. The dsRNA molecules contained in plant tissues are ingested by an insect so that the intended suppression of the target gene expression is achieved.

[0051] A nucleotide sequence provided by the present invention may comprise an inverted repeat separated by a "spacer sequence." The spacer sequence may be a region comprising any sequence of nucleotides that facilitates secondary structure formation between each repeat, where this is required. In one embodiment of the present invention, the spacer sequence is part of the sense or antisense coding sequence for mRNA. The spacer sequence may alternatively comprise any combination of nucleotides or homologues thereof that are capable of being linked covalently to a nucleic acid molecule. The spacer sequence may comprise a sequence of nucleotides of at least about 10-100 nucleotides in length, or alternatively at least about 100-200 nucleotides in length, at least 200-400 about nucleotides in length, or at least about 400-500 nucleotides in length.

[0052] The nucleic acid molecules or fragment of the nucleic acid molecules or other nucleic acid molecules in the sequence listing are capable of specifically hybridizing to other nucleic acid molecules under certain circumstances. As used herein, two nucleic acid molecules are said to be capable of specifically hybridizing to one another if the two molecules are capable of forming an anti-parallel, double-stranded nucleic acid structure. A nucleic acid molecule is said to be the complement of another nucleic acid molecule if they exhibit complete complementarity. Two molecules are said to be "minimally complementary" if they can hybridize to one another with sufficient stability to permit them to remain annealed to one another under at least conventional "low-stringency" conditions. Similarly, the molecules are said to be complementary if they can hybridize to one another with sufficient stability to permit them to remain annealed to one another under conventional "high-stringency" conditions. Conventional stringency conditions are described by Sambrook, *et al.* (1989), and by Haymes *et al.* (1985).

[0053] Departures from complete complementarity are therefore permissible, as long as such departures do not completely preclude the capacity of the molecules to form a double-stranded structure. Thus, in order for a nucleic acid molecule or a fragment of the nucleic acid molecule to serve as a primer or probe it needs only be sufficiently complementary in sequence to be able to form a stable double-stranded structure under the particular solvent and salt concentrations employed.

[0054] Appropriate stringency conditions which promote DNA hybridization are, for example, 6.0 x sodium chloride/sodium citrate (SSC) at about 45°C, followed by a wash of 2.0 x SSC at 50°C, are known to those skilled in the art or can be found in Current Protocols in Molecular Biology (1989). For example, the salt concentration in the wash step can be selected from a low stringency of 2.0 x SSC at 50°C to a high stringency of 0.2 x SSC at 50°C. In addition, the temperature in the wash step can be increased from low stringency conditions at room temperature, about 22°C, to high stringency conditions at about 65°C. Both temperature and salt may be varied, or either the temperature or the salt concentration may be held constant while the other variable is changed. A nucleic acid for use in the present invention may specifically hybridize to one or more of nucleic acid molecules from WCR or complements thereof under such conditions. Preferably, a nucleic acid for use in the present invention will exhibit at least from 80%, or at least from 90%, or at least from 95%, or at least from 98% or even 100% sequence identity with one or more nucleic acid molecules as set forth in SEQ ID NO:704 as set forth in the sequence listing.

[0055] Nucleic acids of the present invention may also be synthesized, either completely or in part, especially where it is desirable to provide plant-preferred sequences, by methods known in the art. Thus, all or a portion of the nucleic acids of the present invention may be synthesized using codons preferred by a selected host. Species-preferred codons may be determined, for example, from the codons used most frequently in the proteins expressed in a particular host species. Other modifications of the nucleotide sequences may result in mutants having slightly altered activity.

[0056] dsRNA or siRNA nucleotide sequences comprise double strands of polymerized ribonucleotide and may include modifications to either the phosphate-sugar backbone or the nucleoside. Modifications in RNA structure may be tailored to allow specific genetic inhibition. In one embodiment, the dsRNA molecules may be modified through an enzymatic process so that siRNA molecules may be generated. The siRNA can efficiently mediate the down-regulation effect for some target genes in some insects. This enzymatic process may be accomplished by utilizing an RNase III enzyme or a DICER enzyme, present in the cells of an insect, a vertebrate animal, a fungus or a plant in the eukaryotic RNAi pathway (Elbashir *et al.*, 2002; Hamilton and Baulcombe, 1999). This process may also utilize a recombinant DICER or RNase III introduced into the cells of a target insect through recombinant DNA techniques that are readily known to the skilled in the art. Both the DICER enzyme and RNase III, being naturally occurring in an insect or being made through recombinant DNA techniques, cleave larger dsRNA strands into smaller oligonucleotides. The DICER enzymes specifically cut the dsRNA molecules into siRNA pieces each of which is about 19-25 nucleotides in length while the RNase III enzymes normally cleave the dsRNA molecules into 12-15 base-pair siRNA. The siRNA molecules produced by the either of the enzymes have 2 to 3 nucleotide 3' overhangs, and 5' phosphate and 3' hydroxyl termini. The siRNA molecules generated by RNase III enzyme are the same as those produced by Dicer enzymes in the eukaryotic RNAi pathway and are hence then targeted and degraded by an inherent cellular RNA-degrading mechanism after they are subsequently

unwound, separated into single-stranded RNA and hybridize with the RNA sequences transcribed by the target gene. This process results in the effective degradation or removal of the RNA sequence encoded by the nucleotide sequence of the target gene in the insect. The outcome is the silencing of a particularly targeted nucleotide sequence within the insect. Detailed descriptions of enzymatic processes can be found in Hannon (2002).

[0057] As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequences or sequence(s) are chosen based on a three-dimensional configuration that is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzymatic active sites and signal sequences. Nucleic acid target motifs include promoter sequences, cis elements, hairpin structures and inducible expression elements (protein binding sequences).

B. Recombinant Vectors and Host Cell Transformation

[0058] A recombinant DNA vector may, for example, be a linear or a closed circular plasmid. The vector system may be a single vector or plasmid or two or more vectors or plasmids that together contain the total DNA to be introduced into the genome of the bacterial host. In addition, a bacterial vector may be an expression vector. Nucleic acid molecules as set forth in SEQ ID NO:704 or fragments or complements thereof can, for example, be suitably inserted into a vector under the control of a suitable promoter that functions in one or more microbial hosts to drive expression of a linked coding sequence or other DNA sequence. Many vectors are available for this purpose, and selection of the appropriate vector will depend mainly on the size of the nucleic acid to be inserted into the vector and the particular host cell to be transformed with the vector. Each vector contains various components depending on its function (amplification of DNA or expression of DNA) and the particular host cell with which it is compatible. The vector components for bacterial transformation generally include, but are not limited to, one or more of the following: a signal sequence, an origin of replication, one or more selectable marker genes, and an inducible promoter allowing the expression of exogenous DNA.

[0059] Expression and cloning vectors generally contain a selection gene, also referred to as a selectable marker. This gene encodes a protein necessary for the survival or growth of transformed host cells grown in a selective culture medium. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, *e.g.*, ampicillin, neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, *e.g.*, the gene encoding D-alanine racemase for *Bacilli*. Those cells that are successfully transformed with a heterologous protein or fragment thereof produce a protein conferring drug resistance and thus survive the selection regimen. An expression vector for producing a mRNA can also contain an inducible promoter that is recognized by the host bacterial organism and is operably linked to the nucleic acid encoding, for example, the nucleic acid molecule coding the *D. v. virgifera* mRNA or fragment thereof of interest. Inducible promoters suitable for use with bacterial hosts include β -lactamase promoter, *E. coli* λ phage PL and PR promoters, and *E. coli* galactose promoter, arabinose promoter, alkaline phosphatase promoter, tryptophan (*trp*) promoter, and the lactose operon promoter and variations thereof and hybrid promoters such as the *tac* promoter. However, other known bacterial inducible promoters are suitable.

[0060] The term "operably linked", as used in reference to a regulatory sequence and a structural nucleotide sequence, means that the regulatory sequence causes regulated expression of the linked structural nucleotide sequence. "Regulatory sequences" or "control elements" refer to nucleotide sequences located upstream (5' noncoding sequences), within, or downstream (3' non-translated sequences) of a structural nucleotide sequence, and which influence the timing and level or amount of transcription, RNA processing or stability, or translation of the associated structural nucleotide sequence. Regulatory sequences may include promoters, translation leader sequences, introns, enhancers, stem-loop structures, repressor binding sequences, and polyadenylation recognition sequences.

[0061] Alternatively, the expression constructs can be integrated into the bacterial genome with an integrating vector. Integrating vectors typically contain at least one sequence homologous to the bacterial chromosome that allows the vector to integrate. Integrations appear to result from recombinations between homologous DNA in the vector and the bacterial chromosome. For example, integrating vectors constructed with DNA from various *Bacillus* strains integrate into the *Bacillus* chromosome (EP 0 127,328). Integrating vectors may also be comprised of bacteriophage or transposon sequences. Suicide vectors are also known in the art.

[0062] Construction of suitable vectors containing one or more of the above-listed components employs standard recombinant DNA techniques. Isolated plasmids or DNA fragments are cleaved, tailored, and re-ligated in the form desired to generate the plasmids required. Examples of available bacterial expression vectors include the multifunctional *E. coli* cloning and expression vectors such as Bluescript™ (Stratagene, La Jolla, CA), in which, for example, a *D. v. virgifera* protein or fragment thereof, may be ligated into the vector in frame with sequences for the amino-terminal Met and the subsequent 7 residues of β -galactosidase so that a hybrid protein is produced and pIN vectors (Van Heeke and Schuster, 1989).

[0063] A yeast recombinant construct can typically include one or more of the following: a promoter sequence, fusion partner sequence, leader sequence, transcription termination sequence, a selectable marker. These elements can be

combined into an expression cassette, which may be maintained in a replicon, such as an extrachromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as yeast or bacteria. The replicon may have two replication systems, thus allowing it to be maintained, for example, in yeast for expression and in a prokaryotic host for cloning and amplification. Examples of such yeast-bacteria shuttle vectors include YEp24 (Botstein *et al.*, 1979), pCI/1 (Brake *et al.*, 1984), and YRp17 (Stinchcomb *et al.*, 1982). In addition, a replicon may be either a high or low copy number plasmid. A high copy number plasmid will generally have a copy number ranging from 5 to 200, and typically 10 to 150. A host containing a high copy number plasmid will preferably have at least 10, and more preferably at least 20.

[0064] Useful yeast promoter sequences can be derived from genes encoding enzymes in the metabolic pathway. Examples of such genes include alcohol dehydrogenase (ADH) (EP 0 284044), enolase, glucokinase, glucose-6-phosphate isomerase, glyceraldehyde-3-phosphatedehydrogenase (GAP or GAPDH), hexokinase, phosphofructokinase, 3-phosphoglycerate mutase, and pyruvate kinase (PyK) (EP 0 3215447). The yeast PHO5 gene, encoding acid phosphatase, also provides useful promoter sequences (Myanohara *et al.*, 1983). In addition, synthetic promoters that do not occur in nature also function as yeast promoters. Examples of such hybrid promoters include the ADH regulatory sequence linked to the GAP transcription activation region (U.S. Patent No. 4,876,197 and 4,880,734). Examples of transcription terminator sequences and other yeast-recognized termination sequences, such as those coding for glycolytic enzymes, are known to those of skill in the art.

[0065] Alternatively, the expression constructs can be integrated into the yeast genome with an integrating vector. Integrating vectors typically contain at least one sequence homologous to a yeast chromosome that allows the vector to integrate, and preferably contain two homologous sequences flanking the expression construct. Integrations appear to result from recombinations between homologous DNA in the vector and the yeast chromosome (Orr-Weaver *et al.*, 1983). An integrating vector may be directed to a specific locus in yeast by selecting the appropriate homologous sequence for inclusion in the vector. See Orr-Weaver *et al.*, *supra*. One or more expression constructs may integrate, possibly affecting levels of recombinant protein produced (Rine *et al.*, 1983).

[0066] The present invention also contemplates transformation of a nucleotide sequence of the present invention into a plant to achieve pest inhibitory levels of expression of one or more dsRNA molecules. A transformation vector can be readily prepared using methods available in the art. The transformation vector comprises one or more nucleotide sequences that is/are capable of being transcribed to an RNA molecule and that is/are substantially homologous and/or complementary to one or more nucleotide sequences encoded by the genome of the insect, such that upon uptake of the RNA there is down-regulation of expression of at least one of the respective nucleotide sequences of the genome of the insect.

[0067] The transformation vector may be termed a dsDNA construct and may also be defined as a recombinant molecule, an insect control agent, a genetic molecule or a chimeric genetic construct. A chimeric genetic construct of the present invention may comprise, for example, nucleotide sequences encoding one or more antisense transcripts, one or more sense transcripts, one or more of each of the aforementioned, wherein all or part of a transcript therefrom is homologous to all or part of an RNA molecule comprising an RNA sequence encoded by a nucleotide sequence within the genome of an insect.

[0068] In one embodiment the plant transformation vector comprises an isolated and purified DNA molecule comprising a promoter operatively linked to one or more nucleotide sequences of the present invention. The nucleotide sequence has SEQ ID NO:704 as set forth in the sequence listing. The nucleotide sequence includes a segment coding all or part of an RNA present within a targeted pest RNA transcript and may comprise inverted repeats of all or a part of a targeted pest RNA. The DNA molecule comprising the expression vector may also contain a functional intron sequence positioned either upstream of the coding sequence or even within the coding sequence, and may also contain a five prime (5') untranslated leader sequence (*i.e.*, a UTR or 5'-UTR) positioned between the promoter and the point of translation initiation.

[0069] A plant transformation vector may contain sequences from more than one gene, thus allowing production of more than one dsRNA for inhibiting expression of two or more genes in cells of a target pest. One skilled in the art will readily appreciate that segments of DNA whose sequence corresponds to that present in different genes can be combined into a single composite DNA segment for expression in a transgenic plant. Alternatively, a plasmid of the present invention already containing at least one DNA segment can be modified by the sequential insertion of additional DNA segments between the enhancer and promoter and terminator sequences. In the insect control agent of the present invention designed for the inhibition of multiple genes, the genes to be inhibited can be obtained from the same insect species in order to enhance the effectiveness of the insect control agent. In certain embodiments, the genes can be derived from different insects in order to broaden the range of insects against which the agent is effective. When multiple genes are targeted for suppression or a combination of expression and suppression, a polycistronic DNA element can be fabricated as illustrated and disclosed in Fillatti, Application Publication No. US 2004-0029283.

[0070] Promoters that function in different plant species are also well known in the art. Promoters useful for expression of polypeptides in plants include those that are inducible, viral, synthetic, or constitutive as described in Odell *et al.* (1985), and/or promoters that are temporally regulated, spatially regulated, and spatio-temporally regulated. Preferred

promoters include the enhanced CaMV35S promoters, and the FMV35S promoter. For the purpose of the present invention, e.g., for optimum control of species that feed on roots, it may be preferable to achieve the highest levels of expression of these genes within the roots of plants. A number of root-enhanced promoters have been identified and are known in the art (Lu *et al.*, 2000; U.S. Patent No. 5,837,848 and 6,489,542).

[0071] A recombinant DNA vector or construct of the present invention will typically comprise a selectable marker that confers a selectable phenotype on plant cells. Selectable markers may also be used to select for plants or plant cells that contain the exogenous nucleic acids encoding polypeptides or proteins of the present invention. The marker may encode biocide resistance, antibiotic resistance (e.g., kanamycin, G418 bleomycin and hygromycin), or herbicide resistance (e.g., glyphosate). Examples of selectable markers include a neo gene which codes for kanamycin resistance and can be selected for using kanamycin, G418, a bar gene which codes for bialaphos resistance; a mutant EPSP synthase gene which encodes glyphosate resistance; a nitrilase gene which confers resistance to bromoxynil; a mutant acetolactate synthase gene (ALS) which confers imidazolinone or sulfonylurea resistance; and a methotrexate resistant DHFR gene. Examples of such selectable markers are illustrated in U.S. Patents 5,550,318; 5,633,435; 5,780,708 and 6,118,047.

[0072] A recombinant vector or construct of the present invention may also include a screenable marker. Screenable markers may be used to monitor expression. Exemplary screenable markers include a β -glucuronidase or *uidA* gene (GUS) which encodes an enzyme for which various chromogenic substrates are known (Jefferson, 1987; Jefferson *et al.*, 1987); an R-locus gene, which encodes a product that regulates the production of anthocyanin pigments (red color) in plant tissues (Dellaporta *et al.*, 1988); a β -lactamase gene (Sutcliffe *et al.*, 1978), a gene which encodes an enzyme for which various chromogenic substrates are known (e.g., PADAC, a chromogenic cephalosporin); a luciferase gene (Ow *et al.*, 1986) a *xylE* gene (Zukowsky *et al.*, 1983) which encodes a catechol dioxygenase that can convert chromogenic catechols; an α -amylase gene (Ikata *et al.*, 1990); a tyrosinase gene (Katz *et al.*, 1983) which encodes an enzyme capable of oxidizing tyrosine to DOPA and dopaquinone which in turn condenses to melanin; an α -galactosidase, which catalyzes a chromogenic α -galactose substrate.

[0073] Preferred plant transformation vectors include those derived from a Ti plasmid of *Agrobacterium tumefaciens* (e.g. U.S. Patent Nos. 4,536,475, 4,693,977, 4,886,937, 5,501,967 and EP 0 122 791). *Agrobacterium rhizogenes* plasmids (or "Ri") are also useful and known in the art. Other preferred plant transformation vectors include those disclosed, e.g., by Herrera-Estrella (1983); Bevan (1983), Klee (1985) and EP 0 120 516.

[0074] In general it is preferred to introduce a functional recombinant DNA at a non-specific location in a plant genome. In special cases it may be useful to insert a recombinant DNA construct by site-specific integration. Several site-specific recombination systems exist which are known to function implants include cre-lox as disclosed in U.S. Patent 4,959,317 and FLP-FRT as disclosed in U.S. Patent 5,527,695.

[0075] Suitable methods for transformation of host cells for use with the current invention are believed to include virtually any method by which DNA can be introduced into a cell, such as by direct delivery of DNA such as by PEG-mediated transformation of protoplasts (Omirulleh *et al.*, 1993), by desiccation/inhibition-mediated DNA uptake (Potrykus *et al.*, 1985), by electroporation (U.S. Patent No. 5,384,253), by agitation with silicon carbide fibers (Kaeppeler *et al.*, 1990; U.S. Patent Nos. 5,302,523; and 5,464,765), by *Agrobacterium*-mediated transformation (U.S. Patent Nos. 5,591,616 and 5,563,055) and by acceleration of DNA coated particles (U.S. Patent Nos. 5,550,318; 5,538,877; and 5,538,880). Through the application of techniques such as these, the cells of virtually any species may be stably transformed. In the case of multicellular species, the transgenic cells may be regenerated into transgenic organisms.

[0076] Methods for the creation of transgenic plants and expression of heterologous nucleic acids in plants in particular are known and may be used with the nucleic acids provided herein to prepare transgenic plants that exhibit reduced susceptibility to feeding by a target pest organism such as corn rootworms. Plant transformation vectors can be prepared, for example, by inserting the dsRNA producing nucleic acids disclosed herein into plant transformation vectors and introducing these into plants. One known vector system has been derived by modifying the natural gene transfer system of *Agrobacterium tumefaciens*. The natural system comprises large Ti (tumor-inducing)-plasmids containing a large segment, known as T-DNA, which is transferred to transformed plants. Another segment of the Ti plasmid, the vir region, is responsible for T-DNA transfer. The T-DNA region is bordered by terminal repeats. In the modified binary vectors the tumor-inducing genes have been deleted and the functions of the vir region are utilized to transfer foreign DNA bordered by the T-DNA border sequences. The T-region may also contain a selectable marker for efficient recovery of transgenic plants and cells, and a multiple cloning site for inserting sequences for transfer such as a dsRNA encoding nucleic acid.

[0077] A transgenic plant formed using *Agrobacterium* transformation methods typically contains a single simple recombinant DNA sequence inserted into one chromosome and is referred to as a transgenic event. Such transgenic plants can be referred to as being heterozygous for the inserted exogenous sequence. A transgenic plant homozygous with respect to a transgene can be obtained by selfing an independent segregant transgenic plant to produce F1 seed. One fourth of the F1 seed produced will be homozygous with respect to the transgene. Germinating F1 seed results in plants that can be tested for heterozygosity or homozygosity, typically using a SNP assay or a thermal amplification assay that allows for the distinction between heterozygotes and homozygotes (*i.e.*, a zygosity assay).

C. Nucleic Acid Expression and Target Gene Suppression

[0078] The present invention provides, as an example, a transformed host or symbiont pest target organism, transformed plant cells and transformed plants and their progeny. The transformed plant cells and transformed plants may be engineered to express one or more of the dsRNA or siRNA sequences described herein to provide a pest-protective effect. These sequences may be used for gene suppression in a pest organism, thereby reducing the predation by the pest on a protected transformed host or symbiont organism. As used herein the words "gene suppression" are intended to refer to any of the well-known methods for reducing the levels of gene transcription to mRNA and/or subsequent translation of the mRNA.

[0079] Gene suppression is also intended to mean the reduction of protein expression from a gene or a coding sequence including posttranscriptional gene suppression and transcriptional suppression. Posttranscriptional gene suppression is mediated by the homology between of all or a part of a mRNA transcribed from a gene or coding sequence targeted for suppression and the corresponding double stranded RNA used for suppression, and refers to the substantial and measurable reduction of the amount of available mRNA available in the cell for binding by ribosomes. The transcribed RNA can be in the sense orientation to effect what is called co-suppression, in the anti-sense orientation to effect what is called anti-sense suppression, or in both orientations producing a dsRNA to effect what is called RNA interference (RNAi).

[0080] Transcriptional suppression is mediated by the presence in the cell of a dsRNA gene suppression agent exhibiting substantial sequence identity to a promoter DNA sequence or the complement thereof to effect what is referred to as promoter *trans* suppression. Gene suppression may be effective against a native plant gene associated with a trait, e.g., to provide plants with reduced levels of a protein encoded by the native gene or with enhanced or reduced levels of an affected metabolite. Gene suppression can also be effective against target genes in plant pests that may ingest or contact plant material containing gene suppression agents, specifically designed to inhibit or suppress the expression of one or more homologous or complementary sequences in the cells of the pest. Post-transcriptional gene suppression by anti-sense or sense oriented RNA to regulate gene expression in plant cells is disclosed in U.S. Pat. Nos. 5,107,065, 5,759,829, 5,283,184, and 5,231,020. The use of dsRNA to suppress genes in plants is disclosed in WO 99/53050, WO 99/49029, U.S. Patent Application Publication Nos. 2003/0175965, and 2003/0061626, U.S. Patent Application No. 10/465,800, and U.S. Patent Nos. 6,506,559, and 6,326,193.

[0081] A beneficial method of post transcriptional gene suppression in plants employs both sense-oriented and anti-sense-oriented, transcribed RNA which is stabilized, e.g., as a hairpin and stem and loop structure. A preferred DNA construct for effecting post transcriptional gene suppression is one in which a first segment encodes an RNA exhibiting an anti-sense orientation exhibiting substantial identity to a segment of a gene targeted for suppression, which is linked to a second segment in sense orientation encoding an RNA exhibiting substantial complementarity to the first segment. Such a construct forms a stem and loop structure by hybridization of the first segment with the second segment and a loop structure from the nucleotide sequences linking the two segments (see WO94/01550, WO98/05770, US 2002/0048814, and US 2003/0018993).

[0082] According to one embodiment of the present invention, there is provided a nucleotide sequence, for which *in vitro* expression results in transcription of a stabilized RNA sequence that is substantially homologous to an RNA molecule of a targeted gene in an insect that comprises an RNA sequence encoded by a nucleotide sequence within the genome of the insect. Thus, after the insect ingests the stabilized RNA sequence incorporated in a diet or sprayed on a plant surface, a down-regulation of the nucleotide sequence corresponding to the target gene in the cells of a target insect is affected.

[0083] Inhibition of a target gene using the stabilized dsRNA technology of the present invention is sequence-specific in that nucleotide sequences corresponding to the duplex region of the RNA are targeted for genetic inhibition. RNA containing a nucleotide sequences identical to a portion of the target gene is preferred for inhibition. RNA sequences with insertions, deletions, and single point mutations relative to the target sequence have also been found to be effective for inhibition. In performance of the present invention, it is preferred that the inhibitory dsRNA and the portion of the target gene share at least from 80% sequence identity, or from 90% sequence identity, or from 95% sequence identity, or from 99% sequence identity, or even 100% sequence identity. Alternatively, the duplex region of the RNA may be defined functionally as a nucleotide sequence that is capable of hybridizing with a portion of the target gene transcript. A less than full length sequence exhibiting a greater homology compensates for a longer less homologous sequence. The length of the identical nucleotide sequences may be at least 25, 50, 100, 200, 300, 400, 500 or at least 1000 bases. Normally, a sequence of greater than 20-100 nucleotides should be used, though a sequence of greater than 200-300 nucleotides would be preferred, and a sequence of greater than 500-1000 nucleotides would be especially preferred depending on the size of the target gene. The invention has the advantage of being able to tolerate sequence variations that might be expected due to genetic mutation, strain polymorphism, or evolutionary divergence. The introduced nucleic acid molecule may not need to be absolute homology, may not need to be full length, relative to either the primary transcription product or fully processed mRNA of the target gene. Therefore, those skilled in the art need to realize that,

as disclosed herein, 100% sequence identity between the RNA and the target gene is not required to practice the present invention.

[0084] Inhibition of target gene expression may be quantified by measuring either the endogenous target RNA or the protein produced by translation of the target RNA and the consequences of inhibition can be confirmed by examination of the outward properties of the cell or organism. Techniques for quantifying RNA and proteins are well known to one of ordinary skill in the art. Multiple selectable markers are available that confer resistance to ampicillin, bleomycin, chloramphenicol, gentamycin, hygromycin, kanamycin, lincomycin, methotrexate, phosphinothricin, puromycin, spectinomycin, rifampicin, and tetracyclin, and the like.

[0085] In certain embodiments gene expression is inhibited by at least 10%, preferably by at least 33%, more preferably by at least 50%, and yet more preferably by at least 80%. In particularly preferred embodiments of the invention gene expression is inhibited by at least 80%, more preferably by at least 90%, more preferably by at least 95%, or by at least 99% within cells in the insect so a significant inhibition takes place. Significant inhibition is intended to refer to sufficient inhibition that results in a detectable phenotype (e.g., cessation of larval growth, paralysis or mortality) or a detectable decrease in RNA and/or protein corresponding to the target gene being inhibited. Although in certain embodiments of the invention inhibition occurs in substantially all cells of the insect, in other preferred embodiments inhibition occurs in only a subset of cells expressing the gene. For example, if the gene to be inhibited plays an essential role in cells in the insect alimentary tract, inhibition of the gene within these cells is sufficient to exert a deleterious effect on the insect.

[0086] dsRNA molecules may be synthesized either *in vivo* or *in vitro*. The dsRNA may be formed by a single self-complementary RNA strand or from two complementary RNA strands. Endogenous RNA polymerase of the cell may mediate transcription *in vivo*, or cloned RNA polymerase can be used for transcription *in vivo* or *in vitro*. Inhibition may be targeted by specific transcription in an organ, tissue, or cell type; stimulation of an environmental condition (e.g., infection, stress, temperature, chemical inducers); and/or engineering transcription at a developmental stage or age. The RNA strands may or may not be polyadenylated; the RNA strands may or may not be capable of being translated into a polypeptide by a cell's translational apparatus.

[0087] A RNA, dsRNA, siRNA, or miRNA of the present invention may be produced chemically or enzymatically by one skilled in the art through manual or automated reactions *or in vivo* in another organism. RNA may also be produced by partial or total organic synthesis; any modified ribonucleotide can be introduced by *in vitro* enzymatic or organic synthesis. The RNA may be synthesized by a cellular RNA polymerase or a bacteriophage RNA polymerase (e.g., T3, T7, SP6). The use and production of an expression construct are known in the art (see, for example, WO 97/32016; U.S. Pat. No's. 5,593,874, 5,698,425, 5,712,135, 5,789,214, and 5,804,693). If synthesized chemically or by *in vitro* enzymatic synthesis, the RNA may be purified prior to introduction into the cell. For example, RNA can be purified from a mixture by extraction with a solvent or resin, precipitation, electrophoresis, chromatography, or a combination thereof. Alternatively, the RNA may be used with no or a minimum of purification to avoid losses due to sample processing. The RNA may be dried for storage or dissolved in an aqueous solution. The solution may contain buffers or salts to promote annealing, and/or stabilization of the duplex strands.

[0088] For transcription from a transgene *in vivo* or an expression construct, a regulatory region (e.g., promoter, enhancer, silencer, and polyadenylation) may be used to transcribe the RNA strand (or strands). Therefore, in one embodiment, the nucleotide sequences for use in producing RNA molecules may be operably linked to one or more promoter sequences functional in a microorganism, a fungus or a plant host cell. Ideally, the nucleotide sequences are placed under the control of an endogenous promoter, normally resident in the host genome. The nucleotide sequence of the present invention, under the control of an operably linked promoter sequence, may further be flanked by additional sequences that advantageously affect its transcription and/or the stability of a resulting transcript. Such sequences are generally located upstream of the operably linked promoter and/or downstream of the 3' end of the expression construct and may occur both upstream of the promoter and downstream of the 3' end of the expression construct, although such an upstream sequence only is also contemplated.

[0089] As used herein, the term "insect control agent", or "gene suppression agent" refers to a particular RNA molecule comprising a first RNA segment and a second RNA segment, wherein the complementarity between the first and the second RNA segments results in the ability of the two segments to hybridize *in vivo* and *in vitro* to form a double stranded molecule. It may generally be preferable to include a third RNA segment linking and stabilizing the first and second sequences such that the entire structure forms into a stem and loop structure, or even more tightly hybridizing structures may form into a stem-loop knotted structure. Alternatively, a symmetrical hairpin could be formed without a third segment in which there is no designed loop, but for steric reasons a hairpin would create its own loop when the stem is long enough to stabilize itself. The first and the second RNA segments will generally lie within the length of the RNA molecule and be substantially inverted repeats of each other and linked together by the third RNA segment. The first and the second segments correspond invariably and not respectively to a sense and an antisense sequence with respect to the target RNA transcribed from the target gene in the target insect pest that is suppressed by the ingestion of the dsRNA molecule. The insect control agent can also be a substantially purified (or isolated) nucleic acid molecule and more specifically nucleic acid molecules or nucleic acid fragment molecules thereof from a genomic DNA (gDNA) or cDNA

library. Alternatively, the fragments may comprise smaller oligonucleotides having from 15 to 250 nucleotide residues, and more preferably, 15 to 30 nucleotide residues.

[0090] As used herein, the term "genome" as it applies to cells of an insect or a host encompasses not only chromosomal DNA found within the nucleus, but organelle DNA found within subcellular components of the cell. The DNA's of the present invention introduced into plant cells can therefore be either chromosomally integrated or organelle-localized. The term "genome" as it applies to bacteria encompasses both the chromosome and plasmids within a bacterial host cell. The DNA's of the present invention introduced into bacterial host cells can therefore be either chromosomally integrated or plasmid-localized.

[0091] As used herein, the term "pest" refers to insects, arachnids, crustaceans, fungi, bacteria, viruses, nematodes, flatworms, roundworms, pinworms, hookworms, tapeworms, trypanosomes, schistosomes, botflies, fleas, ticks, mites, and lice that are pervasive in the human environment and that may ingest or contact one or more cells, tissues, or fluids produced by a pest host or symbiont transformed to express or coated with a double stranded gene suppression agent or that may ingest plant material containing the gene suppression agent. As used herein, a "pest resistance" trait is a characteristic of a transgenic plant, transgenic animal, transgenic host or transgenic symbiont that causes the plant, animal, host, or symbiont to be resistant to attack from a pest that typically is capable of inflicting damage or loss to the plant, animal, host or symbiont. Such pest resistance can arise from a natural mutation or more typically from incorporation of recombinant DNA that confers pest resistance. To impart insect resistance to a transgenic plant a recombinant DNA can, for example, be transcribed into a RNA molecule that forms a dsRNA molecule within the tissues or fluids of the recombinant plant. The dsRNA molecule is comprised in part of a segment of RNA that is identical to a corresponding RNA segment encoded from a DNA sequence within an insect pest that prefers to feed on the recombinant plant. Expression of the gene within the target insect pest is suppressed by the dsRNA, and the suppression of expression of the gene in the target insect pest results in the plant being insect resistant. Fire et al. (U.S. Patent No. 6,506,599) generically described inhibition of pest infestation, providing specifics only about several nucleotide sequences that were effective for inhibition of gene function in the nematode species *Caenorhabditis elegans*. Similarly, Plaetinck et al. (US 2003/0061626) describe the use of dsRNA for inhibiting gene function in a variety of nematode pests. Mesa et al. (US 2003/0150017) describe using dsDNA sequences to transform host cells to express corresponding dsRNA sequences that are substantially identical to target sequences in specific pathogens, and particularly describe constructing recombinant plants expressing such dsRNA sequences for ingestion by various plant pests, facilitating down-regulation of a gene in the genome of the pest and improving the resistance of the plant to the pest infestation.

[0092] The present invention provides for inhibiting gene expression of one or multiple target genes in a target pest using stabilized dsRNA methods. The invention is particularly useful in the modulation of eukaryotic gene expression, in particular the modulation of expression of genes present in pests that exhibit a digestive system pH level that is from 4.5 to 9.5, more preferably from 5.0 to 8.0, and even more preferably from 6.5 to 7.5. For plant pests with a digestive system that exhibits pH levels outside of these ranges, delivery methods may be desired for use that do not require ingestion of dsRNA molecules.

[0093] The modulatory effect of dsRNA is applicable to a variety of genes expressed in the pests including, for example, endogenous genes responsible for cellular metabolism or cellular transformation, including house keeping genes, transcription factors and other genes which encode polypeptides involved in cellular metabolism.

[0094] As used herein, the phrase "inhibition of gene expression" or "inhibiting expression of a target gene in the cell of an insect" refers to the absence (or observable decrease) in the level of protein and/or mRNA product from the target gene. Specificity refers to the ability to inhibit the target gene without manifest effects on other genes of the cell and without any effects on any gene within the cell that is producing the dsRNA molecule. The inhibition of gene expression of the target gene in the insect pest may result in novel phenotypic traits in the insect pest.

[0095] The present invention provides in part a delivery system for the delivery of the insect control agents to insects through their exposure to a diet containing the insect control agents of the present invention. In accordance with one of the embodiments, the stabilized dsRNA or siRNA molecules may be incorporated in the insect diet or may be overlaid on the top of the diet for consumption by an insect. The present invention also provides in part a delivery system for the delivery of the insect control agents to insects through their exposure to a microorganism or host such as a plant containing the insect control agents of the present invention by ingestion of the microorganism or the host cells or the contents of the cells. In accordance with another embodiment, the present invention involves generating a transgenic plant cell or a plant that contains a recombinant DNA construct transcribing the stabilized dsRNA molecules of the present invention. As used herein, the phrase "generating a transgenic plant cell or a plant" refers to the methods of employing the recombinant DNA technologies readily available in the art (e.g., by Sambrook, *et al.*, 1989) to construct a plant transformation vector transcribing the stabilized dsRNA molecules of the present invention, to transform the plant cell or the plant and to generate the transgenic plant cell or the transgenic plant that contain the transcribed, stabilized dsRNA molecules.

[0096] In still another embodiment, non-pathogenic, attenuated strains of microorganisms may be used as a carrier for the insect control agents and, in this perspective, the microorganisms carrying such agents are also referred to as

insect control agents. The microorganisms may be engineered to express a nucleotide sequence of a target gene to produce RNA molecules comprising RNA sequences homologous or complementary to RNA sequences typically found within the cells of an insect. Exposure of the insects to the microorganisms result in ingestion of the microorganisms and down-regulation of expression of target genes mediated directly or indirectly by the RNA molecules or fragments or derivatives thereof.

[0097] The present invention alternatively provides exposure of an insect to the insect control agents of the present invention incorporated in a spray mixer and applied to the surface of a host, such as a host plant. In an exemplary embodiment, ingestion of the insect control agents by an insect delivers the insect control agents to the gut of the insect and subsequently to the cells within the body of the insect. In another embodiment, infection of the insect by the insect control agents through other means such as by injection or other physical methods also permits delivery of the insect control agents. In yet another embodiment, the RNA molecules themselves are encapsulated in a synthetic matrix such as a polymer and applied to the surface of a host such as a plant. Ingestion of the host cells by an insect permits delivery of the insect control agents to the insect and results in down-regulation of a target gene in the host.

[0098] It is envisioned that the compositions of the present invention can be incorporated within the seeds of a plant species either as a product of expression from a recombinant gene incorporated into a genome of the plant cells, or incorporated into a coating or seed treatment that is applied to the seed before planting. The plant cell containing a recombinant gene is considered herein to be a transgenic event.

[0099] It is believed that a pesticidal seed treatment can provide significant advantages when combined with a transgenic event that provides protection from coleopteran pest infestation that is within the preferred effectiveness range against a target pest. In addition, it is believed that there are situations that are well known to those having skill in the art, where it is advantageous to have such transgenic events within the preferred range of effectiveness.

[0100] The present invention provides in part a delivery system for the delivery of insect control agents to insects. The stabilized dsRNA or siRNA molecules of the present invention may be directly introduced into the cells of an insect, or introduced into an extracellular cavity, interstitial space, lymph system, digestive system, into the circulation of the insect through oral ingestion or other means that one skilled in the art may employ. Methods for oral introduction may include direct mixing of RNA with food of the insect, as well as engineered approaches in which a species that is used as food is engineered to express the dsRNA or siRNA, then fed to the insect to be affected. In one embodiment, for example, the dsRNA or siRNA molecules may be incorporated into, or overlaid on the top of, the insect's diet. In another embodiment, the RNA may be sprayed onto a plant surface. In still another embodiment, the dsRNA or siRNA may be expressed by microorganisms and the microorganisms may be applied onto a plant surface or introduced into a root, stem by a physical means such as an injection. In still another embodiment, a plant may be genetically engineered to express the dsRNA or siRNA in an amount sufficient to kill the insects known to infect the plant.

[0101] Specifically, in practicing the present invention in WCR, the stabilized dsRNA or siRNA may be introduced in the midgut inside the insect and achieve the desired inhibition of the targeted genes. The dsRNA or siRNA molecules may be incorporated into a diet or be overlaid on the diet as discussed above and may be ingested by the insects. In any event, the dsRNA's of the present invention are provided in the diet of the target pest. The target pest of the present invention will exhibit a digestive tract pH from 4.5 to 9.5, or from 5 to 8.5, or from 6 to 8, or from 6.5 to 7.7, or about 7.0. The digestive tract of a target pest is defined herein as the location within the pest that food that is ingested by the target pest is exposed to an environment that is favorable for the uptake of the dsRNA molecules of the present invention without suffering a pH so extreme that the hydrogen bonding between the double-strands of the dsRNA are caused to dissociate and form single stranded molecules.

[0102] It is also anticipated that dsRNA's produced by chemical or enzymatic synthesis may be formulated in a manner consistent with common agricultural practices and used as spray-on products for controlling insect infestations. The formulations may include the appropriate stickers and wetters required for efficient foliar coverage as well as UV protectants to protect dsRNAs from UV damage. Such additives are commonly used in the bioinsecticide industry and are well known to those skilled in the art. Such applications could be combined with other spray-on insecticide applications, biologically based or not, to enhance plant protection from insect feeding damage.

[0103] The present inventors contemplate that bacterial strains producing insecticidal proteins may be used to produce dsRNAs for insect control purposes. These strains may exhibit improved insect control properties. A variety of different bacterial hosts may be used to produce insect control dsRNAs. Exemplary bacteria may include *E. coli*, *B. thuringiensis*, *Pseudomonas sp.*, *Photobacterium sp.*, *Xenorhabdus sp.*, *Serratia entomophila* and related *Serratia sp.*, *B. sphaericus*, *B. cereus*, *B. laterosporus*, *B. popilliae*, *Clostridium bifermentans* and other *Clostridium* species, or other spore-forming gram-positive bacteria. In certain embodiments, bacteria may be engineered for control of pests such as mosquitoes.

[0104] The present invention also relates to recombinant DNA constructs for expression in a microorganism. Exogenous nucleic acids from which an RNA of interest is transcribed can be introduced into a microbial host cell, such as a bacterial cell or a fungal cell, using methods known in the art.

[0105] The nucleotide sequences of the present invention may be introduced into a wide variety of prokaryotic and eukaryotic microorganism hosts to produce the stabilized dsRNA or siRNA molecules. The term "microorganism" includes

prokaryotic and eukaryotic microbial species such as bacteria, fungi and algae. Fungi include yeasts and filamentous fungi, among others. 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*, *Actinomycetales*, and *Nitrobacteraceae*. Among eukaryotes are fungi, such as *Phycomycetes* and *Ascomycetes*, which includes yeast, such as *Saccharomyces* and *Schizosaccharomyces*; and *Basidiomycetes*, such as *Rhodotorula*, *Aureobasidium* and *Sporobolomyces*.

[0106] For the purpose of plant protection against insects, a large number of microorganisms known to inhabit the phylloplane (the surface of the plant leaves) and/or the rhizosphere (the soil surrounding plant roots) of a wide variety of important crops may also be desirable host cells for manipulation, propagation, storage, delivery and/or mutagenesis of the disclosed recombinant constructs. These microorganisms include bacteria, algae, and fungi. Of particular interest are microorganisms, such as bacteria, e.g., genera *Bacillus* (including the species and subspecies *B. thuringiensis kurstaki* HD-1, *B. thuringiensis kurstaki* HD-73, *B. thuringiensis sotto*, *B. thuringiensis berliner*, *B. thuringiensis thuringiensis*, *B. thuringiensis tolworthi*, *B. thuringiensis dendrolimus*, *B. thuringiensis alesti*, *B. thuringiensis galleriae*, *B. thuringiensis aizawai*, *B. thuringiensis subtoxicus*, *B. thuringiensis entomocidus*, *B. thuringiensis tenebrionis* and *B. thuringiensis san diego*); *Pseudomonas*, *Erwinia*, *Serratia*, *Klebsiella*, *Zanthomonas*, *Streptomyces*, *Rhizobium*, *Rhodopseudomonas*, *Methylophilus*, *Agrobacterium*, *Acetobacter*, *Lactobacillus*, *Arthrobacter*, *Azotobacter*, *Leuconostoc*, and *Alcaligenes*; fungi, particularly yeast, e.g., genera *Saccharomyces*, *Cryptococcus*, *Kluyveromyces*, *Sporobolomyces*, *Rhodotorula*, and *Aureobasidium*. Of particular interest are such phytosphere bacterial species as *Pseudomonas syringae*, *Pseudomonas fluorescens*, *Serratia marcescens*, *Acetobacter xylinum*, *Agrobacterium tumefaciens*, *Rhodobacter sphaeroides*, *Xanthomonas campestris*, *Rhizobium melioli*, *Alcaligenes eutrophus*, and *Azotobacter vinlandii*; 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 roseus*, *S. odoratus*, *Kluyveromyces veronae*, and *Aureobasidium pollulans*.

D. Transgenic Plants

[0107] The present invention provides seeds and plants having one or more transgenic event. Combinations of events are referred to as "stacked" transgenic events. These stacked transgenic events can be events that are directed at the same target pest, or they can be directed at different target pests. In one embodiment, a seed having the ability to express a nucleic acid provided herein also has the ability to express at least one other insecticidal agent, including an RNA molecule the sequence of which is derived from the sequence of an RNA expressed in a target pest and that forms a double stranded RNA structure upon expressing in the seed or cells of a plant grown from the seed, wherein the ingestion of one or more cells of the plant by the target pest results in the suppression of expression of the RNA in the cells of the target pest.

[0108] In certain embodiments, a seed having the ability to express a dsRNA the sequence of which is derived from a target pest also has a transgenic event that provides herbicide tolerance. One beneficial example of a herbicide tolerance gene provides resistance to glyphosate, N-(phosphonomethyl) glycine, including the isopropylamine salt form of such herbicide.

[0109] In the present method, combination of expression of an insecticidal amount of a dsRNA within the cells of a transgenic seed or plant grown from the seed coupled with treatment of the seed or plant with certain chemical or protein pesticides may be used to provide unexpected synergistic advantages, including unexpectedly superior efficacy for protection against damage to the resulting transgenic plant by the target pest. In particular embodiments, treatment of a transgenic seed that is capable of expressing certain constructs that form dsRNA molecules, the sequence of which are derived from one or more sequences expressed in a corn rootworm, with from 100 g to 400 g of pesticide per 100 kg of seed provides unexpectedly superior protection against corn rootworm. In addition, it is believed that such combinations are also effective to protect the emergent plants against predation by other pests. The seeds of the present invention may also be used to decrease the cost of pesticide use, because less pesticide can be used to obtain a required amount of protection than when such methods are not used. Moreover, because less pesticide is used and because it is applied prior to planting and without a separate field application, it is believed that the subject method is therefore safer to the operator and to the environment, and is potentially less expensive than conventional methods.

[0110] By "synergistic" it is meant to include the synergistic effects of the combination on the pesticidal activity (or efficacy) of the combination of the transgenic event and the pesticide. However, it is not intended that such synergistic effects be limited to the pesticidal activity, but that they should also include such unexpected advantages as increased scope of activity, advantageous activity profile as related to type and amount of damage reduction, decreased cost of pesticide and application, decreased pesticide distribution in the environment, decreased pesticide exposure of personnel who produce, handle and plant corn seeds, and other advantages known to those skilled in the art.

[0111] Pesticides and insecticides that are useful in compositions in combination with the methods and compositions

of the present invention, including as seed treatments and coatings as well as methods for using such compositions can be found, for example, in U.S. Patent 6,551,962. Although it is believed that the seed treatments can be applied to a transgenic seed in any physiological state, it may be preferred that the seed be in a sufficiently durable state that it incurs no damage during the treatment process. Typically, the seed would be a seed that had been harvested from the field; removed from the transgenic plant; and separated from any other non-seed plant material. The seed would preferably also be biologically stable to the extent that the treatment would cause no biological damage to the seed. In one embodiment, for example, the treatment can be applied to seed corn that has been harvested, cleaned and dried to a moisture content below about 15% by weight. In an alternative embodiment, the seed can be one that has been dried and then primed with water and/or another material and then re-dried before or during the treatment with the pesticide. Within the limitations described, it is believed that the treatment can be applied to the seed at any time between harvest of the seed and sowing of the seed. As used herein, the term "unsown seed" is meant to include seed at any period between the harvest of the seed and the sowing of the seed in the ground for the purpose of germination and growth of the plant. When it is said that unsown seed is "treated" with the pesticide, such treatment is not meant to include those practices in which the pesticide is applied to the soil, rather than to the seed. For example, such treatments as the application of the pesticide in bands, "T"-bands, or in-furrow, at the same time as the seed is sowed are not considered to be included in the present invention.

[0112] The pesticide, or combination of pesticides, can be applied "neat", that is, without any diluting or additional components present. However, the pesticide is typically applied to the seeds in the form of a pesticide formulation. This formulation may contain one or more other desirable components including but not limited to liquid diluents, binders to serve as a matrix for the pesticide, fillers for protecting the seeds during stress conditions, and plasticizers to improve flexibility, adhesion and/or spreadability of the coating.

[0113] The subject pesticides can be applied to a seed as a component of a seed coating. Seed coating methods and compositions that are known in the art are useful when they are modified by the addition of one of the embodiments of the combination of pesticides of the present invention. Such coating methods and apparatus for their application are disclosed in, for example, U.S. Patent Nos. 5,918,413, 5,891,246, 5,554,445, 5,389,399, 5,107,787, 5,080,925, 4,759,945 and 4,465,017. Seed coating compositions are disclosed, for example, in U.S. Patent Nos. 5,939,356, 5,882,713, 5,876,739, 5,849,320, 5,834,447, 5,791,084, 5,661,103, 5,622,003, 5,580,544, 5,328,942, 5,300,127, 4,735,015, 4,634,587, 4,383,391, 4,372,080, 4,339,456, 4,272,417 and 4,245,432.

[0114] The pesticides that are useful in the coating are those pesticides that are described herein. The amount of pesticide that is used for the treatment of the seed will vary depending upon the type of seed and the type of active ingredients, but the treatment will comprise contacting the seeds with an amount of the combination of pesticides that is pesticidally effective. When insects are the target pest, that amount will be an amount of the insecticide that is insecticidally effective. As used herein, an insecticidally effective amount means that amount of insecticide that will kill insect pests in the larvae or pupal state of growth, or will consistently reduce or retard the amount of damage produced by insect pests.

[0115] In general, the amount of pesticide that is applied to the seed in the treatment will range from 10 g to 2000 g of the active ingredient of the pesticide per 100 kg of the weight of the seed. Preferably, the amount of pesticide will be within the range of 50 g to 1000 g active per 100 kg of seed, more preferably within the range of 100 g to 600 g active per 100 kg of seed, and even more preferably within the range of 200 g to 500 g of active per 100 kg of seed weight. Alternatively, it has been found to be preferred that the amount of the pesticide be over 60 g of the active ingredient of the pesticide per 100 kg of the seed, and more preferably over 80 g per 100 kg of seed.

[0116] The pesticides that are used in the treatment must not inhibit germination of the seed and should be efficacious in protecting the seed and/or the plant during that time in the target insect's life cycle in which it causes injury to the seed or plant. In general, the coating will be efficacious for 0 to 120 days after sowing. The pesticides of the subject invention can be applied to the seed in the form of a coating.

[0117] Benefits provided by the present invention may include, but are not limited to: the ease of introducing dsRNA into the insect cells, the low concentration of dsRNA which can be used, the stability of dsRNA, and the effectiveness of the inhibition. The ability to use a low concentration of a stabilized dsRNA avoids several disadvantages of anti-sense interference. The present invention is not limited to *in vitro* use or to specific sequence compositions, to a particular set of target genes, a particular portion of the target gene's nucleotide sequence, or a particular transgene or to a particular delivery method, as opposed to some of the available techniques known in the art, such as antisense and co-suppression. Furthermore, genetic manipulation becomes possible in organisms that are not classical genetic models.

[0118] In practicing the present invention, selections can be carried out to ensure that the presence of the nucleotide sequences that are transcribed from the recombinant construct are not harmful to non-pest cells. This can be achieved by targeting genes that exhibit a low degree of sequence identity with corresponding genes in a plant or a vertebrate animal. Preferably the degree of the sequence identity is less than 80%. More preferably the degree of the sequence identity is less than 70%. Most preferably the degree of the sequence identity is less than 60%.

[0119] In addition to direct transformation of a plant with a recombinant DNA construct, transgenic plants can be

prepared by crossing a first plant having a recombinant DNA construct with a second plant lacking the construct. For example, recombinant DNA for gene suppression can be introduced into first plant line that is amenable to transformation to produce a transgenic plant that can be crossed with a second plant line to introgress the recombinant DNA for gene suppression into the second plant line.

[0120] The present invention can be, in practice, combined with other insect control traits in a plant to achieve desired traits for enhanced control of insect infestation. Combining insect control traits that employ distinct modes-of-action can provide insect-protected transgenic plants with superior durability over plants harboring a single insect control trait because of the reduced probability that resistance will develop in the field.

[0121] The mechanism of insecticidal activity of *B. thuringiensis* crystal proteins has been studied extensively in the past decade. It has been shown that the crystal proteins are toxic to the larval form of the insect only after ingestion of the protein. In lepidopteran larvae, an alkaline pH and proteolytic enzymes in the insect mid-gut solubilize the proteins, thereby allowing the release of components that are toxic to the insect. These toxic components disrupt the mid-gut cells, cause the insect to cease feeding, and, eventually, bring about insect death. For this reason, *B. thuringiensis* toxins have proven themselves to be effective and environmentally safe insecticides in dealing with various insect pests. Coleopteran and hemipteran insects, and likely dipteran, lygus and other piercing and sucking insects exhibit a gut pH that is slightly acidic, and so the Bt toxins that are effective against lepidopteran larvae are ineffective against these pests. The slightly acidic pH of the gut of these insects is also believed to be more hospitable to the compositions of the present invention, and without intending to be limited to a particular theory, it is likely that the alkaline pH of the gut of lepidopteran larvae is a contributing reason that prior attempts to exhibit dsRNA efficacy has failed (Fire et al. U.S. Patent No. 6,506,559; Mesa et al. Patent Publication No. US2003/0150017; Rajagopal et al., 2002; Tabara et al., 1998). It is believed therefore that the dsRNA methods disclosed herein should be preferentially used in compositions and in plants to control coleopteran, dipteran, hemipteran, lygus, and piercing and sucking insects. The methods and compositions set forth herein are particularly useful for targeting genes for suppression in insects exhibiting a gut pH of from 4.5 to 9.5, or from 5.0 to 9.0, or from 5.5 to 8.5, or from 6.0 to 8.0, or from 6.5 to 7.7, or from 6.8 to 7.6, or about 7.0. However, insects and other pest species that exhibit a gut pH of from 7.5 to 11.5, or from 8.0 to 11.0, or from 9.0 to 10.0, such as lepidopteran insect larvae, are also intended to be within the scope of the present invention. This is particularly true when a dsRNA specific for inhibiting a gene in a lepidopteran larvae is provided in the diet of the larvae along with one or more Bt proteins, that, with respect to the Bt protein would ordinarily be toxic to that lepidopteran larvae when provided at or above a threshold level. The presence of one or more Bt toxins toxic to the same insect species would effectively reduce the gut pH, providing a stable environment for the double stranded RNA molecules to exert their effects in suppressing a target gene in the insect pest.

[0122] It is anticipated that the combination of certain stabilized dsRNA constructs with one or more insect control protein genes will result in synergies that enhance the insect control phenotype of a transgenic plant. Insect bioassays employing artificial diet- or whole plant tissue can be used to define dose-responses for larval mortality or growth inhibition using both dsRNAs and insect control proteins. One skilled in the art can test mixtures of dsRNA molecules and insect control proteins in bioassay to identify combinations of actives that are synergistic and desirable for deployment in insect-protected plants (Tabashnik, 1992). Synergy in killing insect pests has been reported between different insect control proteins (for review, see Schnepf et al., 1998). It is anticipated that synergies will exist between certain dsRNAs and between certain dsRNAs and certain insect control proteins.

[0123] The invention also relates to commodity products containing one or more of the sequences of the present invention, and produced from a recombinant plant or seed containing one or more of the nucleotide sequences of the present invention are specifically contemplated as embodiments of the present invention. A commodity product containing one or more of the sequences of the present invention is intended to include meals, oils, crushed or whole grains or seeds of a plant, or any food product comprising any meal, oil, or crushed or whole grain of a recombinant plant or seed containing one or more of the sequences of the present invention. The detection of one or more of the sequences of the present invention in one or more commodity or commodity products contemplated herein is defacto evidence that the commodity or commodity product is composed of a transgenic plant designed to express one or more of the nucleotide sequences of the present invention for the purpose of controlling insect infestation using dsRNA mediated gene suppression methods.

E. Obtaining Nucleic acids

[0124] The present invention provides a method for obtaining a nucleic acid comprising a nucleotide sequence for producing a dsRNA or siRNA. In one embodiment, such a method comprises: (a) probing a cDNA or gDNA library with a hybridization probe comprising all or a portion of a nucleotide sequence or a homolog thereof from a targeted insect; (b) identifying a DNA clone that hybridizes with the hybridization probe; (c) isolating the DNA clone identified in step (b); and (d) sequencing the cDNA or gDNA fragment that comprises the clone isolated in step (c) wherein the sequenced nucleic acid molecule transcribes all or a substantial portion of the RNA nucleotide acid sequence or a homolog thereof.

[0125] In another embodiment, a method of the present invention for obtaining a nucleic acid fragment comprising a nucleotide sequence for producing a substantial portion of a dsRNA or siRNA comprises: (a) synthesizing first and a second oligonucleotide primers corresponding to a portion of one of the nucleotide sequences from a targeted insect; and (b) amplifying a cDNA or gDNA template in a cloning vector using the first and second oligonucleotide primers of step (a) wherein the amplified nucleic acid molecule transcribes a substantial portion of a dsRNA or siRNA of the present invention.

[0126] In practicing the present invention, a target gene may be derived from a corn rootworm (CRW), such as a WCR or a SCR, or any insect species that causes damage to the crop plants and subsequent yield losses. It is contemplated that several criteria may be employed in the selection of preferred target genes. The gene is one whose protein product has a rapid turnover rate, so that dsRNA inhibition will result in a rapid decrease in protein levels. In certain embodiments it is advantageous to select a gene for which a small drop in expression level results in deleterious effects for the insect. If it is desired to target a broad range of insect species a gene is selected that is highly conserved across these species. Conversely, for the purpose of conferring specificity, in certain embodiments of the invention, a gene is selected that contains regions that are poorly conserved between individual insect species, or between insects and other organisms. In certain embodiments it may be desirable to select a gene that has no known homologs in other organisms.

[0127] As used herein, the term "derived from" refers to a specified nucleotide sequence that may be obtained from a particular specified source or species, albeit not necessarily directly from that specified source or species.

[0128] In one embodiment, a gene is selected that is expressed in the insect gut. Targeting genes expressed in the gut avoids the requirement for the dsRNA to spread within the insect. Target genes for use in the present invention may include, for example, those that share substantial homologies to the nucleotide sequences of known gut-expressed genes that encode protein components of the vacuolar and plasma membrane proton V-ATPase (Dow *et al.*, 1997; Dow, 1999). This protein complex is the sole energizer of epithelial ion transport and is responsible for alkalization of the midgut lumen. The V-ATPase is also expressed in the Malpighian tubule, an outgrowth of the insect hindgut that functions in fluid balance and detoxification of foreign compounds in a manner analogous to a kidney organ of a mammal. In another embodiment, the V-ATPase may be Vha68-2, or a homolog or ortholog thereof (*e.g.* as found in SEQ ID NO:821).

[0129] In another embodiment, a gene is selected that is essentially involved in the growth, development, and reproduction of an insect. Exemplary genes include but are not limited to a CHD3 gene, a β -tubulin gene, and a gene encoding a protein predicted to be involved in transport. The CHD3 gene in *Drosophila melanogaster* encodes a protein with ATP-dependent DNA helicase activity that is involved in chromatin assembly/disassembly in the nucleus. Similar sequences have been found in diverse organisms such as *Arabidopsis thaliana*, *Caenorhabditis elegans*, and *Saccharomyces cerevisiae*. The beta-tubulin gene family encodes microtubule-associated proteins that are a constituent of the cellular cytoskeleton. Related sequences are found in such diverse organisms as *C. elegans*, and *Manduca sexta*. Proteins predicted to be subunits of the endosomal sorting complex required for transport (ESCRT)-III (Babst *et al.*, 2002), *e.g.* Dv49, are found in diverse organisms including mammals, yeast, and insects such as *D. virgifera*. Another transport-related protein is the β' -coatamer protein, abbreviated as β' Cop, that encodes a product involved in retrograde (Golgi to ER) transport. Similar or predicted sequences have been identified in *C. elegans* and *D. virgifera*, *e.g.* Dv248.

[0130] Other target genes for use in the present invention may include, for example, those that play important roles in the viability, growth, development, reproduction and infectivity. These target genes may be one of the house keeping genes, transcription factors and insect specific genes or lethal knockout mutations in *Drosophila*. The target genes for use in the present invention may also be those that are from other organisms, *e.g.*, from a nematode (*e.g.*, *C. elegans*). Additionally, the nucleotide sequences for use in the present invention may also be derived from plant, viral, bacterial or fungal genes whose functions have been established from literature and the nucleotide sequences of which share substantial similarity with the target genes in the genome of an insect. According to one aspect of the present invention for WCR control, the target sequences may essentially be derived from the targeted WCR insect. Some of the exemplary target sequences from cDNA library from WCR that encode *D. virgifera* proteins or fragments thereof which are homologues of known proteins may be found in the Sequence Listing. Nucleic acid molecules from *D. virgifera* encoding homologs of known proteins are known (Andersen *et al.*, U.S. Patent Application Serial No. 10/205,189).

[0131] For the purpose of the present invention, the dsRNA or siRNA molecules may be obtained from the CRW by polymerase chain (PCRTM) amplification of a target CRW gene sequences derived from a corn rootworm gDNA or cDNA library or portions thereof. The WCR larvae may be prepared using methods known to the ordinary skilled in the art and DNA/RNA may be extracted. Larvae with various sizes ranging from 1 st instars to fully-grown CRWs may be used for the purpose of the present invention for DNA/RNA extraction. Genomic DNA or cDNA libraries generated from WCR may be used for PCRTM amplification for production of the dsRNA or siRNA.

[0132] The target genes may be then be PCRTM amplified and sequenced using the methods readily available in the art. One skilled in the art may be able to modify the PCRTM conditions to ensure optimal PCRTM product formation. The confirmed PCRTM product may be used as a template for *in vitro* transcription to generate sense and antisense RNA with the included minimal promoters.

[0133] The present inventors contemplate that nucleic acid sequences identified and isolated from any insect species

in the insect kingdom may be used in the present invention for control of WCR and another targeted insects. In one aspect of the present invention, the nucleic acid may be derived from a coleopteran species. Specifically, the nucleic acid may be derived from leaf beetles belonging to the genus *Diabrotica* (*Coleoptera*, *Chrysomelidae*) and more specifically the nucleic acid molecules of the present invention may be derived from species in the *virgifera* group. Most specifically, the nucleic acid molecules of the present invention may be derived from *Diabrotica virgifera virgifera* LeConte that is normally referred to as WCR. The isolated nucleic acids may be useful, for example, in identifying a target gene and in constructing a recombinant vector that produce stabilized dsRNAs or siRNAs of the present invention for protecting plants from WCR insect infestations.

[0134] Therefore, in one embodiment, the present invention comprises isolated and purified nucleotide sequences from WCR or *Lygus* that may be used as the insect control agents. The isolated and purified nucleotide sequences may comprise those as set forth in the sequence listing.

[0135] The nucleic acids from WCR or other insects that may be used in the present invention may also comprise isolated and substantially purified Unigenes and EST nucleic acid molecules or nucleic acid fragment molecules thereof. EST nucleic acid molecules may encode significant portions of, or indeed most of, the polypeptides. Alternatively, the fragments may comprise smaller oligonucleotides having from about 15 to about 250 nucleotide residues, and more preferably, about 15 to about 30 nucleotide residues. Alternatively, the nucleic acid molecules for use in the present invention may be from cDNA libraries from WCR, or from any other coleopteran pest species.

[0136] Nucleic acid molecules and fragments thereof from WCR, or other coleopteran pest species may be employed to obtain other nucleic acid molecules from other species for use in the present invention to produce desired dsRNA and siRNA molecules. Such nucleic acid molecules include the nucleic acid molecules that encode the complete coding sequence of a protein and promoters and flanking sequences of such molecules. In addition, such nucleic acid molecules include nucleic acid molecules that encode for gene family members. Such molecules can be readily obtained by using the above-described nucleic acid molecules or fragments thereof to screen, for instance, cDNA or gDNA libraries obtained from *D. v. virgifera* or other coleopterans, or from *Lygus hesperus*. Methods for forming such libraries are well known in the art.

[0137] As used herein, the phrase "coding sequence", "structural nucleotide sequence" or "structural nucleic acid molecule" refers to a nucleotide sequence that is translated into a polypeptide, usually via mRNA, when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by a translation start codon at the 5'-terminus and a translation stop codon at the 3'-terminus. A coding sequence can include genomic DNA, cDNA, EST and recombinant nucleotide sequences.

[0138] The term "recombinant DNA" or "recombinant nucleotide sequence" refers to DNA that contains a genetically engineered modification through manipulation via mutagenesis, restriction enzymes, and the like.

[0139] For many of the insects that are potential targets for control by the present invention, there may be limited information regarding the sequences of most genes or the phenotype resulting from mutation of particular genes. Therefore, the present inventors contemplate that selection of appropriate genes from insect pests for use in the present invention may be accomplished through use of information available from study of the corresponding genes in a model organism such in *Drosophila*, in some other insect species, or even in a nematode species, in a fungal species, in a plant species, in which the genes have been characterized. In some cases it will be possible to obtain the sequence of a corresponding gene from a target insect by searching databases such as GenBank using either the name of the gene or the sequence from, for example, *Drosophila*, another insect, a nematode, a fungus, or a plant from which the gene has been cloned. Once the sequence is obtained, PCR[™] may be used to amplify an appropriately selected segment of the gene in the insect for use in the present invention.

[0140] In order to obtain a DNA segment from the corresponding gene in an insect species, PCR[™] primers may be designed based on the sequence as found in WCR or other insects from which the gene has been cloned. The primers are designed to amplify a DNA segment of sufficient length for use in the present invention. DNA (either genomic DNA or cDNA) is prepared from the insect species, and the PCR[™] primers are used to amplify the DNA segment. Amplification conditions are selected so that amplification will occur even if the primers do not exactly match the target sequence. Alternately, the gene (or a portion thereof) may be cloned from a gDNA or cDNA library prepared from the insect pest species, using the WCR gene or another known insect gene as a probe. Techniques for performing PCR[™] and cloning from libraries are known. Further details of the process by which DNA segments from target insect pest species may be isolated based on the sequence of genes previously cloned from WCR or other insect species are provided in the Examples. One of ordinary skill in the art will recognize that a variety of techniques may be used to isolate gene segments from insect pest species that correspond to genes previously isolated from other species.

[0141] When an insect is the target pest for the present invention, such pests include: from the order Lepidoptera, for example,

Acleris spp., *Adoxophyes* spp., *Aegeria* spp., *Agrotis* spp., *Alabama argillaceae*, *Amylois* spp., *Anticarsia gemmatilis*, *Archips* spp., *Argyrotaenia* spp., *Autographa* spp., *Busseola fusca*, *Cadra cautella*, *Carposina nipponensis*, *Chilo* spp., *Choristoneura* spp., *Clysia ambiguella*, *Cnaphalocrocis* spp., *Cnephasia* spp., *Cochylis* spp., *Coleophora* spp., *Crocid-*

olomia binotalis, *Cryptophlebia leucotreta*, *Cydia* spp., *Diatraea* spp., *Diparopsis castanea*, *Earias* spp., *Ephestia* spp., *Eucosma* spp., *Eupoecilia ambiguella*, *Euproctis* spp., *Euxoa* spp., *Grapholita* spp., *Hedya nubiferana*, *Heliothis* spp., *Hellula undalis*, *Hyphantria cunea*, *Keiferia lycopersicella*, *Leucoptera scitella*, *Lithocollethis* spp., *Lobesia botrana*, *Lymantria* spp., *Lyonetia* spp., *Malacosoma* spp., *Mamestra brassicae*, *Manduca sexta*, *Operophtera* spp., *Ostrinia* *Nubilalis*, *Pammene* spp., *Pandemis* spp., *Panolis flammea*, *Pectinophora gossypiella*, *Phthorimaea operculella*, *Pieris rapae*, *Pieris* spp., *Plutella xylostella*, *Prays* spp., *Scirpophaga* spp., *Sesamia* spp., *Sparganothis* spp., *Spodoptera* spp., *Synanthedon* spp., *Thaumetopoea* spp., *Tortrix* spp., *Trichoplusia ni* and *Yponomeuta* spp.; from the order *Coleoptera*, for example,

Agriotes spp., *Anthonomus* spp., *Atomaria linearis*, *Chaetocnema tibialis*, *Cosmopolites* spp., *Curculio* spp., *Dermestes* spp., *Diabrotica* spp., *Epilachna* spp., *Eremnus* spp., *Leptinotarsa decemlineata*, *Lissorhoptrus* spp., *Melolontha* spp., *Orycaephilus* spp., *Otiorhynchus* spp., *Phlyctinus* spp., *Popillia* spp., *Psylliodes* spp., *Rhizopertha* spp., *Scarabeidae*, *Sitophilus* spp., *Sitotroga* spp., *Tenebrio* spp., *Tribolium* spp. and *Trogoderma* spp.; from the order *Orthoptera*, for example,

Blatta spp., *Blattella* spp., *Gryllotalpa* spp., *Leucophaea maderae*, *Locusta* spp., *Periplaneta* spp., and *Schistocerca* spp.;

from the order *Isoptera*, for example,

Reticulitermes spp.;

from the order *Psocoptera*, for example,

Liposcelis spp.;

from the order *Anoplura*, for example,

Haematopinus spp., *Linognathus* spp., *Pediculus* spp., *Pemphigus* spp. and *Phylloxera* spp.;

from the order *Mallophaga*, for example,

Damalinea spp. and *Trichodectes* spp.;

from the order *Thysanoptera*, for example,

Franklinella spp., *Hercinothrips* spp., *Taeniothrips* spp., *Thrips palmi*, *Thrips tabaci* and *Scirtothrips aurantii*;

from the order *Heteroptera*, for example,

Cimex spp., *Distantiella theobroma*, *Dysdercus* spp., *Euchistus* spp., *Eurygaster* spp., *Leptocoris* spp., *Nezara* spp., *Piesma* spp., *Rhodnius* spp., *Sahlbergella singularis*, *Scotinophara* spp., *Triatoma* spp., *Miridae* family spp. such as *Lygus hesperus* and *Lygus lineolaris*, *Lygaeidae* family spp. such as *Blissus leucopterus*, and *Pentatomidae* family spp.; from the order *Homoptera*, for example,

Aleurothrix floccosus, *Aleyrodes brassicae*, *Aonidiella* spp., *Aphididae*, *Aphis* spp., *Aspidiotus* spp., *Bemisia tabaci*, *Ceroplaster* spp., *Chrysomphalus aonidium*, *Chrysomphalus dictyospermi*, *Coccus hesperidum*, *Empoasca* spp., *Eriosoma lorigerum*, *Erythroneura* spp., *Gascardia* spp., *Laodelphax* spp., *Lacanium corni*, *Lepidosaphes* spp., *Macrosiphus* spp., *Myzus* spp., *Nehotettix* spp., *Nilaparvata* spp., *Paratoria* spp., *Pemphigus* spp., *Planococcus* spp., *Pseudaulacaspis* spp., *Pseudococcus* spp., *Psylla* spp., *Pulvinaria aethiopica*, *Quadraspidotus* spp., *Rhopalosiphum* spp., *Saissetia* spp., *Scaphoideus* spp., *Schizaphis* spp., *Sitobion* spp., *Trialeurodes vaporariorum*, *Trioza erytreae* and *Unaspis citri*;

from the order *Hymenoptera*, for example,

Acromyrmex, *Atta* spp., *Cephus* spp., *Diprion* spp., *Diprionidae*, *Gilpinia polytoma*, *Hoplocampa* spp., *Lasius* spp., *Monomorium pharaonis*, *Neodiprion* spp., *Solenopsis* spp. and *Vespa* spp.;

from the order *Diptera*, for example,

Aedes spp., *Antherigona soccata*, *Bibio hortulanus*, *Calliphora erythrocephala*, *Ceratitis* spp., *Chrysomyia* spp., *Culex* spp., *Cuterebra* spp., *Dacus* spp., *Drosophila melanogaster*, *Fannia* spp., *Gastrophilus* spp., *Glossina* spp., *Hypoderma* spp., *Hyppobosca* spp., *Liriomyza* spp., *Lucilia* spp., *Melanagromyza* spp., *Musca* spp., *Oestrus* spp., *Orseolia* spp., *Oscinella frit*, *Pegomyia hyoscyami*, *Phorbia* spp., *Rhagoletis pomonella*, *Sciara* spp., *Stomoxys* spp., *Tabanus* spp., *Tannia* spp. and *Tipula* spp.,

from the order *Siphonaptera*, for example,

Ceratophyllus spp. and *Xenopsylla cheopis* and

from the order *Thysanura*, for example,

Lepisma saccharina.

[0142] It has been found that the present invention is particularly effective when the insect pest is a *Diabrotica* spp., and especially when the pest is *Diabrotica virgifera virgifera* (Western Corn Rootworm, WCR), *Diabrotica barberi* (Northern Corn Rootworm, NCR), *Diabrotica virgifera zea* (Mexican Corn Rootworm, MCR), *Diabrotica balteata* (Brazilian Corn Rootworm (BZR) or Brazilian Corn Rootworm complex (BCR) consisting of *Diabrotica viridula* and *Diabrotica speciosa*), or *Diabrotica undecimpunctata howardi* (Southern Corn Rootworm, SCR).

EXAMPLES

[0143] The inventors herein have identified means for controlling coleopteran pest infestation by providing a double stranded ribonucleic acid molecules in the diet of pests. Surprisingly, the inventors have discovered double stranded

ribonucleic acid molecules that function upon ingestion by the pest to inhibit a biological function in the pest, resulting in one or more of the following attributes: reduction in feeding by the pest, reduction in viability of the pest, death of the pest, inhibition of differentiation and development of the pest, absence of or reduced capacity for sexual reproduction by the pest, muscle formation, juvenile hormone formation, juvenile hormone regulation, ion regulation and transport, maintenance of cell membrane potential, amino acid biosynthesis, amino acid degradation, sperm formation, pheromone synthesis, pheromone sensing, antennae formation, wing formation, leg formation, development and differentiation, egg formation, larval maturation, digestive enzyme formation, haemolymph synthesis, haemolymph maintenance, neurotransmission, cell division, energy metabolism, respiration, apoptosis, and any component of a eukaryotic cells' cytoskeletal structure, such as, for example, actins and tubulins. Any one or any combination of these attributes can result in an effective inhibition of pest infestation, and in the case of a plant pest, inhibition of plant infestation. For example, when used as a diet composition containing a pest inhibitory sufficient amount of one or more double stranded ribonucleic acid molecules provided topically to a plant, as a seed treatment, as a soil application around a plant, or when produced by a plant from a recombinant DNA molecule present within the cells of a plant, plant pest infestation is unexpectedly dramatically reduced. The Examples set forth herein below are illustrative of the invention when applied to a single pest. Examples not covered by the scope of the claims are for illustrative purpose.

EXAMPLE 1

Identification of Target Nucleotide Sequences For Preparation of dsRNA Useful for Controlling Corn Rootworms.

[0144] Corn rootworm cDNA libraries (LIB149, LIB 150, LIB3027, LIB3373) were constructed from whole larvae, pupae and from dissected midgut sections, and nucleotide sequence information was obtained (see Andersen *et al.*, U.S. Patent Application Serial No. 10/205,189 filed July 24, 2002). In addition, cDNA libraries were constructed from whole larvae at different developmental stages and at different times within each developmental stage in order to maximize the number of different EST sequences from the *Diabrotica* species. Libraries LIB5444 and LIB5462 were constructed respectively from mRNA pools obtained from first (1 g) and third (2.9 g) instar Western Corn Rootworm larvae. Harvested insects were rapidly frozen by insertion into liquid nitrogen. The insects were ground in a mortar and pestle maintained at or below -20°C by chilling on dry ice and/or with the addition of liquid nitrogen to the mortar until the tissue was ground into a fine powder. RNA was extracted using TRIzol® reagent (Invitrogen) according to the manufacturer's instructions. Poly A+ RNA was isolated from the total RNA prep using DYNABEADS Oligo dT (Invitrogen) following the manufacturer's instructions. A cDNA library was constructed from the Poly A+ RNA using the SuperScript™ Plasmid System (Invitrogen). cDNA was size fractionated using chromatography. The fourth and fifth fractions were collected and ligated into the pSPORT1 vector (Life Technologies Inc., Gaithersburg MD) between the *Sal*I and *Not*I restriction endonucleases recognition sites, and transformed into *E. coli* DH10B electro-competent cells by electroporation. The first instar larvae library yielded about 420,000 colony-forming units. The third instar larvae library yielded about 2.78 x 10⁶ colony forming units. Colonies from LIB 149, LIB150 were washed from the plates, mixed to uniformity by vortexing briefly, and pooled into Tris-EDTA buffer. Half of the wash was brought to 10% glycerol, aliquoted into cryovials, and stored at -70°C. The other half was used to produce plasmid DNA using a Quiagen midi-prep purification column, or its equivalent. Purified plasmid DNA was aliquoted to microcentrifuge tubes and stored at -20°C.

[0145] Colonies from the *Diabrotica virgifera* cDNA libraries LIB5444 and LIB5462 were amplified individually in a high viscosity medium. Approximately 200,000 colony-forming units from LIB5444 and 600,000 colony-forming units from LIB5462 were mixed on a stir plate separately in 500 ml LB medium containing 0.3% SeaPrep agarose® and 50 mg/1 carbenecillin at 37°C and then rapidly cooled in a water/ice bath for 1 hour allowing uniform suspension of the bacterial colonies. The inoculated libraries were then grown at 30°C for 42 hours. After incubation, the cells were mixed for 5 minutes on a stir plate. The medium was then transferred to two 250 ml centrifuge bottles. The bacterial cells were pelleted at 10,000 x g for 10 minutes. The medium was removed from the bottles and the cells were resuspended in a total of 20 ml of LB medium with 50 mg/1 carbenecillin. Dimethyl sulfoxide was added to 10% to preserve the cells in freezing. Both libraries were amplified to a final titer of 10⁸ colony-forming units per milliliter. Samples of the *Diabrotica virgifera* cDNA libraries LIB5444 and LIB5462 were combined and adjusted to a DNA concentration of about 1.25 micrograms per microliter in sterile distilled and deionized water and aliquoted into twenty five cryovials, each cryovial containing about 8.75 micrograms of DNA. These samples were deposited by the applicant(s)/inventors with the American Type Culture Collection (ATCC) located at 10801 University Boulevard, Manassas, Virginia, USA ZIP 20110-2209 on June 10, 2004 and referred to as LIB5444/62. The ATCC provided the Applicant with a deposit receipt, assigning the ATCC Deposit Accession No. PTA-6072.

[0146] Corn rootworm high molecular weight cDNA libraries, *i.e.*, LIB5496 and LIB5498, were prepared essentially as described above for the production of corn rootworm cDNA libraries. Libraries LIB5496 and LIB5498 were constructed respectively from mRNA pools obtained from first (1 gram) and second and third (1 gram) instar Western Corn Rootworm larvae. Briefly, insects were quickly frozen in liquid nitrogen. The frozen insects were reduced to a fine powder by grinding

in a mortar and pestle. RNA was extracted using TRIzol® reagent (Invitrogen) following the manufacturer's instructions. Poly A+ RNA was isolated from the total RNA prep using DYNABEADS Oligo dT (Invitrogen). A high molecular weight cDNA library was made from 20 micrograms of Poly A+ RNA using the SuperScript™ Plasmid System (Invitrogen). The cDNA was size fractionated on a 1% agarose gel in TAE, and cDNA between the range of 1 Kb to 10 Kb was collected and ligated into the pSPORT1 vector in between the *Sa*I and *Not*I restriction sites and transformed into *E. coli* DH10B electro-competent cells by electroporation. LIB5496 yielded a total titer of about 3.5×10^6 colony forming units. LIB5498 yielded a total titer of about 1.0×10^6 colony forming units. Colonies from the corn rootworm high molecular weight cDNA libraries LIB5496 and LIB5498 were amplified individually in a high viscosity medium. Approximately 600,000 colony-forming units from LIB5496 and LIB5498 were mixed on a stir plate separately in 500 ml LB medium containing 0.3% SeaPrep agarose® and 50 mg/1 carbenecillin at 37°C and then rapidly cooled in a water/ice bath for 1 hour allowing uniform suspension of the bacterial colonies. The libraries were then grown at 30°C for 42 hours. After incubation, the cells were mixed for 5 minutes on a stir plate. The medium was then transferred to two 250 mL centrifuge bottles. The bacterial cells were pelleted at 10,000 xg for 10 minutes. The medium was removed from the bottles and the cells were resuspended in a total of 20 mL of LB medium with 50 mg/L carbenecillin. Dimethyl sulfoxide was added to 10% to preserve the cells in freezing. Both libraries were amplified to a final titer of 10^8 colony-forming units per milliliter. Inserted cDNA sequence information was obtained from the corn rootworm species-specific plasmid libraries.

[0147] The Andersen *et al.* rootworm libraries together with additional sequences from the libraries LIB5444 and LIB5462 initially produced about 18,415 individual EST sequences consisting of approximately 1.0×10^7 nucleotide residues. The average length of an EST sequence was about 586 nucleotide residues. These EST sequences were subjected to bioinformatics algorithms that resulted in the assembly of contig sequences referred to herein as UNIGENE sequences, and individual EST sequences that could not be compiled by overlap identity with other EST sequences, referred to herein as singletons. The LIB5444 and LIB5462 libraries were then sequenced much deeper, resulting in additional individual EST sequences. EST sequences obtained from libraries, *i.e.*, LIB149, LIB150, LIB3027, LIB3373, LIB5444, LIB5462, LIB5496 and LIB5503 were selected for further investigation in feeding bioassays as set forth below and the corresponding sequences are given in the sequence listing..

[0148] The EST sequences isolated from CRW cDNA libraries were assembled, where possible, into UNIGENE sets and these assembled Unigene sequences are included in the sequence listing. A UNIGENE is a gene-oriented cluster formed from the overlap of individual EST sequences within regions of sequence identity to form a larger sequence. Pontius *et al.* (2003). Each nucleotide sequence as set forth in the sequence listing was analyzed to identify the presence of open reading frames. Amino acid sequence information deduced from open reading frames was compared to known amino acid sequence information available in public databases in order to deduce the extent of amino acid sequence identity or similarity to those known amino acid sequences. Biological function, if any, associated with known amino acid sequences in public databases was annotated to the amino acid sequences deduced from the cDNA library nucleotide sequence information. Annotations provided information that was suggestive of the function of a protein that may be expressed from a particular gene that gave rise to a particular cDNA sequence, but was not outcome determinative. Based on the suggestive annotation information, certain cDNA sequences were characterized as those that encoded a protein that was likely involved in some biological function within corn rootworm cells that was either essential to life, or that was necessary for ensuring health and vitality to a cell, or were likely to be involved in cellular integrity, cell maintenance, reproductive capacity, and the like.

[0149] Sequences selected for further investigation were used in the construction of double stranded RNA molecules for incorporation into CRW diet. Thermal amplification primer pairs were designed based on cDNA and EST starting sequences to obtain sequences used in feeding assays. Primer pairs were constructed either as a pair of nucleotide sequences, each member of a primer pair exhibiting perfect complementarity either to a sense or to an antisense sequence. Some primer pair sequences were constructed so that each member of the pair exhibited a sequence containing a T7 phage RNA polymerase promoter at its 5' end. Preferably a higher fidelity first amplification reaction was carried out using a first primer pair lacking a T7 promoter to generate a first amplicon using CRW genomic DNA as template. Preferably, a cDNA or a mRNA sequence is used as the template for the synthesis of a dsRNA molecule for use in the present invention because eukaryotic genome sequences are recognized in the art to contain sequences that are not present within the mature RNA molecule. A sample of the first amplicon generated from the higher fidelity first amplification reaction was then used as template in a second thermal amplification reaction with a second primer pair containing the T7 promoter sequence to produce a second amplicon that contained a T7 promoter at or embedded within the 5' end of each strand of the second amplicon. The complete nucleotide sequence of the second amplicon was obtained in both directions and compared to the nucleotide sequence as reported for the cDNA, and discrepancies between the two sequences, if any, were noted. Generally, sequences prepared using genome DNA as template were inconsistent with further use as dsRNA molecules for use in achieving significant levels of suppression because of variations within the genome sequences that were not present within the RNA or cDNA sequence.

[0150] An *in vitro* transcription reaction typically contained from about 1 to about 2 micrograms of linearized DNA template, T7 polymerase reaction buffer from a 10X concentrate, ribonucleotides ATP, CTP, GTP, and UTP at a final

concentration of from between 50 and 100 mM each, and 1 unit of T7 RNA polymerase enzyme. The RNA polymerase reaction was incubated at about 37°C, depending on the optimal temperature of the RNA polymerase used according to the manufacturers' instructions, for a period of time ranging from several minutes to several hours. Generally, reactions were carried out for from about 2 to about 6 hours for transcription of template sequences up to about 400 nucleotides in length, and for up to 20 hours for transcription of template sequences greater than about 400 nucleotides in length. Heating the reaction to 65°C for fifteen minutes terminates RNA transcription. RNA transcription products were precipitated in ethanol, washed, air dried and resuspended in RNase free water to a concentration of about 1 microgram per microliter. Most transcripts which took advantage of the opposing T7 promoter strategy outlined above produced double stranded RNA in the *in vitro* transcription reaction, however, a higher yield of double stranded RNA was obtained by heating the purified RNA to 65°C and then slowly cooling to room temperature to ensure proper annealing of sense and antisense RNA segments. Double stranded RNA products were then incubated with DNase I and RNase at 37°C for one hour to remove any DNA or single stranded RNA present in the mixture. Double stranded RNA products were purified over a column according to the manufacturers' instructions (AMBION MEGAscript® RNAi KIT) and resuspended in 10 mM Tris-HCl buffer (pH 7.5) or RNase free water to a concentration of between 0.1 and 1.0 microgram per microliter.

[0151] The following nucleotide sequences were derived first as cDNA sequences identified in a corn rootworm mid-gut cDNA library (Andersen *et al.*, *ibid*), and were adapted for use in constructing double stranded RNA molecules for use in testing the efficacy of inhibiting a biological function in a pest by feeding double stranded RNA molecules in the diet of the pest.

A. Chd3 Homologous Sequences

[0152] CHD genes have been identified in numerous eukaryotes, and the corresponding proteins are proposed to function as chromatin-remodeling factors. The term CHD is derived from the three domains of sequence homology found in CHD proteins: a chromo (chromatin organization modifier) domain, a SNF2-related helicase/ATPase domain, and a DNA-binding domain, each of which is believed to confer a distinct chromatin-related activity. CHD proteins are separated into two categories based on the presence or absence of another domain of sequence homology, a PHD zinc finger domain, typically associated with chromatin related activity. CHD3 related proteins possess a PHD zinc finger domain, but CHD1 related proteins do not. Experimental observations have suggested a role for CHD3 proteins in repression of transcription, and in some species have been shown to be a component of a complex that contains histone deacetylase as a subunit. Deacetylation of histones is correlated with transcriptional inactivation, and so CHD3 proteins have been implicated to function as repressors of transcription by virtue of being a component of a histone deacetylase complex (Ogas *et al.*, 1999). Thus, suppression of CHD3 protein synthesis may be a useful target for double stranded RNA mediated inhibition of coleopteran pests.

B. Beta-tubulin homologous sequences

[0153] Tubulin proteins are important structural components of many cellular structures in all eukaryote cells and principally in the formation of microtubules. Inhibition of microtubule formation in cells results in catastrophic effects including interference with the formation of mitotic spindles, blockage of cell division, and the like. Therefore, suppression of tubulin protein formation may be a useful target for double stranded RNA mediated inhibition.

C. 40 kDa V-ATPase homologous sequences

[0154] Energy metabolism within subcellular organelles in eukaryotic systems is an essential function. Vacuolar ATP synthases are involved in maintaining sufficient levels of ATP within vacuoles. Therefore, vacuolar ATP synthases may be a useful target for double stranded RNA mediated inhibition.

D. EF1 α homologous sequences

[0155] Transcription elongation and transcription termination factors are essential to metabolism and may be advantageous targets for double stranded RNA mediated inhibition.

E. 26S proteasome subunit p28 homologous sequences

[0156] The 26S proteasome is a large, ATP-dependent, multi-subunit protease that is highly conserved in all eukaryotes. It has a general function in the selective removal of various short-lived proteins that are first covalently linked to ubiquitin and then subsequently degraded by the 26S proteasome complex. The ubiquitin pathway plays an important role in the control of the cell cycle by the specific degradation of a number of regulatory proteins including mitotic cyclins

and inhibitors of cyclin-dependent kinases such as p27 of mammalian cells. Thus, the suppression of 26S proteasome synthesis and suppression of synthesis of its component subunits may be preferred targets for double stranded RNA mediated inhibition. (Smith *et al.*, 1997).

F. Juvenile Hormone Epoxide Hydrolase Homologous Sequences

[0157] Insect juvenile hormone controls and regulates a variety of necessary biological processes within the insect life cycle including but not necessarily limited to metamorphosis, reproduction, and diapause. Juvenile hormone (JH) concentrations are required to peak at appropriate times within the haemolymph of the larval form of an insect pest, in particular lepidopteran and coleopteran larvae, and then must be degraded in order to terminate the effects of the hormone response. Enzymes involved in decreasing the concentration of juvenile hormone are effective through two primary pathways of metabolic degradation. One pathway involves juvenile hormone esterase (JHE), which hydrolyzes the methyl ester providing the corresponding acid. The second pathway utilizes juvenile hormone epoxide hydrolase (JHEH) to achieve hydrolysis of the epoxide, resulting in formation of the diol. The contribution of JHE in the degradation of JH is well understood and has been found to be invariable between the lepidoptera and coleoptera species. Inhibition of JH esterase has been associated with severe morphological changes including but not limited to larval wandering, deferred pupation, and development of malformed intermediates. In contrast, the contribution of JHEH in JH metabolism is less well understood and had been shown to vary between the species, but recent studies point to evidence that suggests that JHEH may be the primary route of metabolism of JH (Brandon J. Fetterolf, Doctoral Dissertation, North Carolina State University (Feb. 10, 2002) Synthesis and Analysis of Mechanism Based Inhibitors of Juvenile Hormone Epoxide Hydrolase from Insect *Trichoplusia ni*). In any event, disruption of either JH degradation pathway using gene suppression technology could be an effective target for double stranded RNA mediated pest inhibition.

G. Swelling dependent chloride channel protein homologous sequences

[0158] Swelling dependent chloride channel proteins have been postulated to play a critical role in osmoregulation in eukaryotic animal cell systems. Therefore, a nucleotide sequence exhibiting the ability to express an amino acid sequence that exhibits homology to previously identified swelling dependent chloride channel proteins may be a useful target for RNA inhibition in a pest.

H. Glucose-6-phosphate 1-dehydrogenase protein homologous sequences

[0159] Glucose-6-phosphate 1-dehydrogenase protein (G6PD) catalyzes the oxidation of glucose-6-phosphate to 6-phosphogluconate while concomitantly reducing the oxidized form of nicotinamide adenine dinucleotide phosphate (NADP⁺) to NADPH. NADPH is known in the art as a required cofactor in many eukaryotic biosynthetic reactions, and is known to maintain glutathione in its reduced form. Reduced glutathione acts as a scavenger for dangerous oxidative metabolites in eukaryotic cells, and with the assistance of the enzyme glutathione peroxidase, convert harmful hydrogen peroxide to water (Beutler *et al.*, 1991). Therefore, G6PD may be a preferable target for double stranded RNA mediated inhibition in a coleopteran pest.

I. Act42A protein homologous sequences

[0160] Actin is a ubiquitous and highly conserved eukaryotic protein required for cell motility and locomotion (Lovato *et al.*, 2001). A number of CRW cDNA sequences were identified that were predicted to likely encode actin or proteins exhibiting amino acid sequence structure related to actin proteins. Therefore, genes encoding actin homologues in a pest cell may be useful targets for double stranded RNA mediated inhibition.

J. ADP-ribosylation factor 1 homologous sequences

[0161] ADP ribosylation factors have been demonstrated to be essential in cell function in that they play integral roles in the processes of DNA damage repair, carcinogenesis, cell death, and genomic stability. Thus, it would be useful to be able to selectively disrupt transcription of ADP-ribosylation factors in coleopteran pest species using double stranded RNA mediated inhibition.

K. Transcription Factor IIB protein homologous sequences

[0162] Transcription elongation and transcription termination factors, as indicated above, are essential to metabolism and may be advantageous targets for double stranded RNA mediated inhibition to control or eliminate coleopteran pest

infestation.

L. Chitinase homologous sequences

- 5 **[0163]** Chitin is a $\beta(1 \rightarrow 4)$ homopolymer of N-acetylglucosamine and is found in insect exoskeletons. Chitin is formed from UDP-N-acetylglucosamine in a reaction catalyzed by Chitin synthase. Chitin is a structural homopolymer polysaccharide, and there are many enzymatic steps involved in the construction of this highly branched and cross-linked structure. Chitin gives shape, rigidity and support to insects and provides a scaffolding to which internal organs such as muscles are attached. Chitin must also be degraded to some extent to mediate the steps involved in the insect molting process. Therefore, it is believed that double stranded RNA mediated inhibition of proteins in these pathways would be useful as a means for controlling coleopteran pest infestation.

M. Ubiquitin conjugating enzyme homologous sequences

- 15 **[0164]** The ubiquitin pathway plays an important role in the control of the cell cycle by the specific degradation of a number of regulatory proteins including mitotic cyclins and inhibitors of cyclin-dependent kinases such as p27 of mammalian cells. Thus, genes encoding ubiquitin and associated components may be a preferred target for double stranded RNA mediated inhibition. (Smith *et al.*, 1997). The ubiquitin-dependent proteolytic pathway is one of the major routes by which intracellular proteins are selectively destroyed in eukaryotes. Conjugation of ubiquitin to substrate proteins is mediated by a remarkably diverse array of enzymes. Proteolytic targeting may also be regulated at steps between ubiquitination of the substrate and its degradation to peptides by the multi-subunit 26S protease. The complexity of the ubiquitin system suggests a central role for protein turnover in eukaryotic cell regulation, and implicates other proteins in the pathway including ubiquitin-activating enzyme, ubiquitin-conjugating enzyme, ubiquitin-protein ligase, and 26S proteasome subunit components. Therefore, it is believed that double stranded RNA mediated inhibition of proteins in this pathway would be useful as a means for controlling coleopteran pest infestation.

N. Glyceraldehyde-3-phosphate dehydrogenase homologous sequences

- 30 **[0165]** The glycolytic pathway is an essential pathway in most organisms and is involved in the production of metabolic energy from the degradation of glucose. One important enzyme in the second stage of the glycolytic pathway is glyceraldehyde-3-phosphate dehydrogenase (G3PDH), which, in the presence of NAD⁺ and inorganic phosphate, catalyzes the oxidation of 3-phospho-glyceraldehyde to 3-phosphoglyceroyl-phosphate along with the formation of NADH. The important component of this reaction is the storage of energy through the formation of NADH. Genes encoding enzymes associated with the glycolytic pathway, and particularly genes encoding enzymes involved in the steps useful in formation of energy reserves may be particularly useful targets for double stranded RNA mediated inhibition in coleopteran pest species.

O. Ubiquitin B homologous sequences

- 40 **[0166]** As described above, the ubiquitin protein degradation pathway plays an important role in the control of the cell cycle by the specific degradation of a number of regulatory proteins including mitotic cyclins and inhibitors of cyclin-dependent kinases such as p27 of mammalian cells. Thus, genes encoding ubiquitin and associated components may be a preferred target for double stranded RNA mediated inhibition. (Smith *et al.*, 1997).

P. Juvenile hormone esterase homologs

- 45 **[0167]** As indicated above, insect juvenile hormone controls and regulates a variety of necessary biological processes within the insect life cycle including but not necessarily limited to metamorphosis, reproduction, and diapause. Disruption of JH synthesis or degradation pathways using gene suppression technology could be an effective target for double stranded RNA mediated pest inhibition.

Q. Alpha tubulin homologous sequences

- 55 **[0168]** Eukaryotic cells generally utilize cytoskeletal structural elements that are important, not only as a mechanical scaffold, but also in sustaining the shape of the cell. Semiflexible microfilaments make cells mobile, help them to divide in mitosis (cytokinesis) and, in vertebrate and invertebrate animals, are responsible for muscular contraction. The relatively stiff microtubules which are made up of alpha and beta tubulin proteins play an important role in acting as a sort of highway for transport of vesicles and organelles and in the separation of chromosomes during mitosis (karyokinesis).

The flexible intermediate filaments provide at least additional strength to the overall cellular structure. The cytoskeleton is also known to be involved in signaling across the cell cytoplasm. Taking these functions into account, it is believed that any disruption of the cytoskeleton or even subtle changes of its integrity may cause pathological consequences to a cell.

R. Transport Related Sequences

[0169] As indicated above, sorting and transport of various molecules within a cell, including to appropriate organelles, as well as their secretion is an important physiological function. Such sorting pathways could include those relying on the endosomal sorting complex required for transport (ESCRT), complexes I-III, among others. Thus, functions related to transport of polypeptides and other molecules may also be a preferred target for dsRNA-mediated inhibition.

EXAMPLE 2

Insect Feeding Bioassays

[0170] Samples of double stranded RNA (dsRNA) were subjected to bioassay with a selected number of target pests. The dsRNA was prepared from sequences identified according to Example 1 using either a full contig sequence in the case of SEQ ID Nos:1-6, or a sequence amplified from the assembled contig using the primer pairs as set forth in the sequence listing. Varying doses of dsRNA were applied as an overlay to corn rootworm artificial diet according to the following procedure. *Diabrotica virgifera virgifera* (WCR) eggs were obtained from Crop Characteristics, Inc., Farmington, Minnesota. The non-diapausing WCR eggs were incubated in soil for about 13 days at 24°C, 60% relative humidity, in complete darkness. On day 13 the soil containing WCR eggs was placed between #30 and #60 mesh sieves and the eggs were washed out of the soil using a high pressure garden hose. The eggs were surface disinfested by soaking in LYSOL for three minutes, rinsed three times with sterile water, washed one time with a 10% formalin solution and then rinsed three additional times in sterile water. Eggs treated in this way were dispensed onto sterile coffee filters and hatched overnight at 27°C, 60% relative humidity, in complete darkness.

[0171] To prepare dsRNA, amplicons of selected sequences were cloned into a plasmid vector capable of replication in *E. coli* and sufficient amounts of plasmid DNA was recovered to allow for *in vitro* T7 RNA polymerase transcription from the embedded convergent T7 promoters at either end of the cloned fragment. Double stranded RNA was produced and subjected to bioassay; one RNA segment comprising the sequence as set forth in the sequence listing, the other RNA segment being substantially the reverse complement of the nucleotide sequence, uridines appropriately positioned in place of thymidines. A sample of double stranded RNA (dsRNA) was treated with DICER or with RNase III to produce sufficient quantities of small interfering RNA's (siRNA). Samples containing siRNA or dsRNA were overlayed onto CRW diet bioassay as described above and larvae were allowed to feed as set forth below.

[0172] A sample of double stranded RNA was either added directly to each well containing insect diet as indicated above, or was modified prior to being added to insect diet. Modification of double stranded RNA followed the instructions for RNase III (AMBION CORPORATION, Austin, Texas) or DICER (STRATAGENE, La Jolla, California) provided by the manufacturer. RNase III digestion of double stranded RNA produced twenty-one and twenty-two nucleotide duplexes containing 5' phosphorylated ends and 3' hydroxyl ends with 2-3 base overhangs, similar to the ~21-26 base pair duplexed short interfering RNA (siRNA) fragments produced by the dicer enzyme in the eukaryotic pathway identified by Hamilton *et. al.* (1999) and Elbashir *et. al.* (2001a). This collection of short interfering RNA duplexes was further purified and a sample characterized by polyacrylamide gel electrophoresis to determine the integrity and efficiency of duplex formation. The purity and quantity of the sample was then determined by spectrophotometry at a wavelength of 250 nanometers, and unused sample retained for further use by storage at -20°C.

[0173] Insect diet was prepared essentially according to Pleau *et al.* (2002), with the following modifications. 9.4 grams of SERVA agar was dispensed into 540 milliliters of purified water and agitated until the agar was thoroughly distributed. The water/agar mixture was heated to boiling to completely dissolve the agar, and then poured into a WARING blender. The blender was maintained at low speed while 62.7 grams of BIO-SERV DIET mix (F9757), 3.75 grams lyophilized corn root, 1.25 milliliters of green food coloring, and 0.6 milliliters of formalin was added to the hot agar mixture. The mixture was then adjusted to pH 9.0 with the addition of a 10% potassium hydroxide stock solution. The approximately 600 milliliter volume of liquid diet was continually mixed at high speed and maintained at from about 48°C to about 60°C using a sterilized NALGENE coated magnetic stir bar on a magnetic stirring hot plate while being dispensed in aliquots of 200 microliters into each well of FALCON 96-well round bottom microtiter plates. The diet in the plates was allowed to solidify and air dry in a sterile biohood for about ten minutes.

[0174] Thirty (30) microliter volumes of test samples containing either control reagents or double stranded RNA in varying quantities was overlayed onto the surface of the insect diet in each well using a micro-pipettor repeater. Insect diet was allowed to stand in a sterile biohood for up to one half hour after application of test samples to allow the reagents

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to diffuse into the diet and to allow the surface of the diet to dry. One WCR neonate larva was deposited to each well with a fine paintbrush. Plates were then sealed with MYLAR and ventilated using an insect pin. 12-72 insect larvae were tested per dose depending on the design of the assay. The bioassay plates were incubated at 27°C, 60% relative humidity in complete darkness for 12-14 days. The number of surviving larvae per dose was recorded at the 12-14 day time point. Larval mass was determined using a suitable microbalance for each surviving larva. Data was analyzed using JMP®4 statistical software (SAS Institute, 1995) and a full factorial ANOVA was conducted with a Dunnett's test to look for treatment effects compared to the untreated control ($P < 0.05$). A Tukey-Kramer post hoc test was performed to compare all pairs of the treatments ($P < 0.05$). The results of the CRW larvae feeding assays exhibited significant growth inhibition and mortality compared to controls as explained below.

EXAMPLE 3

Results of Insect Feeding Bioassays

[0175] Artificial diet sufficient for rearing corn rootworm larvae was prepared by applying samples of double stranded RNA sequences identified as described in Example 1 using bioassays carried out as described in Example 2. Corn rootworm larvae were typically allowed to feed on the diet for twelve days and mortality and stunting monitored in comparison to rootworms allowed to feed only on negative and positive control diets. The results of the studies confirmed significant levels ($p < 0.05$) of larval stunting and/or mortality using dsRNAs containing portions sequences homologous to a variety of different gene classes. The sequences and vectors yielding significant stunting and/or mortality and the corresponding SEQ ID NO for the sequence expressed as a dsRNA are given in Tables 1-5 below.

Table 1: dsRNA Constructs Demonstrating Significant Stunting and/or Mortality in Effect in Insect Feeding Bioassays with Southern Corn Rootworm or Western Corn Rootworm

Vector	Sequence Expressed as dsRNA	SEQ ID NO
RNAi-pIC17553:001	Apple	697
RNAi-pIC17504:049	EST Full Length V-ATPase	695
RNAi-pIC17554:001	Rpl 9	698
RNAi-pIC17555:001	Rpl 19	699
RNAi-pIC17504:050	Section 6.0 V-ATPase	711
RNAi-pIC19514:001	WCR mRNA capping enzyme LIB5496-028-A1-M1-A7	696
RNAi-pIC17552:003	LIB5462-042-A1-M1-H10 Dv.6_CG9355 DUSKY STRUCTURAL CONSTITUENT OF CUTICLE	700
RNAi-pIC17546:003	LIB5462-091-A1-M1-G3 Dv.1_CG6217 KNICKKOPF UNK	701
RNAi-pIC17546:001	Dv.1_CG6217	1
RNAi-pIC17549:001	Dv.4_CG1435	4
RNAi-pIC17550:001	LIB5444-065-A1-M1-D5 Dv.5_cg1915_1	5
RNAi-pIC17551:001	LIB5462-012-A1-M2-B2 Dv.5_cg1915_2	703
RNAi-pIC17552:001	Dv.6_CG9355	6
RNAi-pMON78412:002	Dv.7_CG3416; putative Mov34:CG3416 ortholog	10
RNAi-pMON96172:002	Dv.8_CG1088; putative vacuolar H ⁺ ATPase E subunit: CG1088 ortholog	14
RNAi-pMON96168:002	Dv.9_CG2331; putative ATPase activity: CG2331 ortholog	18
RNAi-pMON78424:002	Dv.10_CG6141; putative ribosomal protein L9: CG6141 ortholog	22
RNAi-pMON78425:001	Dv.11_CG2746	26

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(continued)

	Vector	Sequence Expressed as dsRNA	SEQ ID NO
5	RNAi-pMON78444:002	Dv.12_CG1341; putative proteasome regulatory particle, rpt1: CG1341 ortholog	30
	RNAi-pMON78416:002	Dv.13_CG11276; putative ribosomal protein S4: CG11276 ortholog	34
10	RNAi-pMON78434:001	Dv.14_CG17927_2; putative myosin heavy chain: CG17927 ortholog	38
	RNAi-pMON78439:001	Dv.16_CG5394; putative glutamyl-prolyl-tRNA synthetase: CG5394 ortholog	46
15	RNAi-pMON78438:001	Dv.17_CG10149; putative proteasome p44.5 subunit, rpn6: CG10149 ortholog	50
	RNAi-pMON78435:002	Dv.18_CG1404, putative RAN small monomeric GTPase: CG1404 ortholog	54
20	RNAi-pMON78449:002	Dv.19_CG18174; putative proteasome regulatory particle, lid subcomplex, rpn11: CG18174 ortholog	58
	RNAi-pMON78419:001	Dv.20_CG3180_1; putative DNA-directed RNA polymerase II: CG3180 ortholog	62
25	RNAi-pMON78440:002	Dv20_CG3180_2; putative DNA-directed RNA polymerase II: CG3180 ortholog	706
	RNAi-pMON78420:001	Dv.21_CG3320; putative Rab1: CG3320 ortholog	70
	RNAi-pMON78410:002	Dv.22_CG3395; putative Ribosomal protein S9: CG3395 ortholog	74
30	RNAi-pMON78422:001	Dv.23_CG7269; putative helicase: CG7269 ortholog	78
	RNAi-pMON78423:001	Dv.25_CG9012; putative Clathrin heavy chain: CG9012 ortholog	86
35	RNAi-pMON78414:006	DV.26 sec1 ~ 5' half of EST	710
	RNAi-pMON78414:001	Dv.26_CG9261; putative sodium/potassium-exchanging ATPase: CG9261 ortholog	90
	RNAi-pMON78413:001	Dv.27_CG12052; putative RNA polymerase II transcription factor: CG12052 ortholog.	94
40	RNAi-pMON78427:001	Dv.35_CG3762; putative Vha68-2: CG3762 ortholog.	126
	RNAi-pMON97122:001	C1_Dv.35; putative Vha68-2: CG3762 ortholog; concatamer	713
45	RNAi-pMON97127:001	C2_Dv.35; putative Vha68-2: CG3762 ortholog; concatamer	714
	RNAi-pMON97125:001	C3_Dv.35; putative Vha68-2: CG3762 ortholog; concatamer	715
50	RNAi-pMON78441:001	Dv.39_CG9078; putative sphingolipid delta-4 desaturase; stearoyl-CoA 9-desaturase: CG9078 ortholog	142
	RNAi-pMON97114:001	Dv.41_CG2637; Female sterile Ketel; involved in protein-nucleus import: CG2637 ortholog	150
55	RNAi-pMON97140:001	Dv.44_CG1244; Putative nucleic acid binding activity: CG1244 ortholog	162

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(continued)

	Vector	Sequence Expressed as dsRNA	SEQ ID NO
5	RNAi-pMON78429:001	Dv.46_CG10689; putative RNA helicase: CG10689 ortholog.	170
	RNAi-pMON78432:001	Dv.48_CG33196; putative transmembrane receptor protein tyrosine kinase: CG33196 ortholog	178
10	RNAi-pMON78428:001	Dv.49_CG8055_1; putative binding, carrier activity: CG8055_1 ortholog	182
	RNAi-pMON78428:003	Dv.49_CG8055_1; putative binding, carrier activity: CG8055_1 ortholog Free region selected from DV.49	704
15	RNAi-pMON78426:001	Dv.50_CG10110_1; putative Cleavage and polyadenylation specificity factor: CG10110_1 ortholog	186
	RNAi-pMON96185:001	Dv.55_CG5931; putative splicing factor activity, RNA helicase activity: CG5931 ortholog	202
20	RNAi-pMON78442:001	Dv.57_CG2968; putative hydrogen-exporting ATPase: CG2968 ortholog	206
	RNAi-pMON78431:001	Dv.58_CG1751; putative signal peptidase: CG1751 ortholog	210
25	RNAi-pMON96177:001	Dv.61_CG3725_1; putative Calcium ATPase: CG3725 ortholog	222
	RNAi-pMON96183:001	Dv.62_CG3612; putative bellwether: CG3612 ortholog	230
	RNAi-pMON96180:002	Dv.65_CG7033; putative chaperone activity: CG7033 ortholog	242
30	RNAi-pMON96176:001	Dv.66_CG32019; putative bent: CG32019 ortholog	246
	RNAi-pMON96170:002	Dv.67_CG16916; putative endopeptidase activity: CG16916 ortholog	250
35	RNAi-pMON96166:001	Dv.70_CG5771; putative Rab-protein 11: CG5771 ortholog	258
	RNAi-pMON96179:001	Dv.72_CG6831; putative rhea: CG6831 ortholog	266
	RNAi-pMON96186:001	Dv.73_CG10119; putative Lamin C: CG10119 ortholog	270
40	RNAi-pMON96160:002	Dv.74_CG6375; putative pitchoune: CG6375 ortholog	274
	RNAi-pMON97137:001	Dv.77_CG4214; putative Syntaxin 5; involved in intracellular protein transport: CG4214 ortholog	286
	RNAi-pMON96167:001	Dv.82_CG8264; putative Bx42: CG8264 ortholog	302
45	RNAi-pMON96171:001	Dv.83_CG11397; putative gluon: CG11397 ortholog	306
	RNAi-pMON96187:003	Dv.85_CG4494; putative protein binding activity: CG4494 ortholog	314
	RNAi-pMON96174:001	Dv.86_CG5055; putative bazooka: CG5055 ortholog	318
50	RNAi-pMON97126:001	Dv.88_CG8756; function unknown; contains chitin binding domain: CG8756 ortholog	326
	RNAi-pMON97130:001	Dv.93_CG8515; putative structural constituent of cuticle; contains chitin binding domain: CG8515 ortholog	342
55	RNAi-pMON97109:001	Dv.99_CG2446; Unknown; lethal in Drosophila & low homology with human: CG2446 ortholog	366

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(continued)

Vector	Sequence Expressed as dsRNA	SEQ ID NO
RNAi-pMON97111:001	Dv.105_CG1250_1; GTPase activator, involved in intracellular protein transport: CG1250 ortholog	390
RNAi-pMON97112:001	Dv.105_CG1250_2; GTPase activator, involved in intracellular protein transport: CG1250 ortholog	394
RNAi-pMON97107:001	Dv.107_CG14813; COPI vesicle coat; involved in Golgi to ER intracellular protein transport: CG14813 ortholog	398
RNAi-pMON97115:001	Dv.108_CG17248; n-synaptobrevin; involved in intracellular protein transport: CG17248 ortholog	402
RNAi-pMON97133:001	Dv.113; function unknown; WCR unique sequence	422
RNAi-pMON97121:001	Dv.122_CG3164; putative ATP-binding cassette transporter activity: CG3164 ortholog	454
RNAi-pMON97134:001	Dv.127; function unknown; no homology with human	470
RNAi-pMON97171:001	Dv.146; function unknown, WCR unique sequence	514
RNAi-pMON97166:001	Dv.147; function unknown, WCR unique sequence	518
RNAi-pMON97167:001	Dv.149; function unknown, WCR unique sequence	526
RNAi-pMON97169:001	Dv.155; function unknown, WCR unique sequence	550
RNAi-pMON97173:001	Dv.162; function unknown, WCR unique sequence	578
RNAi-pMON97170:001	Dv.170; function unknown, WCR unique sequence	610

Table 2: dsRNA Constructs Causing Significant Stunting Levels in Feeding Bioassays with Western Corn Rootworm (WCR) Larvae

Vector	Sequence Expressed as dsRNA
RNAi-pIC17553:001	Apple
RNAi-pIC17504:049	EST Full Length V-ATPase
RNAi-pIC17554:001	Rpl 9
RNAi-pIC17555:001	Rpl 19
RNAi-pIC17504:050	Section 6.0 V-ATPase
RNAi-pIC16005:001	V-ATPase D subunit 1
RNAi-pIC19514:001	WCR mRNA capping enzyme LIB5496-028-A1-M1-A7
RNAi-pIC17546:001	Dv.1_CG6217
RNAi-pIC17549:001	Dv.4 CG1435
RNAi-pIC17551:001	LIB5462-012-A1-M2-B2 Dv.5_cg1915_2
RNAi-pIC17552:001	Dv.6_CG9355
RNAi-pMON78412:001	Dv.7_CG3416
RNAi-pMON78412:002	Dv.7_CG3416; putative Mov34:CG3416 ortholog
RNAi-pMON96172:002	Dv.8_CG1088; putative vacuolar H ⁺ ATPase E subunit: CG1088 ortholog
RNAi-pMON96168:002	Dv.9_CG2331; putative ATPase activity: CG2331 ortholog
RNAi-pMON78424:002	Dv.10_CG6141; putative ribosomal protein L9: CG6141 ortholog

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(continued)

Vector	Sequence Expressed as dsRNA
RNAi-pMON78425:001	Dv.11_CG2746
RNAi-pMON78444:002	Dv.12_CG1341; putative proteasome regulatory particle, rpt1: CG1341 ortholog
RNAi-pMON78416:002	Dv.13_CG11276; putative ribosomal protein S4: CG11276 ortholog
RNAi-pMON78434:001	Dv.14_CG17927_2; putative myosin heavy chain: CG17927 ortholog
RNAi-pMON78439:001	Dv.16_CG5394; putative glutamyl-prolyl-tRNA synthetase: CG5394 ortholog
RNAi-pMON78435:002	Dv.18_CG1404; putative RAN small monomeric GTPase: CG1404 ortholog
RNAi-pMON78449:002	Dv.19_CG18174; putative proteasome regulatory particle, lid subcomplex, rpn11: CG18174 ortholog
RNAi-pMON78440:002	Dv.20_CG3180_2; putative DNA-directed RNA polymerase II: CG3180 ortholog
RNAi-pMON78420:002	Dv.21_CG3320; putative Rab1: CG3320 ortholog
RNAi-pMON78410:001	Dv.22_CG3395; putative Ribosomal protein S9: CG3395 ortholog
RNAi-pMON78422:001	Dv.23_CG7269; putative helicase: CG7269 ortholog
RNAi-pMON78423:001	Dv.25_CG9012; putative Clathrin heavy chain: CG9012 ortholog
RNAi-pMON78414:001	Dv.26_CG9261; putative sodium/potassium-exchanging ATPase: CG9261 ortholog
RNAi-pMON78413:001	Dv.27_CG12052; putative RNA polymerase II transcription factor: CG12052 ortholog.
RNAi-pMON97122:001	C1_Dv.35; putative Vha68-2: CG3762 ortholog; concatamer
RNAi-pMON97127:001	C2_Dv.35; putative Vha68-2: CG3762 ortholog; concatamer
RNAi-pMON97125:001	C3_Dv.35; putative Vha68-2: CG3762 ortholog; concatamer
RNAi-pMON78427:007	Dv.35_CG3762; putative Vha68-2: CG3762 ortholog.
RNAi-pMON78441:001	Dv.399_CG9078; putative sphingolipid delta-4 desaturase; stearoyl-CoA 9-desaturase: CG9078 ortholog
RNAi-pMON97114:001	Dv.41_CG2637; Female sterile Ketel; involved in protein-nucleus import: CG2637 ortholog
RNAi-pMON78429:001	Dv.46_CG10689; putative RNA helicase: CG10689 ortholog.
RNAi-pMON78432:001	Dv.48_CG33196; putative transmembrane receptor protein tyrosine kinase: CG33196 ortholog
RNAi-pMON78428:001	Dv.49_CG8055_1; putative binding, carrier activity: CG8055_1 ortholog
RNAi-pMON78428:003	Dv.49_CG8055_1; putative binding, carrier activity: CG8055_1 ortholog Free region selected from DV.49
RNAi-pMON78426:001	Dv.50_CG10110_1; putative Cleavage and polyadenylation specificity factor: CG10110_1 ortholog

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(continued)

	Vector	Sequence Expressed as dsRNA
5	RNAi-pMON96185:001	Dv.55_CG5931; putative splicing factor activity, RNA helicase activity: CG5931 ortholog
	RNAi-pMON78442:001	Dv.57_CG2968; putative hydrogen-exporting ATPase: CG2968 ortholog
10	RNAi-pMON78431:001	Dv.58_CG1751; putative signal peptidase: CG1751 ortholog
	RNAi-pMON96177:001	Dv.61_CG3725_1; putative Calcium ATPase: CG3725 ortholog
	RNAi-pMON96182:001	Dv.61_CG3725_2; putative Calcium ATPase: CG3725 ortholog
	RNAi-pMON96183:001	Dv.62_CG3612; putative bellwether: CG3612 ortholog
15	RNAi-pMON96180:002	Dv.65_CG7033; putative chaperone activity: CG7033 ortholog
	RNAi-pMON96180:001	Dv.65_CG7033; putative chaperone activity: CG7033 ortholog
	RNAi-pMON96176:001	Dv.66_CG32019; putative bent: CG32019 ortholog
20	RNAi-pMON96170:002	Dv.67_CG16916; putative endopeptidase activity: CG16916 ortholog
	RNAi-pMON96166:001	Dv.70_CG5771; putative Rab-protein 11: CG5771 ortholog
	RNAi-pMON96179:001	Dv.72_CG6831; putative rhea: CG6831 ortholog
25	RNAi-pMON96186:001	Dv.73_CG10119; putative Lamin C: CG10119 ortholog
	RNAi-pMON96160:002	Dv.74_CG6375; putative pitchoune: CG6375 ortholog
	RNAi-pMON96160:001	Dv.74_CG6375; putative pitchoune: CG6375 ortholog
30	RNAi-pMON97137:002	Dv.77_CG4214; putative Syntaxin 5; involved in intracellular protein transport: CG4214 ortholog
	RNAi-pMON96167:001	Dv.82_CG8264; putative Bx42: CG8264 ortholog
	RNAi-pMON96171:001	Dv.83_CG11397; putative gluon: CG11397 ortholog
35	RNAi-pMON96187:003	Dv.85_CG4494; putative protein binding activity: CG4494 ortholog
	RNAi-pMON97126:001	Dv.88_CG8756; function unknown; contains chitin binding domain: CG8756 ortholog
40	RNAi-pMON97109:001	Dv.99_CG2446; Unknown; lethal in Drosophila & low homology with human: CG2446 ortholog
	RNAi-pMON97111:001	Dv.105_CG1250_1; GTPase activator, involved in intracellular protein transport: CG1250 ortholog
45	RNAi-pMON97107:001	Dv.107_CG14813; COPI vesicle coat; involved in Golgi to ER intracellular protein transport: CG14813 ortholog
	RNAi-pMON97115:001	Dv.108_CG17248; n-synaptobrevin; involved in intracellular protein transport: CG17248 ortholog
50	RNAi-pMON97121:001	Dv.122_CG3164; putative ATP-binding cassette transporter activity: CG3164 ortholog
	RNAi-pMON97171:001	Dv.146; function unknown, WCR unique sequence
	RNAi-pMON97166:001	Dv.147; function unknown, WCR unique sequence
55	RNAi-pMON97167:001	Dv.149; function unknown, WCR unique sequence
	RNAi-pMON97169:001	Dv.155; function unknown, WCR unique sequence
	RNAi-pMON97173:001	Dv.162; function unknown, WCR unique sequence

(continued)

Vector	Sequence Expressed as dsRNA
RNAi-pMON97170:001	Dv.170; function unknown, WCR unique sequence

Table 3: dsRNA Constructs Causing Significant Mortality Levels in Feeding Bioassays with Western Corn Rootworm (WCR) Larvae

Vector	Sequence Expressed as dsRNA
RNAi-pIC17553:001	Apple
RNAi-pIC17504:049	EST Full Length V-ATPase
RNAi-pIC17555:001	Rpl 19
RNAi-pIC17554:001	Rpl 9
RNAi-pIC17504:050	Section 6.0 V-ATPase
RNAi-pIC17504:054	V-ATPase subunit 2 sequence from <i>Diabrotica virgifera virgifera</i> Full EST sequence serving as positive control
RNAi-pIC19514:001	WCR mRNA capping enzyme LIB5496-028-A1-M1-A7
RNAi-pIC17546:001	Dv.1_CG6217
RNAi-pIC17549:001	Dv.4_CG1435
RNAi-pIC17550:001	LIB5444-065-A1-M1-D5 Dv.5_cg1915_1
RNAi-pMON78412:002	Dv.7_CG3416; putative Mov34:CG3416 ortholog
RNAi-pMON96172:001	Dv.8_CG1088; putative vacuolar H ⁺ ATPase E subunit: CG1088 ortholog
RNAi-pMON96168:001	Dv.9_CG2331; putative ATPase activity: CG2331 ortholog
RNAi-pMON78424:002	Dv.10_CG6141; putative ribosomal protein L9: CG6141 ortholog
RNAi-pMON78425:001	Dv.11_CG2746
RNAi-pMON78444:001	Dv.12_CG1341; putative proteasome regulatory particle, rpt1: CG1341 ortholog
RNAi-pMON78416:002	Dv.13_CG11276; putative ribosomal protein S4: CG11276 ortholog
RNAi-pMON78434:001	Dv.14_CG17927_2; putative myosin heavy chain: CG17927 ortholog
RNAi-pMON78435:001	Dv.18_CG1404; putative RAN small monomeric GTPase: CG1404 ortholog
RNAi-pMON78449:001	Dv.19_CG18174; putative proteasome regulatory particle, lid subcomplex, rpn11: CG18174 ortholog
RNAi-pMON78440:001	Dv.20_CG3180; putative DNA-directed RNA polymerase II: CG3180 ortholog
RNAi-pMON78420:001	Dv.21_CG3320; putative Rab1: CG3320 ortholog
RNAi-pMON78410:001	Dv.22_CG3395; putative Ribosomal protein S9: CG3395 ortholog
RNAi-pMON78422:001	Dv.23_CG7269; putative helicase: CG7269 ortholog
RNAi-pMON78414:006	DV.26 sec1 ~ 5' half of EST

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(continued)

	Vector	Sequence Expressed as dsRNA
5	RNAi-pMON78414:001	Dv.26_CG9261; putative sodium/potassium-exchanging ATPase: CG9261 ortholog
	RNAi-pMON97122:001	C1_Dv.35; putative Vha68-2: CG3762 ortholog; concatamer
	RNAi-pMON97127:001	C2_Dv.35; putative Vha68-2: CG3762 ortholog; concatamer
10	RNAi-pMON97125:001	C3_Dv.35; putative Vha68-2: CG3762 ortholog; concatamer
	RNAi-pMON78427:001	Dv.35_CG3762; putative Vha68-2: CG3762 ortholog.
	RNAi-pMON97114:001	Dv.41_CG2637; Female sterile Ketel; involved in protein-nucleus import: CG2637 ortholog
15	RNAi-pMON97140:001	Dv.44_CG1244; Putative nucleic acid binding activity: CG1244 ortholog
	RNAi-pMON78429:001	Dv.46_CG10689; putative RNA helicase:CG10689 ortholog.
20	RNAi-pMON78428:001	Dv.49_CG8055_1; putative binding, carrier activity: CG8055_1 ortholog
	RNAi-pMON78428:003	Dv.49_CG8055_1; putative binding, carrier activity: CG8055_1 ortholog Free region selected from DV.49
25	RNAi-pMON78426:001	Dv.50_CG10110_1; putative Cleavage and polyadenylation specificity factor: CG10110_1 ortholog
	RNAi-pMON96185:001	Dv.55_CG5931; putative splicing factor activity, RNA helicase activity: CG5931 ortholog
	RNAi-pMON78431:001	Dv.58_CG1751; putative signal peptidase: CG1751 ortholog
30	RNAi-pMON96177:001	Dv.61_CG3725_1; putative Calcium ATPase: CG3725 ortholog
	RNAi-pMON96182:001	Dv.61_CG3725_2; putative Calcium ATPase: CG3725 ortholog
	RNAi-pMON96180:001	Dv.65_CG7033; putative chaperone activity: CG7033 ortholog
35	RNAi-pMON96176:001	Dv.66_CG32019; putative bent: CG32019 ortholog
	RNAi-pMON96170:001	Dv.67_CG16916; putative endopeptidase activity: CG16916 ortholog
	RNAi-pMON96166:001	Dv.70_CG5771; putative Rab-protein 11: CG5771 ortholog
40	RNAi-pMON96160:001	Dv.74_CG6375; putative pitchoune: CG6375 ortholog
	RNAi-pMON97137:001	Dv.77_CG4214; putative Syntaxin 5; involved in intracellular protein transport: CG4214 ortholog
	RNAi-pMON96167:001	Dv.82_CG8264; putative Bx42: CG8264 ortholog
45	RNAi-pMON96187:002	Dv.85_CG4494; putative protein binding activity: CG4494 ortholog
	RNAi-pMON97126:001	Dv.88_CG8756; function unknown; contains chitin binding domain: CG8756 ortholog
50	RNAi-pMON97130:001	Dv.93_CG8515; putative structural constituent of cuticle; contains
		chitin binding domain: CG8515 ortholog
	RNAi-pMON97111:001	Dv.105_CG1250_1; GTPase activator, involved in intracellular protein transport: CG1250 ortholog
55	RNAi-pMON97107:001	Dv.107_CG14813; COPI vesicle coat; involved in Golgi to ER intracellular protein transport: CG14813 ortholog

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(continued)

Vector	Sequence Expressed as dsRNA
RNAi-pMON97115:001	Dv.108_CG17248; n-synaptobrevin; involved in intracellular protein transport: CG17248 ortholog
RNAi-pMON97133:001	Dv.113; function unknown; WCR unique sequence
RNAi-pMON97121:001	Dv.122_CG3164; putative ATP-binding cassette transporter activity: CG3164 ortholog
RNAi-pMON97134:001	Dv.127; function unknown; no homology with human

Table 4: dsRNA Constructs Causing Significant Stunting Levels in Feeding Bioassays with Southern Corn Rootworm (SCR) Larvae

vector	Sequence Expressed as dsRNA
RNAi-pMON96172:001	Dv8_CG1088; putative vacuolar H ⁺ ATPase E subunit: CG1088 ortholog
RNAi-pMON96168:001	Dv9_CG2331; putative ATPase activity: CG2331 ortholog
RNAi-pMON78424:001	Dv.10_CG6141
RNAi-pMON96155:002	Dv.10_CG6141; putative ribosomal protein L9: CG6141 ortholog.
RNAi-pMON78425:001	Dv.11_CG2746
RNAi-pMON96158:002	Dv.11_CG2746; putative Ribosomal protein L19: CG2746 ortholog.
RNAi-pMON78416:001	Dv.13_Cog11276
RNAi-pMON78434:001	Dv.14_CG17927_2; putative myosin heavy chain: CG17927 ortholog
RNAi-pMON78435:001	Dv.18_CG1404; putative RAN small monomeric GTPase: CG1404 ortholog
RNAi-pMON78449:001	Dv.19_CG18174; putative proteasome regulatory particle, lid subcomplex, rpn11: CG18174 ortholog
RNAi-pMON78419:001	Dv.20_CG3180
RNAi-pMON78420:001	Dv.21_CG3320; putative Rab1: CG3320 ortholog
RNAi-pMON78414:001	Dv.26_CG9261; putative sodium/potassium-exchanging ATPase: CG9261 ortholog
RNAi-pMON97122:001	C1_Dv35; putative Vha68-2: CG3762 ortholog; concatamer
RNAi-pMON97125:001	C3_Dv35; putative Vha68-2: CG3762 ortholog; concatamer
RNAi-pMON78427:008	Dv.35_CG3762; putative Vha68-2: CG3762 ortholog.
RNAi-pMON78428:001	Dv.49_CG8055_1; putative binding, carrier activity: CG8055_1 ortholog
RNAi-pMON78442:001	Dv.57_CG2968; putative hydrogen-exporting ATPase: CG2968 ortholog
RNAi-pMON96177:001	Dv61_CG3725 1; putative Calcium ATPase: CG3725 ortholog
RNAi-pMON96166:001	Dv70_CG5771; putative Rab-protein 11: CG5771 ortholog
RNAi-pMON97126:001	Dv88_CG8756; function unknown; contains chitin binding domain: CG8756 ortholog

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(continued)

vector	Sequence Expressed as dsRNA
RNAi-pMON97111:001	Dv105_CG1250_1; GTPase activator, involved in intracellular protein transport: CG1250 ortholog
RNAi-pMON97112:001	Dv105_CG1250_2; GTPase activator, involved in intracellular protein transport: CG1250 ortholog
RNAi-pMON97107:001	Dv107_CG14813; COPI vesicle coat; involved in Golgi to ER intracellular protein transport: CG14813 ortholog
RNAi-pMON97121:001	Dv122_CG3164; putative ATP-binding cassette transporter activity: CG3164 ortholog

Table 5: dsRNA Constructs Causing Significant Mortality Levels in Feeding Bioassays with Southern Corn Rootworm (SCR) Larvae

Vector	Sequence Expressed as dsRNA
RNAi-pIC17546:003	LIB5462-091-A1-M1-G3 Dv1_CG6217 KNICKKOPF UNK
RNAi-pIC17504:055	V-ATPase subunit 2 sequence from <i>Diabrotica virgifera virgifera</i> Full EST sequence serving as positive control
RNAi-pMON96155:001	Dv.10_CG6141; putative ribosomal protein L9: CG6141 ortholog
RNAi-pMON96158:001	Dv.11_CG2746; putative Ribosomal protein L19: CG2746 ortholog
RNAi-pMON78416:001	Dv.13_CG11276
RNAi-pMON96154:003	Dv.14_CG17927; putative myosin heavy chain: CG17927 ortholog; cells grown in S Complete medium.
RNAi-pMON78438:001	Dv.17_CG10149; putative proteasome p44.5 subunit, rpn6: CG10149 ortholog
RNAi-pMON78449:001	Dv.19_CG18174; putative proteasome regulatory particle, lid subcomplex, rpn11:CG18174 ortholog
RNAi-pMON78440:001	Dv.20_CG3180; putative DNA-directed RNA polymerase II: CG3180 ortholog
RNAi-pMON96156:001	Dv.20_CG3180; putative RNA polymerase II 140kD subunit: CG3180 ortholog
RNAi-pMON78420:001	Dv.21_CG3320; putative Rab1: CG3320 ortholog
RNAi-pMON78427:006	Dv.35_CG3762; putative Vha68-2: CG3762 ortholog.
RNAi-pMON78428:001	Dv.49_CG8055_1; putative binding, carrier activity: CG8055_1 ortholog
RNAi-pMON96177:001	Dv61_CG3725_1; putative Calcium ATPase: CG3725 ortholog
RNAi-pMON96166:001	Dv70_CG5771; putative Rab-protein 11: CG5771 ortholog
RNAi-pMON96174:001	Dv86_CG5055; putative bazooka: CG5055 ortholog
RNAi-pMON97111:001	Dv105_CG1250_1; GTPase activator, involved in intracellular protein transport: CG1250 ortholog
RNAi-pMON97107:001	Dv107_CG14813; COPI vesicle coat; involved in Golgi to ER intracellular protein transport: CG14813 ortholog

EXAMPLE 4**Transgenic Plant Transformation and Bioassays**

[0176] Briefly, the sequence encoding a dsRNA construct as described above is linked at the 5' end to a sequence consisting of a 35S promoter operably linked to a maize hsp70 intron and at the 3' end to a Nos3' transcription termination and polyadenylation sequence. This expression cassette is placed downstream of a glyphosate selection cassette. These linked cassettes are then placed into an *Agrobacterium tumefaciens* plant transformation functional vector, used to transform maize tissue to glyphosate tolerance, and events selected and transferred to soil. R₀ plant roots are fed to western corn rootworm larvae (WCR, *Diabrotica virgifera*). Transgenic corn roots are handed-off in Petri dishes with MS0D 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.

[0177] Transgenic corn plants (R₀) 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.

EXAMPLE 5**Implementing Insect Pest Gene Suppression Using A ta-siRNA Mediated Silencing Method**

[0178] An alternative method to silence genes in a plant pest uses the recently discovered class of trans-acting small interfering RNA (ta-siRNA) (Dalmay *et al.*, 2000; Mourrain *et al.*, 2000; Peragine *et al.*, 2004; Vazquez *et al.*, 2004). ta-siRNA are derived from single strand RNA transcripts that are targeted by naturally occurring miRNA within the cell. Methods for using microRNA to trigger ta-siRNA for gene silencing in plants are described in US Provisional Patent Application Serial No. 60/643,136 (Carrington *et al.* 2004), incorporated herein by reference in its entirety. At least one pest specific miRNA expressed in gut epithelial cells of corn rootworm larvae is identified. This pest specific miRNA is then used to identify at least one target RNA transcript sequence complementary to the miRNA that is expressed in the cell. The corresponding target sequence is a short sequence of no more than 21 contiguous nucleotides that, when part of a RNA transcript and contacted by its corresponding miRNA in a cell type with a functional RNAi pathway, leads to slicer-mediated cleavage of said transcript. Once miRNA target sequences are identified, at least one miRNA target sequence is fused to a second sequence that corresponds to part of a pest gene that is to be silenced using this method. For example, the miRNA target sequence(s) is fused to any of SEQ ID NO:1 through SEQ ID NO:906, or a fragment thereof, such as a sequence of the corn rootworm vacuolar ATPase (V-ATPase) gene. The miRNA target sequence can be placed at the 5' end, the 3' end, or embedded in the middle of the target sequence. It may be preferable to use multiple miRNA target sequences corresponding to multiple miRNA genes, or use the same miRNA target sequence multiple times in the chimera of the miRNA target sequence and the target gene sequence. The target gene sequence can be of any length, with a minimum of 21 bp.

[0179] The chimera of the miRNA target sequence(s) and the target gene sequence is expressed in plant cells using any of a number of appropriate promoter and other transcription regulatory elements, as long as the transcription occurs in cell types subject to being provided in the diet of the pest, e.g. corn roots for control of corn rootworm.

[0180] This method may have the additional advantage of delivering longer RNA molecules to the target pest. Typically, dsRNAs produced in plants are rapidly processed by Dicer into short RNA's that may not be effective when fed exogenously to some pests. In this method, a single strand transcript is produced in the plant cell, taken up by the pest, and

converted into a dsRNA in the pest cell where it is then processed into ta-siRNA capable of post-transcriptionally silencing one or more genes in one or more target pests.

EXAMPLE 6

Method For Providing A DNA Sequence For dsRNA-Mediated Gene Silencing

[0181] This example illustrates a method for providing a DNA sequence for dsRNA-mediated gene silencing. More specifically, this example describes selection of an improved DNA useful in dsRNA-mediated gene silencing by (a) selecting from a target gene an initial DNA sequence including more than 21 contiguous nucleotides; (b) identifying at least one shorter DNA sequence derived from regions of the initial DNA sequence consisting of regions predicted to not generate undesirable polypeptides and not exhibiting identity with known sequences such as homologs/orthologs, and (c) selecting a DNA sequence for dsRNA-mediated gene silencing that includes the at least one shorter DNA sequence. Undesirable polypeptides include, but are not limited to, polypeptides homologous to allergenic polypeptides and polypeptides homologous to known polypeptide toxins.

[0182] WCR V-ATPase has been demonstrated to function in corn rootworm feeding assays to test dsRNA mediated silencing as a means of controlling larval growth. A cDNA sequence from a target gene, such as vacuolar ATPase gene (V-ATPase) from Western corn rootworm (WCR) (*Diabrotica virgifera virgifera* LeConte), is selected for use as an initial DNA sequence. This initial DNA sequence can be screened to identify regions within which every contiguous fragment including at least 21 nucleotides matches fewer than 21 out of 21 contiguous nucleotides of known vertebrate sequences. Sequence segments that are greater than about 100 contiguous nucleotides free of such 21/21 hits are identified. Thus criteria including segment length, GC content, sequence, predicted function based on sequence or function of a corresponding gene in a model organism, and predicted secondary structure (e.g. Elbashir, *et al.*, 2001b) may be used to select and design sequence(s) for use. Different combinations of these sequence segments are combined to construct chimeric DNA sequences for expression as dsRNA and use in insect feeding bioassays as described above.

EXAMPLE 7

Additional Results of Insect Feeding Bioassays with Sequences selected from EST Database

[0183] This example illustrates additional sequences found to be effective in causing larval stunting and/or mortality when ingested by rootworm larvae as double stranded RNA sequences. Methods for rearing corn rootworm larvae, application of dsRNA, and insect bioassays are as described in Examples 1-3. The results of the studies confirmed significant levels ($p < 0.05$) of larval stunting and/or mortality using dsRNAs containing portions of sequences homologous to a variety of different gene classes. The sequences and vectors yielding significant stunting and/or mortality and the corresponding SEQ ID NO for the sequence expressed as a dsRNA are given in Table 6 below. pMON98503, an exemplary binary vector used in corn transformation, contains the following elements between the right and left T-DNA borders for transfer into a plant cell: e35S - HSP70 - DV49 (antisense orientation) - universal spacer - DV49 (sense orientation) - hsp17; ACT (promoter and intron) - CTP2 transit signal - CP4 - NOS. pMON98504, another exemplary binary vector used in corn transformation, contains the following elements between the right and left borders: e35S - HSP70 - C1 (antisense orientation) - universal spacer - C1 (sense orientation) - hsp17; ACT (promoter and intron) - CTP2 transit signal - CP4 - NOS.

Table 6: Additional dsRNA Constructs Demonstrating Significant Stunting and/or Mortality Effect in Insect Feeding Bioassays with Southern Corn Rootworm or Western Corn Rootworm

Vector	Sequence Expressed as dsRNA	SEQ ID NO
pMON98356	Dv164; function unknown, WCR unique sequence	726
pMON98354	Dv172; function unknown, WCR unique sequence	727
pMON97191	Dv189; function unknown, WCR unique sequence	728
pMON98359	Dv200; function unknown, WCR unique sequence	729
pMON38880	Dv207_F39H11.5; putative pbs-7, endopeptidase: F39H11.5 ortholog	730
pMON101054	Dv208_F58F12_1; putative Mitochondrial F1F0-ATP synthase, subunit delta/ATP16: F58F12_1 ortholog	731

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(continued)

Vector	Sequence Expressed as dsRNA	SEQ ID NO
pMON98437	Dv210_K11H12_2; putative rpl-15, structural constituent of ribosome: K11H12_2 ortholog	732
pMON98435	Dv211_R12E2_3; putative rpn-8, translation initiation factor, 26S proteasome regulatory complex, subunit RPN8: R12E2_3 ortholog	733
pMON98447	Dv212_C17H12_14; putative vha-8, hydrogen-exporting ATPase: C17H12_14 ortholog	734
pMON98448	Dv213_B0464_1; putative drs-1, tRNA ligase: B0464_1 ortholog	735
pMON101059	Dv214_F53G12_10; putative rpl-7, structural constituent of ribosome: F53G12_10 ortholog	736
pMON98442	Dv216_C52E4_4; putative rpt-1, ATPase subunit of the 19S regulatory complex of the proteasome: C52E4_4 ortholog	737
pMON98441	Dv218_K01G5_4; putative ran-1, small monomeric GTPase: K01G5_4 ortholog	738
pMON98440	Dv219_C15H11_7; putative pas-1, endopeptidase: C15H11_7 ortholog	739
pMON101081	Dv223_R10E11.1; putative cbp-1, homolog of transcriptional cofactors CBP and p300: R10E11.1 ortholog	740
pMON101050	Dv224_F11C3_3; putative unc-54, ATP binding; motor activity: F11C3_3 ortholog	741
pMON101051	Dv225_C37H5_8; putative hsp-6, heat shock protein 6: C37H5_8 ortholog	742
pMON38888	Dv226_C47D12.5; putative uba-1, ubiquitin activating enzyme: C47E12.5 ortholog	743
pMON38887	Dv227_F54A3.3; putative Chaperonin complex component, TCP-1 gamma subunit: F54A3.3 ortholog	744
pMON101110	Dv229_D1081.8; putative Myb-like DNA binding: D1081.8 ortholog	745
pMON101052	Dv230_F55A11_2; putative syn-3, protein transporter; syntaxin: F55A11_2 ortholog	746
pMON101107	Dv231_C30C11.1; putative mitochondrial ribosomal protein L32: C30C11.1 ortholog	747
pMON101055	Dv232_B0250_1; putative rpl-2, structural constituent of ribosome: B0250_1 ortholog	748
pMON98446	Dv233_F54C9_5; putative rpl-5, 5S rRNA binding, structural constituent of ribosome: F54C9_5 ortholog	749
pMON101139	Dv235_C04F12.4; putative rpl-14, large ribosomal subunit L14 protein: C04F12.4 ortholog	750
pMON98449	Dv236_C01G8_5; putative erm-1, Ezrin/Radixin/Moesin (ERM) family of cytoskeletal linkers: C01G8_5 ortholog	751
pMON98439	Dv237_F57B9_10; putative rpn-6, proteasome Regulatory Particle, Non-ATPase-like: F57B9_10 ortholog	752
pMON98436	Dv240_F53A3_3; putative rps-22, structural constituent of ribosome: F53A3_3 ortholog	753

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(continued)

Vector	Sequence Expressed as dsRNA	SEQ ID NO
pMON101078	Dv241_F32H2.5; putative alcohol dehydrogenase, zinc-dependent: F32H2.5 ortholog	754
pMON101058	Dv242_B0336_2; putative arf-1, small monomeric GTPase: B0336_2 ortholog	755
pMON101057	Dv244_C14B9_7; putative rpl-21, structural constituent of ribosome: C14B9_7 ortholog	756
pMON98444	Dv245_C26F1_4; putative rps-30, Ribosomal Protein, Small subunit: C26F1_4 ortholog	757
pMON98434	Dv247_C13B9_3; putative delta subunit of the coatomer (COPI) complex: C13B9_3 ortholog	758
pMON101053	Dv248_F38E11_5; putative vesicle coat complex COPI, beta' subunit: F38E11_5 ortholog	759
pMON98445	Dv249_F37C12_9; putative rps-14, structural constituent of ribosome: F37C12_9 ortholog	760
pMON101056	Dv250_CD4_6; putative pas-6, endopeptidase: CD4_6 ortholog	761
pMON101104	Dv251_D1007.12; putative rpl-24.1, structural constituent of ribosome: D1007.12 ortholog	762
pMON101088	Dv252_C49H3.11; putative rps-2, structural constituent of ribosome: C49H3.11 ortholog	763
pMON101079	Dv253_C26D10.2; putative hel-1, ATP-dependent RNA helicase: C26D10.2 ortholog	764
pMON101085	Dv254_B0336.10; putative rpl-23, structural constituent of ribosome: B0336.10 ortholog	765
pMON38879	Dv255_C36A4.2; putative member of Cytochrome P450 family: C36A4.2 ortholog	766
pMON101087	Dv256_K05C4.1; putative pbs-5, proteasome beta subunit: K05C4.1 ortholog	767
pMON101082	Dv257_F29G9.5; putative rpt-2, 26S proteasome regulatory complex: F29G9.5 ortholog	768
pMON101084	Dv258_F40F8.10; putative rps-9, structural constituent of ribosome: F40F8.10 ortholog	769
pMON101083	Dv259_K07D4.3; putative rpn-11, 26S proteasome regulatory complex, subunit RPN11: K07D4.3 ortholog	770
pMON101080	Dv260_F49C12.8; putative rpn-7, proteasome Regulatory Particle, Non-ATPase-like: F49C12.8 ortholog	771
pMON101115	Dv261_D1054.2; putative pas-2, endopeptidase: D1054.2 ortholog	772
pMON101141	Dv263_F55A3.3; putative metalloexopeptidase: F55A3.3 ortholog	773
pMON101126	Dv264_F56F3.5; putative rps-1, structural constituent of ribosome: F56F3.5 ortholog	774
pMON101133	Dv266_C09D4.5; putative rpl-19, structural constituent of ribosome: C09D4.5 ortholog	775
pMON38881	Dv268_R06A4.9; putative Polyadenylation factor I complex, subunit PFS2: R06A4.9 ortholog	776

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(continued)

Vector	Sequence Expressed as dsRNA	SEQ ID NO
pMON101135	Dv271_F37C12.4;putative rpl-36, structural constituent of ribosome:F37C12.4 ortholog	777
pMON101132	Dv273_F54E7.2;putative rps-12, structural constituent of ribosome: F54E7.2 ortholog	778
pMON101139	Dv274_C23G10.4 ;putative rpn-2, proteasome Regulatory Particle, Non-ATPase-like: C23G10.4 ortholog	779
pMON101130	Dv275_C03D6.8;putative rp1-24.2, structural constituent of ribosome: C03D6.8 ortholog	780
pMON101119	Dv276_C26E6.4;putative DNA-directed RNA polymerase: C26E6.4 ortholog	781
pMON101134	Dv277_R13A5.8 ;putative rpl-9, structural constituent of ribosome: R13A5.8 ortholog	782
pMON101127	Dv279_F42C5.8;putative rps-8, structural constituent of ribosome: F42C5.8 ortholog	783
pMON101122	Dv280_F13B10.2;putative rpl-3, large ribosomal subunit L3: F13B10.2 ortholog	784
pMON101116	Dv281_T05C12.7;putative cct-1, Chaperonin complex component, TCP-1 alpha subunit: T05C12.7 ortholog	785
pMON101125	Dv282_F07D10.1;putative rpl-11.2, structural constituent of ribosome: F07D10.1 ortholog	786
pMON38883	Dv283_T05H4.6;putative Peptide chain release factor 1 (eRF1): Dv283_T05H4.6 ortholog	787
pMON101124	Dv284_C47E8.5;putative daf-21, Heat shock 90 protein, chaperone activity: C47E8.5 ortholog	788
pMON101120	Dv285_M03F4.2;putative act-4, actin: M03F4.2 ortholog	789
pMON101137	Dv286_F25H5.4;putative eft-2, translation elongation factor: F25H5.4 ortholog	790
pMON101140	Dv287_F26D10.3;putative hsp-1, Heat shock protein: F26D10.3 ortholog	791
pMON101117	Dv288_F28D1.7;putative rps-23, structural constituent of ribosome: F28D1.7 ortholog	792
pMON38886	Dv290_CG11979;putative H-exporting ATPase: CG11979 ortholog	793
pMON38885	Dv291_CG13628;putative H-exporting ATPase: CG13628 ortholog	794
pMON101103	Dv293_CG31237;putative DNA-directed RNA polymerase II: CG31237 ortholog	795
pMON101096	Dv294_CG8669;putative cryptocephal; transcription factor, involved in molting cycle, pupariation and metamorphosis: CG8669 ortholog	796
pMON101095	Dv295_CG8048;putative Vacuolar H ⁺ ATPase 44kD C subunit: CG8048 ortholog	797
pMON101100	Dv298_CG9032;putative H-exporting ATPase: CG9032 ortholog	798
pMON101111	Dv299_CG17369;putative H-exporting ATPase: CG17369 ortholog	799
pMON101129	Dv303_CG4152;putative ATP-dependent RNA helicase: CG4152 ortholog	800

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(continued)

Vector	Sequence Expressed as dsRNA	SEQ ID NO
pMON101136	Dv305_CG4916;putative ATP-dependent RNA helicase: CG4919 ortholog	801
pMON101131	Dv315_CG9160;putative NADH dehydrogenase: CG9160 ortholog	802
pMON101123	Dv316_CG8764;putative ubiquinol-cytochrome-c reductase: CG8764 ortholog	803
pMON98364	C4_Dv49_CG8055 concatemer; putative binding, carrier activity: CG8055 ortholog	804
pMON98365	C5_Dv49_CG8055 concatemer; putative binding, carrier activity: CG8055 ortholog.	805
pMON98368	C6 concatemer of highly effective WCR targets, ~50% GC criterion, consisting of segments in order 5'-3' from Dv26, Dv49, Dv23, Dv20, Dv13, Dv22, Dv18	806
pMON98369	C7 concatemer of insect-specific targets, ~50% GC criterion, consisting of segments in order 5'-3' from Dv6, Dv1, Dv88, Dv93, Dv4, Dv9113, Dv127, Dv99	807
pMON98372	C8 concatemer; putative sodium/potassium-exchanging ATPase: CG9261 ortholog	808
pMON98373	C9 concatemer; putative sodium/potassium-exchanging ATPase: CG9261 ortholog	809
pMON98366	C10 concatemer of genes with putative same/different mode of action, ~50% GC criterion	810
pMON98367	C12 concatemer of highly effective WCR targets, ~50% GC criterion, consisting of segments in order 5'-3' from Dv23-Dv13-Dv26-Dv18-Dv49-Dv22-Dv20.	811
pMON98371	C14 concatemer of gene targets active in several different organisms, ~50% GC criterion	812
pMON98503	Comprising DV49 putative ESCRT-III (endosomal sorting complex required for transport III) complex subunit from <i>Diabrotica virgifera</i>	820
pMON98504	Comprising putative Vha68-2: CG3762 ortholog; 250bp concatamer C1;	821
pMON102862	Dv319_CG14750;putative ESCRTII, Vps25: CG14750 ortholog	835
pMON102863	Dv320_CG9712;putative ESCRTI, Vps23: CG9712 ortholog	836
pMON102861	Dv321_CG12770;putative ESCRTI, Vps28: CG12770 ortholog	837
pMON102865	Dv322_CG14542;putative ESCRT III, Vps2: CG14542 ortholog	838
pMON102866	Dv323_CG4071;putative ESCRT III, Vsp20: CG4071 ortholog	839
pMON102871	Dv326_CG3564;putative protein carrier, component of the COPI vesicle coat: CG3564 ortholog	840
pMON102873	Dv327_CG6223;putative coatomer, component of the COPI vesicle coat: CG6223 ortholog	841
pMON102877	Dv328_CG6948;putative Clathrin light chain, coat of coated pit: CG6948 ortholog	842
pMON102872	Dv330_CG9543;putative COPI vesicle coat: CG9543 ortholog	843
pMON102879	Dv331_CG5183;putative KDEL sequence binding:CG5183 ortholog	844

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(continued)

Vector	Sequence Expressed as dsRNA	SEQ ID NO
pMON102867	Dv335_F11C1.6;putative nhr-25, DNA binding: F11C1.6 ortholog	845
pMON102870	Dv337_CG18734;putative furin 2, serine-type endopeptidase: CG18734 ortholog	846
pMON102875	Dv329_CG7961;putative coatomer, component of the COPI vesicle coat: CG7961 ortholog	874

[0184] Efficacy tests were conducted as follows, utilizing progeny of corn plants transformed with selected insect control constructs:

1. Seven days post planting: incubate 10,000 WCR eggs per event (10 plants per event) at 25° C, 60%RH in complete darkness for seven days.
2. Fourteen days post infestation: plants are transplanted from 4"peat pots to 8" pots; v4 root tip samples may be taken for gene expression studies.
3. Fourteen days post planting: wash the WCR eggs out of the soil. Place the eggs and soil into a 60-mesh screen and place a 30-mesh screen on top of the 60 -mesh screen to protect the eggs from the water stream. Rinse thoroughly with warm water using a spray nozzle until the soil is removed.
4. Suspend the eggs in a 2% (w/v) Difco agar solution, 25 mL of solution per 1 mL of eggs. The eggs are infested into the soil in about 3 or 4 aliquots using, for example, an Eppendorf repeater pipette, about 1000 eggs per plant. Holes are made into the soil using a spatula prior to infestation and covered after infestation.
5. Twenty-eight days post planting v8 root tip samples may be taken for gene expression studies.
6. Thirty-five days post planting; the assay is evaluated. Plants are cut down using pruning sheers, leaving about 6" of stalk. Plant stakes containing the event information are hole-punched and zip tied to the stalk. As much soil as possible is removed from the root system. The remainder of the soil is washed off using a spray hose.
7. The roots are examined and given a root damage rating by using the Olsen (0-3) NIS scale for WCR larvae damage.

[0185] FIG. 1 and FIG. 2 illustrate insect control results obtained following challenge of F1 corn plants (derived from plants transformed with either pMON98503 or pMON98504) with WCR. In growth chamber efficacy tests performed essentially as described above, NIS scores at or below the economic injury threshold were seen in progeny of events derived by transformation with pMON98503 or pMON98504.

[0186] Full length EST DNA sequences were assembled for selected genes described in Examples 3 and 7 displaying significant activity versus Western Corn Rootworm. These EST sequences are listed in Table 7:

Table 7: Assembled EST Sequences for WCR Targets

Assembled Sequence	SEQ ID NO
Dv9 full length (aka Apple); putative ortholog of CG2331	813
Dv10 full length (Rp19); putative ortholog of CG6141	814
Dv11 full length (Rp119); putative ortholog of CG2746	815
Dv13 full length (Rps4); putative ortholog of CG11276	816
Dv35 full length v-ATPase A; ortholog of CG3762	817
Dv49 full length ortholog of CG8055	818
Dv248 full length putative ortholog of CG6699	819

EXAMPLE 8

Creation and Efficacy Results for Dv49 and Dv248 sequences

[0187] Portions of the assembled EST and adjacent sequences of Dv49 (SEQ ID NO:818) and Dv248 (SEQ ID NO:819) were selected for further bioactivity assays based on criteria including predicted function, phenotype of knockout mutants of corresponding coding regions in other organisms, segment length, GC content, similarity to known sequences, and

predicted secondary structure (e.g. Elbashir, *et al.*, 2001b). The respective Dv49 and Dv248 sequences were synthesized *in vitro* based on their predicted activity against WCR individually, as well as grouped as shown in FIGs. 3-4, and Table 8, and applied to WCR larvae.

Table 8: Dv49 and Dv248 Fragments Assessed for Efficacy Against WCR

Fragment	SEQ ID NO
F1	822
F2	823
F3	824
F4	825
F5	826
F6	827
F7	828
F8	829
F9	830
F10	831
F11	832
F12	833
F13	834

[0188] Fragments F1- F3 correspond to portions of the full length Dv49 transcript. Fragments F4- F6 correspond to portions of the Dv248 transcript or flanking region. Fragments F7- F13 are concatemers of two or more of fragments F1- F6, as shown in FIG. 4. Fragment F13 (SEQ ID NO:834) represents the C38 (Dv49-Dv248) concatemer.

[0189] Dose Response data for F1- F13 is shown in FIGs. 5-7. As shown in FIG. 5, activity (larval % mortality) of fragments F4-F6, comprising Dv248-derived sequences (FIG. 4), was significantly better than the control when fed to WCR larvae at 0.1 ppm. Fragment F6 displayed significant activity when fed at 0.02 ppm as well. Activity of fragment F5 at the lowest dose is likely an artifact, since surviving larvae displayed no stunting.

[0190] As shown in FIG. 6, each of fragments F7- F10 displays statistically significant activity when fed to WCR larvae at 0.1 ppm. Fragments F9 and F10 also displayed statistically significant activity when fed to WCR larvae at 0.02 ppm, and fragment F10 displayed statistically significant activity when fed to WCR larvae at 0.01 ppm as well. Activity of F8 at 0.01 ppm may be an artifact.

[0191] As shown in FIG. 7, fragments F11- F13 display statistically significant activity when fed to WCR larvae at 0.02 ppm or higher. Additionally, the largest fragments (F12 and F13) show activity at 0.005 ppm and higher.

EXAMPLE 9

Additional Active Concatemer Sequences Derived from Concatemer C6

[0192] As shown in Table 9, portions of active concatemer C6 (SEQ ID NO:806), derived from pMON98368, were identified in diet overlay bioassays (performed as described e.g. in Example 2) as inhibiting the growth and/or survival of corn rootworm (WCR). The C6 full length concatemer contains 7 target subfragments of 70bp each, as noted in Table 6 and Table 9.

Table 9 Efficacy of full length C6 concatemer and selected sub-portions in rootworm diet bioassay (SEQ ID NOs:806, 847-873).

Concatemer	Segments	% Mortality at 1 ppm	SEQ ID NO
C6_full length	Dv26-Dv49-Dv23-Dv20-Dv13-Dv22-Dv18	100	806
C6.1	Dv26-Dv49	35.3	847

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(continued)

Concatemer	Segments	% Mortality at 1 ppm	SEQ ID NO
C6.2	Dv26-Dv49-Dv23	57.1	848
C6.3	Dv26-Dv49-Dv23-Dv20	84.7	849
C6.4	Dv26-Dv49-Dv23-Dv20-Dv13	51	850
C6.5	Dv26-Dv49-Dv23-Dv20-Dv13-Dv22	41.3	851
C6.6	Dv49-Dv23	94.6	852
C6.7	Dv49-Dv23-Dv20	75.6	853
C6.8	Dv49-Dv23-Dv20-Dv13	50	854
C6.9	Dv49-Dv23-Dv20-Dv13-Dv22	56.4	855
C6.10	Dv49-Dv23-Dv20-Dv13-Dv22-Dv 18	52.5	856
C6.11	Dv23-Dv20	74.6	857
C6.12	Dv23-Dv20-Dv13	63.4	858
C6.13	Dv23-Dv20-Dv13-Dv22	58.5	859
C6.14	Dv23-Dv20-Dv13-Dv22-Dv18	60.8	860
C6.15	Dv20-Dv13	57.5	861
C6.16	Dv20-Dv13-Dv22	20	862
C6.17	Dv20-Dv13-Dv22-Dv18	44.8	863
C6.18	Dv13-Dv22	71.1	864
C6.19	Dv13-Dv22-Dv18	52.5	865
C6.20	Dv22-Dv18	44.6	866
C6.28	Dv26	58.9	867
C6.29	Dv49	72.3	868
C6.30	Dv23	71.9	869
C6.31	Dv20	62.6	870
C6.32	Dv13	54.2	871
C6.33	Dv22	56.7	872
C6.34	Dv18	44.6	873

[0193] Full length concatemer C7 contains 8 target sub-fragments of 70 bp each, as noted in Table 6. Similarly, full length concatemer C12 contains 7 target sub-fragments from Dv23-Dv13-Dv26-Dv18-Dv49-Dv22-Dv20, ranging in length between 53-80 bp, as noted in Table 6 and Table 10.

Table 10 Composition of full length C12 concatemer and selected sub-portions (SEQ ID NOs:811, 887-892).

Concatemer	Segments	Included sequence (SEQ ID NO) in 5'-3' direction
C12_full length	Dv23-Dv13-Dv26-Dv18-Dv49-Dv22-Dv20	811
C12.1	Dv23-Dv13	887
C12.2	Dv23-Dv13-Dv26	888
C12.3	Dv23-Dv13-Dv26-Dv18	889
C12.4	Dv23-Dv13-Dv26-Dv18-Dv49	890

(continued)

Concatemer	Segments	Included sequence (SEQ ID NO) in 5'-3' direction
C12.5	Dv23-Dv13-Dv26-Dv18-Dv49-Dv22	891
C12.6	Dv13-Dv26	892
C12.7	Dv13-Dv26-Dv18	893
C12.8	Dv13-Dv26-Dv18-Dv49	894
C12.9	Dv13-Dv26-Dv18-Dv49-Dv22	895
C12.10	Dv13-Dv26-Dv18-Dv49-Dv22-Dv20	896
CC12.11	Dv26-Dv18	897
C12.12	Dv26-Dv18-Dv49	898
C12.13	Dv26-Dv18-Dv49-Dv22	899
C12.14	Dv26-Dv18-Dv49-Dv22-Dv20	900
C12.15	Dv18-Dv49	901
C12.16	Dv18-Dv49-Dv22	902
C12.17	Dv18-Dv49-Dv22-Dv20	903
C12.18	Dv49-Dv22	904
C12.19	Dv49-Dv22-Dv20	905
C12.20	Dv22-Dv20	906

[0194] Table 11 lists additional sequences for use in targeting other coleopteran pests, including *Diabrotica* sp. and other *Coccinellidae* and *Chrysomelidae*.

Table 11: Additional Coleopteran Target Sequences

Sequence and source	SEQ ID NO
Dbar248_CG6699 (<i>D. barberi</i>)	875
Dbal248_CG6699 (<i>D. balteata</i>)	876
Du248_CG6699 (<i>D. undecimpunctata howardi</i>)	877
Dz248_CG6699 (<i>D. virgifera zea</i>)	878
Dv248_CG6699 (<i>D. virgifera virgifera</i>)	879
Ev248_CG6699 (<i>Epilachna varivestis</i>)	880
Ld248_CG6699 (<i>Leptinotarsa decemlineata</i>)	881
Dbal49_CG8055_2 (<i>D. balteata</i>)	882
Db49_CG8055_2 (<i>D. barberi</i>)	883
Du49_CG8055_2 (<i>D. undecimpunctata howardi</i>)	884
Dz49_CG8055_2 (<i>D. virgifera zea</i>)	885
Dv49_CG8055_2 (<i>D. virgifera virgifera</i>)	886

References**[0195]**

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- 4,735,015; 4,759,945; 4,876,197; 4,880,734; 4,886,937; 4,959,317; 5,080,925; 5,107,065; 5,107,787; 5,231,020;
5,283,184; 5,300,127; 5,302,523; 5,328,942; 5,384,253; 5,389,399; 5,464,765; 5,501,967; 5,527,695; 5,538,877;
5,538,880; 5,550,318; 5,554,445; 5,563,055; 5,580,544; 5,591,616; 5,593,874; 5,622,003; 5,633,435; 5,661,103;
5,698,425; 5,712,135; 5,759,829; 5,780,708; 5,789,214; 5,791,084; 5,804,693; 5,834,447; 5,837,848; 5,849,320;
5,876,739; 5,882,713; 5,891,246; 5,918,413; 5,939,356; 6,118,047; 6,326,193; 6,489,542 and 6,506,559.
U.S. Patent Applic. Ser. Nos.: 10/205,189; 10/465,800 and 60/643,136.
U.S. Patent Publn. Nos.: 2002/0048814; 2002/0048814; 2003/0018993; 2003/0061626; 2003/0150017;
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SEQUENCE LISTING

[0196]

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<213> *Diabrotica virgifera*

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<210> 34

<211> 733

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<213> *Diabrotica virgifera*

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45 <210> 37
 <211> 25
 <212> DNA
 <213> *Diabrotica virgifera*

<400> 37
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50 <210> 38
 <211> 672
 <212> DNA
 <213> *Diabrotica virgifera*

55 <400> 38

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20
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 <213> Diabrotica virgifera

50
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 <211> 34
 <212> DNA
 <213> Diabrotica virgifera

<400> 41
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<210> 42
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 <212> DNA
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 <213> *Diabrotica virgifera*

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<210> 45

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<211> 33
<212> DNA
<213> *Diabrotica virgifera*

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<210> 46
<211> 790
10 <212> DNA
<213> *Diabrotica virgifera*

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45

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55

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25

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 <211> 34
 <212> DNA
 <213> Diabrotica virgifera

30

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35

<210> 49
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 <212> DNA
 <213> Diabrotica virgifera

40

<400> 49
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45

<210> 50
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50

<400> 50

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<400> 54

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<400> 56
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45 <210> 57
 <211> 27
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50 <400> 57
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55 <210> 58
 <211> 564
 <212> DNA
 <213> *Diabrotica virgifera*

<400> 58

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<210> 59

<211> 1156

<212> DNA

<213> Diabrotica virgifera

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<212> DNA

<213> Diabrotica virgifera

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<210> 61

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<212> DNA

<213> Diabrotica virgifera

<400> 61

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<210> 62

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<211> 677
 <212> DNA
 <213> *Diabrotica virgifera*

5 <400> 62

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 15 gggccgtgca agagacgggtg gtctacgttt cgggtgagatg gaacgagatt gtcaaatttc 480
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 <211> 1156
 <212> DNA
 <213> *Diabrotica virgifera*

25

<400> 63

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 40 cgagacttat ggtactgtag tgtttttaag taaataaata aatgtcctta tctaagagga 780
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 <212> DNA
 <213> *Diabrotica virgifera*

<400> 64

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<210> 65
 <211> 27

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<212> DNA

<213> Diabrotica virgifera

<400> 65

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<210> 66

<211> 677

<212> DNA

10 <213> Diabrotica virgifera

<400> 66

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cggatgatgct acacctttca acgatgcccgt caacgtacag aaaatctcca ctttggttaca 240

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25 atgtaagggt tgcaaaaata agacacagat atcgcaagtt agactgcctt atgctgcgaa 660
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<210> 67

<211> 919

30 <212> DNA

<213> Diabrotica virgifera

<400> 67

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<210> 68

<211> 27

<212> DNA

<213> Diabrotica virgifera

55

<400> 68

caaactctg ctgattggag attcagg 27

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<210> 69
<211> 25
<212> DNA
<213> *Diabrotica virgifera*

5

<400> 69
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<210> 70
<211> 521
<212> DNA
<213> *Diabrotica virgifera*

15

<400> 70

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25

aacctcagct	aagaatgcaa	ccaatgtaga	acaggccttt	atgactatgg	ccgctgaaat	480
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<210> 71
<211> 755
<212> DNA
<213> *Diabrotica virgifera*

<400> 71

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<210> 72
<211> 31
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<213> *Diabrotica virgifera*

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<210> 73
<211> 21

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<212> DNA

<213> Diabrotica virgifera

<400> 73

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<210> 74

<211> 490

<212> DNA

10 <213> Diabrotica virgifera

<400> 74

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<210> 75

25 <211> 857

<212> DNA

<213> Diabrotica virgifera

<220>

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<222> (818)

<223> n = a, c, g or t/u

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 45 aattgcccgc atatcgttgt ggggtactcca ggaagaattt tagcattgggt cagatcgaaa 600
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 50 caacattatg taaaact 857

<210> 76

<211> 34

<212> DNA

55 <213> Diabrotica virgifera

<400> 76

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<210> 77
<211> 32
<212> DNA
<213> *Diabrotica virgifera*

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<400> 77
cttgaacatc acgtctcatg tctaataact cc 32

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<210> 78
<211> 627
<212> DNA
<213> *Diabrotica virgifera*

15

<400> 78

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25

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<210> 79
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<212> DNA
<213> *Diabrotica virgifera*

<400> 79

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40

45

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<213> *Diabrotica virgifera*

<400> 80
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<210> 81
<211> 30
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5

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10

<210> 82
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<213> *Diabrotica virgifera*

15

<400> 82

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<223> n = a, c, g or t/u

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<400> 83

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<210> 84

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<211> 25
<212> DNA
<213> *Diabrotica virgifera*

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<210> 85
<211> 26
10 <212> DNA
<213> *Diabrotica virgifera*

<400> 85
15 cgtgcttctc caatttctga gccaaag 26

<210> 86
<211> 686
<212> DNA
20 <213> *Diabrotica virgifera*

<400> 86

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35 <210> 87
<211> 999
<212> DNA
<213> *Diabrotica virgifera*

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<222> (743)..(827)
<223> n = a, c, g or t/u

45 <400> 87

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55

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      <213> Diabrotica virgifera

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      <212> DNA
      <213> Diabrotica virgifera

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30 <213> Diabrotica virgifera

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35 <210> 93

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<212> DNA

<213> *Diabrotica virgifera*

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<211> 25

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<212> DNA

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<211> 441

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45 <210> 100
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<213> Diabrotica virgifera

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<210> 101

55 <211> 32

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<212> DNA

50 <213> *Diabrotica virgifera*

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<211> 27

<212> DNA

<213> *Diabrotica virgifera*

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<210> 106
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<400> 106

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<400> 107

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<210> 113

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<211> 27
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<210> 114
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<211> 29

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<212> DNA

<213> Diabrotica virgifera

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<213> Diabrotica virgifera

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<210> 121

<211> 28

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<213> *Diabrotica virgifera*

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<210> 122

<211> 542

<212> DNA

10 <213> *Diabrotica virgifera*

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<222> (1772)

<223> n = a, c, g or t/u

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      gttcatgttt agaggacttc agggccacac cgttcatcga atgtaacggt gctcaaggat 1920
40      catgtcacta ttctgccaac acccttagtt tctggctcgc gaccatcgac aacaaccaac 1980
      aattccagaa acctcagaaa cagacactca aagc                                     2014

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<210> 128

<211> 24

<212> DNA

<213> *Diabrotica virgifera*

<400> 128

gtgaacaagg agcaccagga atgg 24

<210> 129

<211> 24

<212> DNA

<213> *Diabrotica virgifera*

<400> 129

ccaggcggtc catogtaacc tctg 24

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<210> 130
 <211> 838
 <212> DNA
 <213> *Diabrotica virgifera*

5

<400> 130

ccaggcggttc catcgtaacc tctgtctcct ttttctcccg gatagcctga gattccttgc 60

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aatcctgttt gtccacgata tcccttttgt cccggagctc cgaaagcacc ggggttacct 120
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 ccggttggtc cttgtggtcc tggagctcca tcaaaacctc gatctccctt ctgcccttga 240
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 ggttcaccaa tttgccctgg ggtgccaggt ataccttctc ttccgttttt gccaggtatt 360
 ccaggcaaac ctttctcccc cttgattgtc aacctgggta atccagctac cccagaaaga 420
 cctcgttcac ctttagctcc tggacgccct gggctaccaa gatttccttt aacaccaggg 480
 aaacctacat cccctttctc tccctcgtag ccaatagctc cagagaatcc acggtctcct 540
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 tgcaccaacg gaccggagg acctgtttct cctacgtcac ctttttctcc tgggttcgccg 660
 aagggtccgg tggaaacctg tgggcctctt tcaccttttt gtccttcata tccatcaaga 720
 cctgacaaac ctcggtctcc tttctctcct gtaaaaccgg gcgtcctgc aaatcctcta 780
 tcaccttttt ctccattggt tcctggaaaa ccgtccattc ctggtgctcc ttgttcac 838

25

<210> 131
 <211> 771
 <212> DNA
 <213> *Diabrotica virgifera*

30

<400> 131

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 ctttttataa actgtgattt aatggatggt cgagatgcat tcctaacact cgcccgtaga 180
 aaacattatg aattctcttc tttaagaagg gccaaatata gtactttgtc tatgttatat 240
 gaattgcata atcaagggtc agataaattt gtatatactt gtaatagttg taaagcccat 300
 gtggaaacaa ggtatcattg tactgtgtgt gaagactttg acttgtgcat ccaatgttat 360
 gagaaagaag gtcacctca caaatggag aaacttggat tggatattga tgatggaagt 420
 tcacctagtg atagcaaagc caatccagga gaagctagaa aattatctat acagcgttgt 480
 atccattctt tggtagatgc ttgtcaatgc agagatgcca attgtcgggt accaagctgt 540
 cagaagatga aacgagtcac aaatcacacc aaattgtgca agaggaaaac aaatgggtgg 600
 tgccctatth gcaacaact catcgctcta tgttgctatc atgccaaca ctgccagaa 660
 aacaagtgtc ctgtaccatt ctgttcatgc ataaagcaca aactaaaaca acaacaattg 720
 caacaaaggt tgcaacaggt gcaactactt agtataagaa tggtagttat g 771

45

<210> 132
 <211> 22
 <212> DNA
 <213> *Diabrotica virgifera*

50

<400> 132
 gattcctaa cactgccc tg 22

55

<210> 133
 <211> 27
 <212> DNA
 <213> *Diabrotica virgifera*

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<400> 133
ggacacttgt ttctgggca gtgttg 27

<210> 134
<211> 515
<212> DNA
<213> Diabrotica virgifera

<400> 134

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gcattcctaa cactcgcccg tgaaaaacat tatgaattct cttctttaag aagggccaaa 60
tatagtactt tgtctatggt atataaattg cataatcaag gtcaagataa atttgtatat 120
acttgtaata gttgtaaagc ccatgtggaa acaaggatc attgtactgt gtgtgaagac 180
tttgacttgt gcatccaatg ttatgagaaa gaaggatc ctcacaaaat ggagaaactt 240
ggattggata ttgatgatgg aagttcacct agtgatagca aagccaatcc aggagaagct 300

agaaaattat ctatacagcg ttgtatccat tctttggtag atgcttgtca atgcagagat 360
gccaattgtc ggttaccaag ctgtcagaag atgaaacgag tcacaaatca caccaaattg 420
tgcaagagga aaacaaatgg tggttgccct atttgcaaac aactcatcgc tctatgttgc 480
tatcatgcc aacactgccc agaaaacaag tgtcc 515
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<210> 135
<211> 1120
<212> DNA
<213> Diabrotica virgifera

<400> 135

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gatggaagta cggacggaat aatattaaat aaaagtgcaa agaaacgtaa caaaaataaa 120
aagaaaaaga atgaaaaacca agaagaaaac agtgaccaa gcaacgaggt tgtccaagcc 180
gaaaacaact tattatctaa cttatcgaac cctattaata caatatcaat taaggagcta 240
aaagcagcca tggaggtatt tactctatca caaaaacctg ccaagagttc agaggaagct 300
ctaaagaaga cattccagtt ttggaatacc cagcctgttc ccaaaatgga cgaaaaaata 360
actgttaacg aagccattga accagacaaa gaacctgctg acattagaca agaaccgtac 420
agtttgccctg atggttttat gtgggacact cttaatctag atgaaccgtt ggtgctcaa 480
gagttatata cgttactcaa tgaaaactat gttgaagatg acgattgtat gtttagattt 540
gattatcaac ctgaattttt gaaatgggct ttgcaacccc cagggtggaa gcgagaatgg 600
cattgtggag tcagagttgt aaaaagtggg agattagtgg gatttatctc tgcaattcca 660
gcaactctaa acatttataa aaagacacaa agaatggtgg agataaattt tctatgtgta 720
cataaaaagc tacgttccaa acgagtcgca ccagtgttga ttcgagaaat caccgcaga 780
gtacacctga acggcctatt tcaagcagtg tacaccgccg gcatagtcct accgaaacca 840
gtgagtactt gtacctactg gcatcgatcg ctgaatccga aaaaattaat cgaggtgaag 900
ttttctcatt tgtctcgtaa tatgacgctg caacggactc tcaagttgta caaactgccg 960
gacaagccta agactccggg atttagaaaa atgacagccg aagatatacc tcaagctcac 1020
aaattactag tagagtattt aagtcgattc gacctagcgc catattttta cgaagaagag 1080
ttcacacatt ggttcctacc tagaacgaac ataatcgaca 1120
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<210> 136
<211> 24
<212> DNA
<213> Diabrotica virgifera

<400> 136
gtgaccaaag caacgaggt gtcc 24

<210> 137
<211> 31
<212> DNA

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<213> Diabrotica virgifera

<400> 137

gtagggtacaa gtactcactg gtttcggtag g 31

<210> 138

<211> 707

<212> DNA

<213> Diabrotica virgifera

<400> 138

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aaaaacctgc caagagttca gaggaagctc taaagaagac attccagttt tgggaataccc 180
agcctgttcc caaaatggac gaaaaaataa ctgttaacga agccattgaa ccagacaaag 240
aacctgctga cattagacaa gaaccgtaca gtttgccctga tgggttttatg tgggacactc 300
ttaatctaga tgaaccgttg gtgctcaaag agttatatac gttactcaat gaaaactatg 360
ttgaagatga cgattgtatg tttagatttg attatcaacc tgaatttttg aaatgggctt 420
tgcaaccccc aggggtggaag cgagaatggc attgtggagt ccgagttgta aaaagtggta 480

gattagtggg atttatctct gcaattccag caactctaaa catttataaa aagacacaaa 540
gaatgggtgga gataaatttt ctatgtgtac ataaaaagct acgttcctaaa cgagtcgcac 600
cagtgttgat tgcagaaatc acccgagag tacacctgaa cggcctcttt caagcagtg 660
acaccgccgg tatagtccta ccgaaaccag tgagtacttg tacctac 707

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<210> 139

<211> 940

<212> DNA

<213> Diabrotica virgifera

<400> 139

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gtgagtcgtg agtgaatcgt atcgtatcgt ggtatcgtat ccggtccggt tagctaagaa 120
tgtgtcaaac aggggaagttt tttaaattgtt aatttagaag ttaatttttt gattaagtta 180
tacctaagtg cgaaattttc aaaaatgggc caacacgtat ctagaacaga tttcgaatgg 240
gtatataccg aggaacctca cgtagccgc aggaagcaaa tcttagaaaa atatcccaa 300
atcaagaaac tctttggata cgatccgaac ttcaaattggg tcgtaacgag catgggtactt 360
acacaattcg tacttctgta cttactcaaa gataggtcat ggccagtgtt aatttttagta 420
gcgatattgt taggaggtgt catcaatcac tcgttaatgt tggctatata tgaaatttcc 480
cacaattttg cgtttggaca cgcacggccg ttgcacaata aattattttg attttttgcc 540
aatttgccaa taggattacc gattactata agcttttaaaa aataccactt ggaacaccac 600
agatatcaag gtgacgaaca gaaagatacg gacatcccaa cgtacataga ggccaaacta 660
ttttgcacga cttttggaaa attcattttg gtgatactgc aaccgttttt ctactctttc 720
cgccactcg tagtttatcc gaagccgcct acgctttttg aattcgtaaa cctggtaatt 780
caactcgcct tcgatgctct cgttgtttat tttttcggag gaagaatgtt gggatatctc 840
cttattggat ctgtcatggc tatgggtctt catccggtag cgggacactt catcagtga 900
cattacatgt tcaaaaaggg ctacgaaacg tacagctact 940

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<210> 140

<211> 34

<212> DNA

<213> Diabrotica virgifera

<400> 140

gtcaggttg tcaattcagt attcagaata gtag 34

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<210> 141
<211> 27
<212> DNA
<213> *Diabrotica virgifera*

5

<400> 141
ggataaacta cgagtgggag gaaagag 27

10

<210> 142
<211> 746
<212> DNA
<213> *Diabrotica virgifera*

15

<400> 142

20

25

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taagaatgtg tcaaacaggg aagtttttaa attgttaatt tagaagttaa ttttttgatt 180
aagttatacc taagtgcgaa attttcaaaa atggggccaa acgtatctag aacagatttc 240
gaatgggtat ataccgagga acctcacgct agccgcagga agcaaactct agaaaaatat 300
ccccaaatca agaaactctt tggatacgat ccgaacttca aatgggtcgt aacgagcatg 360
gtacttacac aattcgtact tctgtactta ctcaaagata ggtcatggcc agtgctaatt 420
ttagtagcgt attgcttagg aggtgtcatc aatcactcgt taatgttggc tatacatgaa 480
atttcccaca atttggcggt tggacacgca cggccgttgc acaataaatt atttggattt 540
tttgccaatt tgccaatagg attaccgatt actataagct ttaaaaaata ccacttggaa 600
caccacagat atcaaggtga cgaacagaaa gatacggaca tcccaacgta catagaggcc 660
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30

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aaactatatt gcacgacctt tggaaaattc atttgggtga tactgcaacc gtttttctac 720
tctttccgcc cactcgtagt ttatcc 746
```

35

<210> 143
<211> 1049
<212> DNA
<213> *Diabrotica virgifera*

<400> 143

40

45

50

55

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gccagcgcgt ctcatagata agattgaaaa gaaagtccga gagcacaaca gaaaactcaa 120
gaaagaaaat aagaacaacc ctaaaaagaa aaaggaaata atgcaaacc caaacatatg 180
tcttttttaa gaggacattc ttaaagaagt agaagcacta aagaaacaaa aggaagaaga 240
aaaacttaag ctaagagaag ctgcaaaatt ggaaaggcaa aaggagaaaag aggaaagtta 300
aaaagagaaa cttactgcag gacttcaggg attagtgcga aatgctgaac taaggagtta 360
acttcatgaa catttaacac cagataataa tgtaaaacag cacgagacaa ataatgagca 420
gtccctgaaa caatattaca aagagtttaa gaaggttatc gaagctgcag atgttattct 480
agaagtagtt gacgctagag atccttttag gactagatgt aagcaagtag agcaggctgt 540
gttagatata aaaggtaata aaagactagt cttagtatta aacaaggcag acttagttcc 600
tagagaaaatt ttggatcaat ggctaaaagta cttgaagaaa accactccca ctatagcatt 660
caaagcatca actcaaaatc aaagtaaaaa gttaggacag agaaagcttg gaaagggaaa 720
taaggatttg cagagttcaa attctgtagg agcagaattg ttaatgtctc tgctagcaaa 780
ctattgtagg aacaagggtta tcaaaacttc tataagagtt ggaattgtag gtttgcctaa 840
tgtaggaaaa agttcaatta ttaacagctt aaaaaggctc agagcttgta atgttgggtgc 900
aacacctggt gttactaggg caatgcagga agtacaatta gactcaaaga taaaactttt 960
ggattctcct ggtatagttt ttgcatctgg aaatgacagt agtgcttctt tgagaaatgc 1020
agttcgaatt tctgccttga gtgatcctg 1049
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<210> 144

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<211> 35
<212> DNA
<213> Diabrotica virgifera

5 <400> 144
gtctcagata taagattgaa aagaaagtcc gagag 35

<210> 145
<211> 30
10 <212> DNA
<213> Diabrotica virgifera

<400> 145
gcttgaatg ctatagtggg agtggtttc 30

<210> 146
<211> 598
<212> DNA
20 <213> Diabrotica virgifera

<400> 146

25	ttctcagata	taagattgaa	aagaaagtcc	gagagcacia	cagaaaactc	aagaaagaaa	60
	ataagaacaa	ccctaaaaag	aaaaaggaaa	taatacaaat	cccaaacata	tgtcctttta	120
	aagaggacat	tcttaaagaa	gtagaagcac	taaagaaaca	aaaggaagaa	gaaaaactta	180
	agctaagaga	agctgcaaaa	ttggaaaggc	aaaaggagaa	agaggaaagt	aaaaaagaga	240
	aacttactgc	agaacttcag	ggattagtgc	aaaatgctga	actaaggagt	aaacttcacg	300
	aacatctaac	accagataat	aatgtaaaac	agcacgagac	aaataatgag	cagtccctga	360
	aacaatatta	caaagagttt	aagaaggtta	togaagctgc	agatgttatt	ctagaagtag	420
30	ttgacgctag	agatccttta	gggactagat	gtaagcaagt	agagcaggct	gtgttagata	480
	caaaaggtaa	taaaagacta	gtcttagtat	taaacaaggc	agacttagtt	cctagggaaa	540
	ttttggatca	atggctaaag	tacttgaaga	aaaccactcc	cactatagca	ttcaaagc	598

<210> 147
35 <211> 889
<212> DNA
<213> Diabrotica virgifera

<400> 147

45	gtaaaatagt	ttcaaaatgc	atcaggaggc	catacaactc	atccaggtgc	tagaaaaaac	60
	agtttcaccg	gataaaaatg	aattggaaca	agcgtcatcg	tttctcgaac	aagctgcagt	120
	gactaaccta	ctagaattca	tcaaaaactct	atcagatata	ttaagacatg	gcggaaatag	180
	ccctgtggcc	cgaatggccg	cagggtttgca	gttaaaaaat	caactcacct	ctaaagactc	240
	caacataaag	accacctacc	aacaacggtg	gttggctttc	ccagaggacg	ttcgggggta	300
	tattaaaaat	aacgttgtgt	gcgcacttgg	aaccgaaaca	agcagaccat	catccgcagc	360
	tcagtgcgta	gcatacgtcg	cagtaacaga	actaccacaa	gggcaatggc	cagatctcat	420
	agcaacggtg	gtcaacaatg	tttgccatgc	aaattccaca	gaaatgcaaa	aggaagccac	480
	attagaagct	atcgggtata	tatgccaaaga	aatcgactcg	gacgtattag	tatctcaacc	540
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	tcgttttagca	gctacacagg	ccctattaaa	ctctctagaa	ttcaciaaagg	ccaactttga	660
	ccaaccgacg	gaacggaact	atatcatgga	agtcgtctgt	gaagccacgc	agtctccaga	720
	ttcacagatc	agagtggccg	ctttgcagtg	tctagttaag	attatgtctt	tgtattatca	780
	acacatggaa	ccttatatgg	ctcctgctct	attccctatc	actctagaag	ccatgaagtc	840
55	ggaaaaacga	tgctgtttct	ctacagggta	togaattctg	gtctaactgt		889

<210> 148
<211> 26

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<212> DNA

<213> *Diabrotica virgifera*

<400> 148

5 gccatacaac tcattccaggt gctaga 26

<210> 149

<211> 31

<212> DNA

10 <213> *Diabrotica virgifera*

<400> 149

gtgataggga atagagcagg agccatataa g 31

<210> 150

<211> 792

<212> DNA

<213> *Diabrotica virgifera*

<400> 150

25 gccatacaat tcattccagtg ctagaaaaaa cagtttcacc ggataaaaaat gaatggaaca 60
agcgtcatcg tttctcgaac aagctgcagt gactaaccta ctagaattca tcaaaactct 120
atcagatata ttaagacatg gcggaaatag ccctgtggcc cgaatggccg cagggtttgca 180
gttaaaaaaat caactcacct ctaaagactc caacataaag accacctacc aacaacgggtg 240
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aaccgaaaca agcagaccat catccgcagc tcagtgcgtg gcatacgtcg cagtaacaga 360
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aaattccaca gaaatgcaaa aggaagccac attagaagct atcggttata tatgccaaga 480
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agtcgtctgt gaagccacgc agtctccaga ttcacagatc agagtggccg ctttgcaagt 720
tctagttaag attatgtctt tgtattatca acacatggaa ccttatatgg ctccctgctct 780
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<210> 151

<211> 685

<212> DNA

40 <213> *Diabrotica virgifera*

<400> 151

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ctgatagagc tataaatatg gcctgcaaga ctggaagatg ggtcatgctg aagaacgtac 120
acttggtccc tcaatgggta gtccagctgg agaagaagct tcattcactt caacctcacg 180
ccaacttttag actattcctc accatggaaa ttaatccgaa actaccagtt aatcttctta 240
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cattcaacac agttccagtc agtaggatga tgaaagcacc aaacgaaaca gcaagacttt 360
50 acttcttatt ggcgtgggtc cacgcgattg tccaggagag gttgatatat tgccctctag 420
gttgagcaaa acattatgaa tttagtgaat catattttaag agtcgcctgc gatactttgg 480
atacttggtat tgataccacg gctatgggaa tgactaactt gccggcagag aaactctcat 540
gtgacaccct agccactctg ctctcgcaat ccatctatgg tggtaaaatc gataacgatt 600
ccgatcaacg actgttacat tccttcctga atctgctttt tactcccata agctttgaaa 660
55 gcgacttttcg cttcaagtcc aacat 685

<210> 152

<211> 23

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<212> DNA
<213> *Diabrotica virgifera*

<400> 152
ggatcatgcc gaagcgattc aac 23

<210> 153
<211> 27
<212> DNA
<213> *Diabrotica virgifera*

<400> 153
gaatgtaaca gtcgttgatc ggaatcg 27

<210> 154
<211> 588
<212> DNA
<213> *Diabrotica virgifera*

<400> 154

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gaagcttcat	tcacttcaac	ctcacgccaa	ctttagacta	ttcctcacca	tggaaattaa	180
tccgaaacta	ccagttaatc	ttcttagagc	aggaagaata	tttgtattcg	aacctccacc	240
gggtattaga	gctaacctct	tgagaacatt	cagcacagtt	ccagccagta	ggatgatgaa	300
agcaccaaac	gaaagagcaa	gactttactt	cttattggcg	tggttccacg	cgattgtcca	360
ggagagggttg	agatattgcc	ctctagggttg	ggcaaaacat	tatgaattta	gtgaatcaga	420
tttaagagtt	gcctgtgata	ctttgggatac	ttggattgat	acaacggcta	tgggaaggac	480
gaacttgccg	ccagagaaaag	tcccatggga	cgccttagtc	actctgctct	cgcaatccat	540
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<210> 155
<211> 946
<212> DNA
<213> *Diabrotica virgifera*

<220>
<221> modified_base
<222> (802)..(849)
<223> n = a, c, g or t/u

<400> 155

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	taaatatgtt	gctaatatgc	atggggatga	agccatagga	agacagttga	tgattttacct	180
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	tagagatttt	ccagatcagt	ttgatgctac	aaaagcagga	acaattctgt	ctggtaggca	420
	gcctgaaacg	atagctatga	tgacttggat	tattttccaga	ccatttgttt	tatctggaaa	480
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10	atgctgtgta	gagagtagat	caccagataa	taatattttc	aaaacgtag	cattaaacta	600
	cgctcaatcg	aatcctgtga	tgaaaaaggg	taatgcttgt	aaagacgata	catttgatca	660
	gggcatcaca	aatgggtgctt	tttgggtatga	agtgagaggt	ggcatgcaag	acttcaacta	720
	cgttcactcc	aactgtttcg	aagtaacttt	tgaactgagt	tgctgtaaat	ttccgtagc	780
	caaaactcta	cctcaggaat	gngcaacaac	aaggaagccc	tactaacttt	catggagtca	840
15	acacattgng	gcgctaaggg	attgggttaga	aacgaaaacg	gtgacgccgt	tttggacgcc	900
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<210> 156

<211> 30

<212> DNA

<213> Diabrotica virgifera

<400> 156

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<210> 157

<211> 28

<212> DNA

<213> Diabrotica virgifera

<400> 157

gttggagtga acgtagttga agtcttgc 28

<210> 158

<211> 689

<212> DNA

<213> Diabrotica virgifera

<400> 158

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	tgtaaacacc	aatgttttaa	tatgttgcta	atatgcatgg	ggatgaagcc	ataggaagac	120
	agttgatgat	ttacctggct	ctctatttaa	ttcacaatta	tggcactaat	gataggggtga	180
	ccagattggg	taattcaact	gatatttatt	taatgccttc	aatgaaccct	gatgggttatg	240
45	aaaattcaga	agagggcaga	tgtgaatcta	aaaaacaata	tgttgggaaga	gaaaatgaaa	300
	atagtgttga	tttaaataga	gattttccag	atcagtttga	tgctacaaaa	gcaggaacaa	360
	ttctgtctgg	taggcagcct	gaaacgatag	ctatgatgac	ttggattatt	tccagaccat	420
	ttgttttatc	tggaaatttg	cacggaggtg	cagtagtagc	tagctatccg	tatgatgatt	480
	ctaactctgg	tcgaagatgc	tgtgtagaga	gtagatcacc	agataataat	attttcaaaa	540
50	cgtagcatt	aaactacgct	caatcgaatc	ctgtgatgaa	aaagggtaat	gcttgtaaag	600
	acgatacatt	tgatcagggc	atcacaaatg	gtgctttttg	gtatgaagtg	agaggtggca	660
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<210> 159

<211> 658

<212> DNA

<213> Diabrotica virgifera

<400> 159

5

10

20

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<213> Diabrotica virgifera

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25

<211> 28

<213> Diabrotica virgifera

30

gatacatcct ccaagaactc gttcgtca 28

35

<212> DNA

<213> Diabrotica virgifera

40

45

<211> 888

<213> Diabrotica virgifera

55

<221> modified base

$\langle 222 \rangle$ (771)

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<223> n = a, c, g or t/u

<400> 163

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      agagcaaagt tttgtagtca aaatggctgg agtattcgat ttagaactgc atgatgttga 180
      aactgtagaa gtagatgatt cagacgatgc aatcgaaatt gaagaggatg aatatgatca 240
      aaatcctaataa attaatgcaa ttgtagaatc cgatgataca gaaacgggttc atctgactga 300
10     acaaattgtg aatccggggcc aggaaaaaac cggaccccat gactttgaat tacgcaaagt 360
      cctgggcaaa ggaggttatg gcaaagtatt tcaagttaga aaaattacgg ggaaagatgc 420

      caatactgtc tttgccatga aggttctccg caaggcttcc atagttagaa atcaaaaaga 480
      tactgcccatacgcgaaagcag aacgaaatat tttagaagaa gtttaagcatc cttttatagt 540
15     ggatttgata tatgccttcc aaacgggtgg aaaattgtac ttaatttttag aatacctcag 600
      cgggggcgaa ctttttatgc atttagaaag agaaggaata ttttttagagg ataccgcttg 660
      cttttatttta tccgaaatca ttctcgccct agaacattta catggacaag gaattattta 720
      tagagatcta aagcctgaaa atattttact tgacgcccac ggtcacgtta nattgacaga 780
      tttcgggtctg tgtaaaaaca cattaacgaa ggcatattga cccacaccgt tttgtggaac 840
20     tattgaatat atggcacctg aaatttaact agacatggcc atggaaaa 888

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<210> 164

<211> 33

<212> DNA

25 <213> *Diabrotica virgifera*

<400> 164

gcatgatgtt gaaactgtag aagtagatga ttc 33

30 <210> 165

<211> 27

<212> DNA

<213> *Diabrotica virgifera*

35 <400> 165

gtgtgggtca atatgccttc gttaatg 27

<210> 166

<211> 658

40 <212> DNA

<213> *Diabrotica virgifera*

<400> 166

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      atctgactga acaaattgtg aacccggggcc aggaaaaaac cggaccccat gactttgaat 180
      tacgcaaagt cctgggcaaa ggaggttatg gcaaagtatt tcaagttaga aaaattacgg 240
      ggaaagatgc caatactgtc tttgccatga aggttctccg caaggcttcc atagttagaa 300
50     atcaaaaaga tactgcccatacgcgaaagcag aacgaaatat tttagaagaa gtttaagcatc 360
      cttttatagt ggatttgata tatgccttcc aaacgggtgg aaaattgtac ttaatttttag 420
      aatacctcag cgggggcgaa ctttttatgc atttagaaag agaaggaata ttttttagagg 480
      ataccgcttg cttttatttta tccgaaatca ttctcgccct agaacattta catggacaag 540
      gaattatttta tagagatcta aagcctgaaa atattttact tgacgcccac ggtcacgtta 600
55     aattgacaga tttcgggtctg tgtaaagaac acattaacga aggcattattg acccacac 658

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<210> 167

<211> 886

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<212> DNA

<213> Diabrotica virgifera

<220>

<221> modified_base

<222> (805)

<223> n = a, c, g or t/u

<400> 167

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ttcagatagt gtcgacagca ctgaagaagc tcgccgaaga gatctgaagg aaagagatga 180
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tgataagcgc gcttatgaag aggctgctaa aagacttaaa ttggacaatg cagaaaaaga 300
gaaacttatt cctgcactca gagttgcttc caggaggaag tatttggaga agagaaagga 360
ggacaaacta caagaattgg aagctgatat tgccgatgat gagtaccttt ttgaggaaga 420

tgttttgact gaaagagaga aaaaagatcg tgtacacaag aaagagctgt taaaattggc 480
gcaggaacat gaaaaggcca gggaacttga gcgggttcaa aggtatcaca tgcccagaga 540
tttgggcaag gactccactg ctgattacat tgaagttgat gacttggaga aggtaccaca 600
atctgaacag aagaaatggg aaaaagatca gatggcctcg gcagtgttta agtttggagc 660
aaaagatggg attaaaaaag aagagtatga gttagtgtta gaagatcaaa ttcagtttat 720
acaagcacta caaatgccag gagtgtctga taagaaagaa cccgaactaa cggaaacaga 780
aaagaaaaaa cttactatag aaganacaaa gaaaagcctt ccgatatacc ctttttaaaga 840
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<210> 168

<211> 31

<212> DNA

<213> Diabrotica virgifera

<400> 168

cgaccaagta caagtaagcg aaatgtctt g 31

<210> 169

<211> 31

<212> DNA

<213> Diabrotica virgifera

<400> 169

gttcttctt atcagacact cctggcattt g 31

<210> 170

<211> 679

<212> DNA

<213> Diabrotica virgifera

<400> 170

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cgcgatgaag aacgtactag aaacgtttgcc agtacttctg ataagcgcgc ttatgaagag 180
gctgctaaaa gacttaaatt ggacaatgca gaaaaagaga aacttattcc tgcactcaga 240
gttgcttcca ggaggaagta tttggagaag agaaaggagg acaaactaca agaattggaa 300
gctgatattg ccgatgatga gtaccttttt gaggaagatg ttttgactga aagagagaaa 360
aaagatcgtg tacacaagaa agagctgtta aaattggcgc aggaacatga aaaggccagg 420
gaacttgagc gggttcaaag gtatcacatg cccagagatt tgggcaagga ctccactgct 480
gattacattg aagttgatga cttggagaag gtaccacaat ctgaacagaa gaaatgggaa 540
aaagatcaga tggcctcggc agtgtttaag tttggagcaa aagatgggat taaaaagaa 600
gagtatgagt tagtgttaga agatcaaatt cagtttatac aagcactaca aatgccaggga 660
gtgtctgata agaaagaac
679

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<210> 171
<211> 910
<212> DNA
<213> Diabrotica virgifera

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<400> 171

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aaattcgtat gaccaaagac gaagaattca taagacagtt cgctacgtta gacgaagcgc 180
agaaggaaga gatgaagaga gagaagcgac ggatacagga gcaactgagg cggatcaaga 240
gaaaccaaga gaaggaaaag atgggaggtg ggcatacgca tatgcattcg acgcctatcg 300
taccgcctgc agggactgcg attgaaaagt tgccaaatcc aagtgactct ctttcgacac 360
ctgtttacacc aacttctagt aagagtatgt cctcgtctcc tcctaaatca aggaggaaaa 420
ccaaactcaa gccagatctc aaactcaagt gtggagcctg tggaaatgtc ggccatatga 480
gaacaaacaa agcctgccct ctttatcaag ccacaactgg tcagaaccgg cctattaacg 540
ttgccatgac tgaagaacaa gaagaagata tcgagaagca aattaatata gacgatgaag 600
atctcgtaaa cgtagatgga accaaagtta aattgtctgg aaagttgttg aagaattact 660

ttcagcatgc cgaggagatt aagcgtagga gcttaatgtt aaaagtcctt aaggacgctt 720
taggtaaccg aaaaagaaga agaggggtgc aagatttaca ttgtgattat ttgaagaaac 780
acaacaggcc agcgaataga agacgaacgg atccggttgt cgttttgtct actattttag 840
agaatatact caatgaaatg cgagatatgc cagacgtcca gccttttctt attccctgtc 900
aatcaaaaac
910

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<210> 172
<211> 27
<212> DNA
<213> Diabrotica virgifera

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<400> 172
cagaactttt aggaaccag aaggacg 27

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<210> 173
<211> 25
<212> DNA
<213> Diabrotica virgifera

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<400> 173
gatccgttcg tottctattc gctgg 25

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<210> 174
<211> 776
<212> DNA
<213> Diabrotica virgifera

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<400> 174

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	gttcgctacg	ttagacgaag	cgcagaagga	agagatgaag	agagagaagc	gacggatata	180
	ggagcaactg	aggcggatca	agagaaacca	agagaaggaa	aagatgggag	gtgggcatac	240
	gcatatgcat	tcgacgccta	tcgtaccgcc	tgcagggact	gcgattgaaa	agttgccaaa	300
	tccaagtgac	tctcttttcga	cacctgttac	accaacttct	agtaagagta	tgtcctcgtc	360
	tcctcctaaa	tcaaggagga	aaaccaaact	caagccagac	ctcaaactca	agtgtggagc	420
10	ctgtggaaat	gtcggccata	tgagaacaaa	caaagcctgc	cctctttatc	aagccacaac	480
	tggtcagaac	ccgcctatta	acgttgccat	gactgaagaa	caagaagaag	atatcgagaa	540
	gcaaattaat	acagacgatg	aagatctcgt	aaacgtagat	ggaaccaaag	ttaaattgtc	600
	tggaaagttg	ttgaagaatt	actttcagca	tgccgaggag	attaagcgca	ggagtttaac	660
	gttaaaaagtc	cctaaggacg	ctttaggtaa	ccgaaaaaga	agaagagggg	tgcaagattt	720
15	acattgtgat	tatttgaaga	agcacaatag	gccagcgaat	agaagacgaa	cggatc	776

<210> 175

<211> 365

<212> DNA

20 <213> Diabrotica virgifera

<400> 175

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	ggtctcattg	cctgtcacga	aaccttttgc	gacaatcaaa	aatgtacaga	aaacctcgtt	180
	tgcaaagatt	ctgaagttct	ggttcccaag	ggaaccattt	gcggatgttg	cgacgactgc	240
	tacagaaaac	taaatgaagg	cgatgcttgc	aggtcacggt	ttattggagg	aggtccattc	300
	agaggaaaat	gtgtagatgg	attagtatgt	aacgctgaag	gaaaatgcgc	caaagcctaa	360
30	attat						365

<210> 176

<211> 29

<212> DNA

35 <213> Diabrotica virgifera

<400> 176

cgttatcag gcagtagatg gtctcattg 29

40 <210> 177

<211> 30

<212> DNA

<213> Diabrotica virgifera

45 <400> 177

gcatttcct tcagcgttac atactaatcc 30

<210> 178

<211> 247

50 <212> DNA

<213> Diabrotica virgifera

<400> 178

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5 cgtttatcag gcagtagatg gtctcattgc ctgtcacgaa accttttgcg acaatcaaaa 60
 atgtacagaa aacctcgttt gcaaagattc tgaagttctg gttcccaagg gaaccatttg 120
 cggatggtgc gacgactgct acagaaaact aaatgaaggc gatgcttgca ggtcacgttt 180
 tattggagga ggtccattca gagggaaatg tgtagatgga ttagtatgta acgctgaagg 240
 aaaatgc 247

<210> 179

<211> 870

<212> DNA

10 <213> Diabrotica virgifera

<400> 179

15 acgcgtgggt tcgtatTTTT ttcttaacaa aagggcaaaa tgagctTTTT tggaaaattg 60
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 gagactgaag aaatgttaat aaaaaaacag gatttttttag aaaagaagat agaagaattt 180
 accatggtag caaagaaaaa tgcgtcgaaa aataaaagag ttgcactcca agccctcaaa 240
 aagaagaaac gattggaaaa gacccaacta caaatagatg gaacccttac aactattgaa 300
 atgcagaggg aagccctcga aggagctagc acaaatactg ctgtattaga ttctatgaaa 360
 aatgctgcag atgcccttaa gaaagctcat aagaatttga atgtagatga tgttcacgat 420
 atcatggatg acatagccga acaacacgac atagccaacg aaatcacaaa cgctattagc 480
 aatcctgtcg gattcaccga cgatctggat gacgatgaat tagaaaaaga attagaagag 540
 ctcgaacaag aaggattgga agaagacctg ctccaagtgc cagggtccaac tcaactgccg 600
 gctgtgcctg ctgatgcagt tgctactaaa ccaatcaaac cagcagctaa aaaagttgaa 660
 gatgatgacg atatgaaaga attggaagcc tgggcctcgt aaaattcctg aaatctggat 720
 atgtgtaaac gaaatcacc atctaagatg aaaacattat aaatatatag gtaataacag 780
 ctaaaaacgt ttcaatgtag aacaagcttt tgctgaaaag gcgtcttgca aaaaatgttg 840
 ataatttaga attctctata tattatatat 870

30 <210> 180

<211> 26

<212> DNA

<213> Diabrotica virgifera

35 <400> 180

gtcctgggga ggctattcaa aaactc 26

<210> 181

<211> 29

40 <212> DNA

<213> Diabrotica virgifera

<400> 181

caggctcca attcttcat atogtcac 29

45

<210> 182

<211> 601

<212> DNA

<213> Diabrotica virgifera

50

<400> 182

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ataaaagagt tgcactccaa gccctcaaaa agaagaaacg attggaaaag acccaactac 180
aaatagatgg aacccttaca actattgaaa tgcagaggga agccctcgaa ggagctagca 240
5 caaatactgc tgtattagat tctatgaaaa atgctgcaga tgcctttaag aaagctcata 300
agaatttgaa tgtagatgat gttcacgata tcatggatga catagccgaa caacacgaca 360
tagccaacga aatcacaaac gctattagca atcctgtcgg attcaccgac gatctggatg 420
acgatgaatt agaaaaagaa ttagaagagc tcgaacaaga aggattggaa gaagacctgc 480
tccaagtgcc aggtccaact caactgccgg ctgtgtctgc tgatgcagtt gctactaaac 540
10 caatcaaacc agcagctaaa aaagttgaag atgatgacga tatgaaagaa ttggaagcct 600
g 601

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<210> 183

<211> 860

<212> DNA

<213> *Diabrotica virgifera*

<220>

<221> modified_base

<222> (804)

<223> n = a, c, g or t/u

<400> 183

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atttttagtac caattttttg aaacctctga cttttctgtt agcgaaagggt ttaggaaatt 180
ccacactaac tccccatcga ttatagatct agcagggttg ttttgtagtt ttctccaact 240
tttaaagtgc ctgaaagcct tgggatttag gccggcaata tgagctcctt gggaaactaa 300
30 tacattttgc aacataagta aacggcgata tgttttctct ggaactggca taatgtatcc 360
tatacctcca tccaaagtag caaacattgt aataaacctt ctatctgctc cagaaaaatg 420
ctttttatca tcgcctagtt cacctagttt acatttaatt ttaaagaatg tgttgacagt 480
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ttctgggtga tacatatata tggctagatt ttgttctcca tctgatacta aaaatcctag 600
35 tgatgaatta tctatcatgt attctattga atatacttcg tttgggttga aatccctaga 660
taccattgac agtggttcggt actcttcttg aaaccttaac aacgcgatag atttgtagac 720
atcaccaacc aacagcaaac ttttgatagt aagtatttga tgagtataga cttgtgtatc 780
tataaatgct actccaataa atcngtatct ttgagttgcc aaatatatat cttttgtccc 840
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<210> 184

<211> 32

<212> DNA

<213> *Diabrotica virgifera*

<400> 184

ctctggaact ggcataatgt atcctatacc tc 32

<210> 185

<211> 31

<212> DNA

<213> *Diabrotica virgifera*

<400> 185

ctgttggttg gtgatgtcta caaatctatc g 31

<210> 186

<211> 399

EP 2 431 473 B1

<212> DNA

<213> *Diabrotica virgifera*

<400> 186

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      ccttctatct gctccagaaa aatgcttttt atcatcgccct agttcaccta gtttacattt 120
      aatttttaaag aatgtgttga cagtttggcc taaatggaaa tccgctttcc ttaatagtct 180
10     ttgacctcct aaagattctc ttgattctgg ttgatacata tacatggcta gattttgttc 240
      tccatctgat actaaaaatc ctagtgatga attatctatc atgtattcta ttgaatatac 300
      ttcgtttggg ttgaaatccc tagataccat tgacagtgtt cgggtactctt cttgaaacct 360
      taacaacgcg atagatttgt agacatcacc aaccaacag          399

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<210> 187

<211> 816

<212> DNA

<213> *Diabrotica virgifera*

<400> 187

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      tcggagacac tcaaagacag caacatgtac gtatacgggt tgcgacattac atagacgtgt 120
      aatatgcgtg cgagtgcctt atcacgggtga agttctggcg tgaacgggtg ctcggaggaa 180
25     tcatggcgtc ggtggcgggc tcgcaagaac agccgcccgc cgcgcacggc catagcttct 240
      gcaagaagac cttccacaag cccacctact gccaccactg cagcgacatg ttatggggcc 300
      tcatccagca gggcttcctc tgcgaagttt gcaacttcgt agtgcgatgat cgctgcttaa 360
      ggactgtggg atccccgtgt tccagcgtct ccgccagtca aataagaaat ccggttgcac 420
      actgttggtc ggagtcgttt caccataaaa gaaaattttg caacgtatgt agaaaacggg 480
30     tagatgacag cgaatccatt cattgcgaaa tttgtgagta tttcgtacat gtggagtgcc 540
      aggattttgc agtagctgac tgtaaagaaa atgcaactta tcttccggga aaacaactta 600
      ccttcgtgcg tcatcaacat cactggcgcg aaggaaatct tccaagcaat tccaagtgt 660
      gctctctgta aaaagacgtg ctggactact gaatgtttat cccggatata gatgcgaatg 720
      gtgggtgaatg acgagccatg cctcctgtcc tacgagtatt aatagtgaat ggactttttg 780
      gaattctgga acccattcat ctacccccgc aggctg          816

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<210> 188

<211> 26

<212> DNA

<213> *Diabrotica virgifera*

<400> 188

ccttaggcat gtaagtgtgg ctgtcg 26

<210> 189

<211> 23

<212> DNA

<213> *Diabrotica virgifera*

<400> 189

ctcgtaggac aggaggcatg gct 23

<210> 190

<211> 717

<212> DNA

<213> *Diabrotica virgifera*

<400> 190

ccttaggcat gtaagtgtgg ctgtcggaga tactcaaaga cagcaacatg tacgtatacg 60

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 gcgtgaacgg tggctcggag gaatcatggc gtccggtggcg ggctcgcaag aacagccgcc 180
 cgccgcgcac ggccatagct tctgcaagaa gaccttccac aagcccacct actgccacca 240
 ctgcagcgac atgttatggg gcctcatcca gcagggttc atctgcgaag tttgcaactt 300
 cgtagtgcac gatcgctgct taaggactgt ggtatccccg tgttccagcg tctccgccag 360
 10 tcaaataaga aatccggttg cacactgttg gtccgagtcg tttcaccata aaagaaaatt 420
 ttgcaacgta tgtagaaaac ggtagatga cagcgaatcc attcattgag aaatttgtga 480
 gtatttcgta catgtggagt gccaggattt tgcagtagct gactgtaaag aaaatgcaac 540
 ttatcttccg ggaaaacaac ttacctctcg gcgtcatcaa catcactggc gcgaaggaaa 600
 tcttccaagc aattccaagt gtgctctctg taaaagacg tgctggacta ctgaatgttt 660
 atccggatac agatgcgaat ggtgtggaat gacgagccat gcctcctgtc ctacgag 717

<210> 191

<211> 826

<212> DNA

<213> *Diabrotica virgifera*

<220>

<221> modified_base

<222> (752)

<223> n = a, c, g or t/u

<400> 191

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 gtcactagta ctagcatgat tcaaggaaat agtacgacgc ctacatctaa caccctggc 120
 acaggcgaga ataataatgg tgtaagaga attagtata atagaaggag taacaagcct 180
 attatggaga aaaggcggag ggcgaggata aataactgtc tcaatgagtt gaaaacgctc 240
 atattggacg ccatgaaaaa agatcctgcc agacattcaa agctggaaaa agctgacatc 300
 ctggagatga cagtcaagca ttacagaaac cttcaaagac agcaagtcgc tatgtcagcg 360
 35 gcagcagatc ccttagtagt taataaattc agagcagggg ttagcgagtg cgcttcagaa 420
 gtcggcagat ttccaggctc agatccaatc gtccgacgaa gggtactcca gcatctagcc 480
 aactgtctca gccaaaggctc caaaccacaa gaagttcctc aagtacaagt tcacatactt 540
 ccaaactc aaaaaccttt agaacagcaa gtaccccaaa gcagtggcat tattcttagt 600
 aacggtaacg gtactggagt tcaactagta ccaacaagac taccgaatgg agatttagct 660
 ctggtacttc ctacgacctt acaaacacag cccagttatt caccggcggc agtaccatta 720
 40 ttagtgccga tagtaccgga aagaaccgct tncaccacat cagcgaccag cagttactcg 780
 aattatttct ccagtcatag tccagagcct atggagtcta tgtaca 826

<210> 192

<211> 31

<212> DNA

<213> *Diabrotica virgifera*

<400> 192

gcagttttgt gatttaagaa gattacgatg g 31

<210> 193

<211> 30

<212> DNA

<213> *Diabrotica virgifera*

<400> 193

gctgtgtttg taaggctgta ggaagtacca 30

<210> 194
 <211> 679
 <212> DNA
 <213> *Diabrotica virgifera*

5

<400> 194

10

gcagttttgt gatttaagaa gattacgatg gttactacca cgaatgcggg cactagtact 60

15

20

agcatgattc aaggaaatag tacgacgcct acatctaaca cccctggcac aggcgagaat 120
 aataatggtg ttaagagaat tagtgataat agaaggagta acaagcctat tatggagaaa 180
 aggcggaggg cgaggataaa taactgtctc aatgagttga aaacgctcat atcggacgcc 240
 atgaaaaaag atcctgccag acattcaaag ctggaaaaag ctgacatcct ggagatgaca 300
 gtcaagcatt tacagaacct tcaaagacag caagtcgcta tgtcagcggc agcagatccc 360
 ttagtagtta ataacttcag agcagggttt agcagagtgcg cttcagaagt cggcagattt 420
 ccaggtctag atccaatcgt ccgacgaagg ttactccagc atctagccaa ctgtctcagc 480
 caaggttcca aaccacaaga agttcctcaa gtacaagttc acatacttcc aaacactcaa 540
 aaaccttttag aacagcaagt accccaaagc agtggcatta ttcttagtaa cggtaacggg 600
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 acgaccttac aaacacagc 679

25

<210> 195
 <211> 873
 <212> DNA
 <213> *Diabrotica virgifera*

30

<220>
 <221> modified_base
 <222> (709)..(772)
 <223> n = a, c, g or t/u

<400> 195

35

40

45

50

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 tacacttcaa gctgggttgc gtacgttaca tgaggctggg ccagaactga aacgcgccat 180
 ctcaggcaat ctatgatgaat taattgatga caatcccgaa ccaatgcatc gtagaaatca 240
 ttcactcttc ggaagtgtat ggtcttcaat gagacgaggt catactttca atagagcgaa 300
 atctctgaag ttaaattcaa cccaaatcaa aattacaccg gcttccagcg tcgactatct 360
 tccatacaat tctattaaga atgccgtcac agaagggatg aatcacatta cttccatgac 420
 gaaaaacggt caaaaccgtg ttagcgctag ttccctgaac aatcaggata actataagga 480
 tgaagaaatt cctctgaggt ctcttagtaa tctgcataat ggagatgaga agaataacta 540
 cacggctcatc gataaatctg gcttcctgca ccctaactac aagggttgag cagggtgaggc 600
 gaatgggtcac gtgggaccag agcgtcttag ccattcactg cctggcagtc cggccgaccg 660
 tagacttgct tccttcgaag tcgtaggctc tgccggaaagc ctggtaggnc gaatcctagc 720
 cgagcaaggc ttaggtaagt actgtgatca ggatttcgtg cgctacacct nncgaagaga 780
 tgcagaggca ttggatatga ctcaggagga aatggatcgc gcagcccacc agattctttt 840
 cacagagaaa cttatacatc atcctctgca gca 873

55

<210> 196
 <211> 25
 <212> DNA
 <213> *Diabrotica virgifera*

<400> 196
 cgacgaagtc accgtgggta aattc 25

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<210> 197
<211> 24
<212> DNA
<213> Diabrotica virgifera

5

<400> 197
cgaaggaagc aagtctacgg tcgg 24

10

<210> 198
<211> 677
<212> DNA
<213> Diabrotica virgifera

15

<400> 198

20

cgacgaagtc	accgtgggta	aattctacgc	gactttcctc	attcaggatt	acttcaggcg	60
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tacacttcaa	gctggggttc	gtacgttaca	tgatgctggt	ccagaactga	aacgcgccat	180
ctcaggcaat	ctagatgaat	taattgatga	caatcccga	ccaatgcac	gtagaaatca	240
ttcactcttc	ggaagtgtat	ggtcttcaat	gagacgaggt	catactttca	atagagcgaa	300
atctctgaag	ttaaattcaa	cccaaataca	aattacaccg	gcttccagcg	tcgactatct	360
tccatacaat	tctattaaga	atgccgtcac	agaagggatg	aatcacatta	cttccatgac	420
gaaaaacgtt	caaaaccgtg	ttagcgttag	ttccttgaac	aatcaggata	actataagga	480
tgaagaaatt	cctctgaggt	ctcttagtaa	tctgcataat	ggagatgaga	agaataacta	540
cacgggtcac	gataaatctg	gcttcctgca	ccctaactac	aagggtggag	cagggtgaggc	600
gaatgggtcac	gtgggaccag	agcgtcttag	ccattcactg	cctggcagtc	cggccgaccg	660
tagacttgct	tccttcg					677

25

<210> 199
<211> 418
<212> DNA
<213> Diabrotica virgifera

30

<400> 199

35

acggaaacac	agttacctgt	atcggtccga	catttgattt	tgcccagaga	aaacttccct	60
cctactgaat	tgctggactt	gcaaccgctg	cctattactg	ctttgagaaa	cgaacaattt	120
gagtctttat	acgccgataa	gtttccacag	tttaataccta	tacaaacaca	ggttttcaac	180
tcagtataca	atggagacga	caacatattc	ataggcgctc	ccacgggatc	aggaaagacc	240
acaatagcaa	aatttgccat	cctcagactc	ttcgattgaa	atcctgaagg	tcgatgtgtt	300
tatctagttc	ctaaggacgc	cctcgttgaa	ctgattttcg	ccgattggca	taataagttt	360
ggacaggcct	tggtcaaaga	agtgggtattg	ctgactggag	aaactgggtac	tgatctaa	418

40

<210> 200
<211> 29
<212> DNA
<213> Diabrotica virgifera

45

<400> 200
cacagttacc tgtatcggtc cgacatttg 29

50

<210> 201
<211> 31
<212> DNA
<213> Diabrotica virgifera

55

<400> 201
gatcagttacc agtttctcca gtcagcaata c 31

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<210> 202
<211> 408
<212> DNA
<213> *Diabrotica virgifera*

5

10

15

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cacagttacc tgtatcgttc cgacatttga ttttgcccga gaaaaacttc cctccgactg 60
aattgctgga cttgcaaccg ctgcctatta ctgctttgag aaacgaacaa tttgagtctt 120
tatacgccga taagtttcca cagtttaatc ctatacaaac acagggtttc aactcagtat 180
acaatggaga cgacaacata ttcataggcg ctcccacggg atcaggaaag accacaatag 240
cagaatttgc catcctcaga ctcttcgata gaaatcctga aggtcgatgt gtttatctag 300
ttcctaagga cgccctcgct gaactgattt tgcgcgattg gcataataag tttggacagg 360
ccttggcaaa gaaagtggta ttgctgactg gagaaactgg tactgatc 408

```

<210> 203
<211> 735
<212> DNA
<213> *Diabrotica virgifera*

20

25

30

35

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cactgtcatt cgtcattctc atacattttt tttgggtact ttgggttgta cttgggataa 60
aagacctttt tgtatttcca aatacattgt catataaatt aaaaaagaaa tggctgccat 120
cagatctatg tctcgcttcc ttattaatag atcacttcaa accactgcaa agaggacctt 180
tgccgaccaa atgaacttca catttgcagc tggaatcag gtttactata ctgcaacttc 240
agttaaacia gtagatgtac catctttctc tggtagcttt ggtatccttc ccgcccattg 300
accacactg gctgtgctaa aacctggagt agtcactgtt tacgaagatg gtggtaatgt 360
taagaaaatc tttgtttcca gtggtactgt caccatcaat gatgattcat cagttcagat 420
tcttgcgtga gaagcccacc cagtagaaaa cattgatgtc aatgcagcaa gagacatcct 480
taccaaagcc cagagccagt tatcatctgc aagtacagat gaggcgaaag ctgaagcctc 540
cattgctgtt gaagtgggag aagcgttagt caaagcggct gaataataat ttaatttttg 600
taattttatg taaatttaaa aaatttagtg ctcaatggta ctgttcattt taaaacaaca 660
acatattaga tctatacctc tatgagttga caatttttac aaaaacgaga atcaatccaa 720
atacataatt tttgt 735

```

<210> 204
<211> 31
<212> DNA
<213> *Diabrotica virgifera*

40

45

```

<400> 204
ggtactttgg gttgtacttg ggataaaaga c 31

```

<210> 205
<211> 27
<212> DNA
<213> *Diabrotica virgifera*

50

55

```

<400> 205
gcttgacta acgcttctcc cacttca 27

```

<210> 206
<211> 542
<212> DNA
<213> *Diabrotica virgifera*

<400> 206

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5 ggtacttttg gttgtacttg ggataaaaga cttttttgta tttccaaata cattgtcata 60
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 cttcaaacca ctgcaaagag gacctatgcc gaccaaatga acttcacatt tgcagctgga 180
 aatcagggtt actatactgc aacttcagtt aaacaagtag atgtgccatc tttctctggt 240
 agctttggta tcctccccgc ccatgtaccc acactggctg tgctaaaacc tggagtagtc 300
 actgtttacg aagatggttg taatgttaag aaaatctttg tttccagtgg tactgtcacc 360
 atcaatgatg attcatcagt tcagattctt gctgaagaag cccaccagat agaaaacatt 420
 gatgtcaatg cagcaagaga catccttacc aaagcccaga gccagttatc atctgcaagt 480
 10 acagatgagg cgaaagctga agcctccatt gccgttgaag tgggagaagc gttagtcaaa 540
 gc 542

<210> 207

<211> 686

<212> DNA

15 <213> *Diabrotica virgifera*

<400> 207

20 tatatttaaat aattaatata gattttttaag tatggcacca aaggaaaaag atgatgaaat 60
 cgtatcaata aataaatggg atggagtagc cgtcaaaaat gcattagatg atgcagttaa 120
 agaggtagctt acaaagaaat acaattatgc tgaaaatttt gctctcatgg atggtaggtt 180
 gatttatatgt ggcatagctg taggtgttgc aatgtttgac ttgatttggg attatttgta 240
 cccattccca caatctaagc ctattttaat attttctgtt actacatatt tttttatgat 300
 25 gggaatttta actttatata ctacatacaa agagaaagga atctttgctg tttgtattca 360
 gaaagatagt tctaagaagg aaaatacttg ggaagctagc tcttatattc aaaagtatga 420
 tgataagtat actttgaatc ttgcatatat tgatggaaaa acacgcaaaa gaagagagca 480
 agtattataa aggagtattg ccagggtacat agaccagcaa ggaactgtag ttaaagaaaa 540
 tggtgaagat gaaatcacca aaatgcacaa ttctctacta agtgagagga aagaaaaaatg 600
 30 atgtacacag agactaccta ctaaaagaag ttgacgtgta aattatttca ttttttatat 660
 ttttcaataa gtttttttgg tttgag 686

<210> 208

<211> 28

35 <212> DNA

<213> *Diabrotica virgifera*

<400> 208

gtatggcacc aaaggaaaaa gatgatga 28

40

<210> 209

<211> 30

<212> DNA

<213> *Diabrotica virgifera*

45

<400> 209

cattttggtg attcatctt caacatttc 30

<210> 210

50 <211> 536

<212> DNA

<213> *Diabrotica virgifera*

<400> 210

55

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gtatggcacc aaaggaaaaa gatgatgaaa tcgtatcaat aaataaatgg gatggagtgg 60
 ccgtcaaaaaa tgcattagat gatgcagtta aagagggtact taaaaagaaa tacaattatg 120
 ctgaaaaattt tgctctcatg gatggtaggt tagttatatg tggcatagct gtaggtgttg 180
 caatgtttgc cttgatttgg gattatttgt acccattccc acaatctaag cctattttaa 240
 5 tattttctgt tactacatat ttttttatga tgggaatttt aactttatat actacataca 300
 aagagaaaagg aatctttgct gtttgtattc agaaagatag ttctaagaag gaaaatactt 360
 gggaagctag ctcttatatt caaaagtatg atgataagta tactttgaat cttgcatata 420
 ttgatggaaa aacacgcaa agaagagagc agagtattaa aaggagtatt gccaggtaca 480
 tagaccagca aggaactgta gttaaagaaa atgttgaaga tgaaatcacc aaaatg 536

10

<210> 211
 <211> 901
 <212> DNA
 <213> *Diabrotica virgifera*

15

<220>
 <221> modified_base
 <222> (707)
 <223> n = a, c, g or t/u

20

<400> 211

25

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 attccattga ttattaaaaa tctagatgaa catactgatg ggggtctgtaa taatgctgct 120
 tgggtgattg gaaagttgtg tgctgtgatg ggcaatgcaa tccaaccttt ccttccagaa 180
 atccttaatg cctttgttca tatattaaga acaccagctg tagctcgtac catgcacaaa 240
 actgtagcta tttccttatg catcgtattc tatgtgtgcc ccgatgtgac tattccagaa 300
 atggatgtga ttgttaagaa ttgctgtatg ttagtgagaa atgttaggga ttcagatgag 360
 aaggatcttg cttttcgagg cttgtgtgag gtgattataa ggcatccaga attcaacaag 420
 30 aactacttca tcttcttttg tgatgctgca gcttcctgga tcaatatccg tgtagatttg 480
 aagcagacaa ttcgcaatgt tctattggca tttaaacaac aatgtggtga ggataactgg 540
 cgccaatttt attgtcagtt tcctgaagct cttaaactta aacttcaaga gttatatggg 600

30

35

gtatgaaata aacaatctac aaaaaacggg gaattcgaca tatgggtggg aaagcttgag 660
 tgcacctgcc ttgagtttat cgcgtaatag tatttaaata tcgtccngtg agggaggggc 720
 gtcttgccgg tatcttagag tcacgcgtta ataaaaaat cgagaaggat ttttttagac 780
 agattaattt ttttgtttta tgggtagttt cttagttaat caactaaata atgtttattt 840
 aattattttt taaggaattt tataacaaat atggtaattt atattgtgga agtgttttta 900
 t 901

40

<210> 212
 <211> 27
 <212> DNA
 <213> *Diabrotica virgifera*

45

<400> 212
 cgtgggctaa tagcattgtg ttatcca 27

50

<210> 213
 <211> 28
 <212> DNA
 <213> *Diabrotica virgifera*

55

<400> 213
 gaacattgcg aattgtctgc ttcaaac 28

<210> 214
 <211> 496

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<212> DNA
<213> *Diabrotica virgifera*

<400> 214

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5      cgtgggctaa tagcattgtg ttatccattt ttagcttcta gtgtcaatga gtacattcca 60
      ttgattatta aaaatctaga tgaacatact gatggggtct gtaataatgc tgcttgggtg 120
      attggaaagt tgtgtgctgt gatgggcaat gcaatccaac ctttccttcc agaaatcctt 180
10     aatgcctttg ttcatatatt aagaacacca gctgtagctc gtacatgca caaaactgta 240
      gctatttcct tatgcatcgt attctatgtg tgccccgatg tgactattcc agaaatggat 300
      gtgattgtta agaattgctg tatgttagtg agaaatgtta gggattcaga tgagaaggat 360
      cttgcttttc gagccttgtg tgaggtgatt ataaggcatc cagaattcaa caagaactac 420
      ttcattcttct tttgtgatgc tgcagcttcc tggatcaata tccgtgtaga tttgaagcag 480
      acaattcgca atgttc                                     496

```

<210> 215
<211> 916
<212> DNA
<213> *Diabrotica virgifera*

<220>
<221> modified_base
<222> (870)
<223> n = a, c, g or t/u

<400> 215

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30     ctgtcgggat gtaagagcta tgattgaaag gcaggcgtct agacattgcg atcggcaggc 60
      agaatagcag gaaagcaaga caaatcctaa agatcaagcg tcatcgggtt tagaccggca 120
      tacagcatgc gaccgcatgg gcataaggag atcgcagtga tcgcaccctg atcggcctaat 180
      agacacagac acagacacgg tgtgttcgggt atttttagtt agtctgttcg cgaccggcga 240
      agaagtagcg cgtgtgttta aatagagagt tatggtgata acgtcaacgt gtgttgtgac 300
      ggtgtttaag atcaacgggc gccaccggag tcgacaacgc cagtgcgcaa gcagtgcgac 360
      actatgtccc agtcatgggtg aaaacgtttc tgggactgtt agctgcttca atttgtggtc 420
35     tcgtatacgc tgctccatta gctgactctt gcaataatct gaccctttt cgaacagata 480
      gcacaacccc tacttcttca gaagagtcac tgctagagga tccagcagca cgcaacgaaa 540
      gaagcacaaa tctctctcac gtcactggta ccgccagaaa aatacaaatg ttcatacaaga 600
      atcgacattt acaaatctt cctgacggga cagtcaacgg aaccactgac gacactagtg 660

40     cttattcgat attacaaagg acgacgggtg gaattggtca aatgaaaatt caagggtgtg 720
      ttacctgtca gtatttgtgc atggccagggt gtggattgct ctatggatcg agagaatttg 780
      gacaagaatg cgtattcaat gagaccatcg agcaatccaa ctacaacacg tattcctccc 840
      agtaatactc aaacgagaaa agaacccttn atctagcact gaatcaaaga ggccaatcga 900
      gaaagggtcgt cctacg                                     916

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<210> 216
<211> 26
<212> DNA
<213> *Diabrotica virgifera*

<400> 216
gctatgattg aaaggcaggc gtctag 26

<210> 217
<211> 27
<212> DNA
<213> *Diabrotica virgifera*

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<400> 217
gggtcattg aatagcatt ctgtcc 27

<210> 218
<211> 789
<212> DNA
<213> *Diabrotica virgifera*

<400> 218

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gctatgattg aaaggcaggc gtctagacat tgcgatcggc aggcagaata gcaggaaagc 60
aagacaaatc ctaaagatca agcgtcatcg ggttttagacc ggcatacagc atgacgaccgc 120
atgggcataa ggagatcgca gtgatcgcac ccgtatcggc taatagacac agacacagac 180
acggtgtgtt cggtatTTTT agttagtctg ttccgacgac gcgaagaagt agcgcgtgtg 240
tttaaataga gagttatggt aataacgtca acgtgtgttg tgacggtgtt taagatcaac 300
ggtcggcacc ggagtcgaca acgccagtga gcaagcagtg cgacactatg tcccagtcac 360
ggtgaaaacg tttctgggac tgttagctgc ttcaatttgt ggtctcgtat acgctgctcc 420
atagctgact cttgcaataa tctgacctct tttcgaacag atagcacaac ccctacttct 480
tcagaagagt cattgctaga ggatccagca gcacgcaacg aaagaagcac aaatctctct 540
cacgtcactg gtaccgccag aaaaatacaa atgttcatca agaatcgaca ttacaaaatt 600
cttcctgacg ggacagtcaa cggaaccact gacgacacta gtgcttattc gatattacaa 660
aggacgacgg tgggaattgg tcaaataaaa attcaaggtg tgggtacctg tcagtatttg 720
tgcattggcca ggtgtggatt gctctatgga tcgagagaat ttggacaaga atgcgtattc 780
aatgagacc                                     789

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<210> 219
<211> 2176
<212> DNA
<213> *Diabrotica virgifera*

<400> 219

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caaaattatt taagtagtgg agtccaaata gactatttct tcttttgggc tttttctgca 60
gcttttgtga cttttccagt agtatcttca tcttcagtga atacaccaat acgtctgcaa 120
atggcttcag cagtagcttt gttgtcacca gtgataacaa taactctgat accagcagcg 180
cggcattgaa caatggagtc aaatacttct ttacgtgggg gatccaacat accaacaaca 240
ccaacgaatg taagattgac ttcatatgtg tagaatttgg ttgaatcgcc aaggtccatt 300
tcgtctggtt tcatgggggtt atcagcagtt gctagggcaa gacaacgcaa tgtgtcgcgt 360
ccacaacatc attgagcggg aagatcagtg attctctttt taagagtgtt ggtaagtggg 420
actttttgag atccaacacg agcgtgtgta cacttttcca aaacaccttc tggagctcct 480
ttaacgaaga gtttaggtcc attaccaata cgagatgggt tgaggggtgt gcagtaggaa 540
gacatagatt tacgatcacg tgagaattcc aaagtgaatt ccttcttcca tttagtttca 600
atgtcttgtc taacacagat ggcaacctgt ctacgatctc cagttttact gacagagaag 660
ggattcattt tttctgctaa tacaatgaga gcagtttcag tagcttcacc aactttttcg 720

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```

aaagcttggt tgaattcatt gaaatcaatg gcggagtcac tgcacataat acaaattggta 780
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agatatggaa actttatgtg ctcatctgtt tgaaagagtt gaagtaagct taaagcaatg 1080
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<210> 236
 <211> 23
 <212> DNA
 <213> *Diabrotica virgifera*

<400> 236
 ctgtcgaaa ggctggtga atc 23

<210> 237

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<211> 31
<212> DNA
<213> *Diabrotica virgifera*

5 <400> 237
ctcttcacgt cactggacac atctttatcg t 31

<210> 238
<211> 862
10 <212> DNA
<213> *Diabrotica virgifera*

<400> 238

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	catcatg	cgt	tgctttt	tttct	ggaaaga	aacc	gcatatt	ggg	agttgcg	ggc	aaaaatc	cagc	120
	aagtcac	caa	tatgaaga	aac	actgtat	atg	ggctaaaa	aag	gctgttag	ggt	agaaagt	ttta	180
	gggatc	cctca	tgtcaaaaa	aaa	gaaattc	cagt	ttttacc	ata	tacagtt	gta	gaagaaaa	aaa	240
	acggggg	gtat	tgggaatt	tagg	gtaaatt	tatt	taaatga	aga	acataaa	attt	tcaccaga	aac	300
20	aatgttt	ggc	catgttg	tta	acaaaatt	taa	aagatagt	gc	tatgacag	ct	ctacaaact	c	360
	ccataaat	ga	ttgtgtt	ata	tcagttc	cctt	cttacttt	tac	aaacaat	gag	aggaagg	cac	420
	tattagatt	c	tgacagc	cata	gcaggtc	tta	atactcta	aag	gttattt	aat	gaaacaac	ag	480
	ctacggc	cctt	gtcatat	ggc	atttaca	aagc	aggattt	tacc	agctgtt	gaa	gaaaagc	cctc	540
	gtaaatat	tat	ttttgtc	gat	tgtggcc	att	catcctt	taca	agtattt	gca	gttgcatt	ta	600
25	ataaggg	caa	attgaag	atg	cttaccac	tg	ctgcagat	cc	caatttag	ggt	ggtaggg	act	660
	ttgatct	cat	cattgct	gag	cattttt	gca	aacaatt	tcca	aaccaa	atac	aacatgg	atg	720
	caaaatc	taa	tccaagag	ct	tttctaag	at	tgctaac	gga	ggtagaaa	aag	ttgaaga	aagc	780
	agatgtc	tgc	aaattct	taca	accttacc	cac	tcaacat	aga	atgtttc	atg	aacgata	aaag	840
	atgtgtc	cag	tgacatg	aa	g								862

30 <210> 239
<211> 1188
<212> DNA
<213> *Diabrotica virgifera*

35 <400> 239

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	acattgc	cagt	tttaaaaa	aga	attaaaaa	atg	gtatccct	taa	atcccgt	aag	aatttct	caag	120
	caagaag	ccg	aggaagaa	aag	ggcagaga	att	gcccga	actca	gtagttt	tgt	aggtgct	tata	180
	gctatag	gag	atgttggt	tag	aagcacct	tg	ggaccaaa	aag	gaatgg	ataa	aattttt	tagta	240
	tccagt	ggta	gatctgc	cagg	atcagtt	gaa	gttactaa	cag	acggag	caac	tatccta	aaaa	300
	tcgggt	gggtg	ttgataat	cc	tgctgct	aaa	attttgg	tgg	atatgt	caaa	agtccag	gat	360
	gatgaag	tag	gagatgg	cac	cacatcag	tg	acagtatt	tag	catctga	act	acttaa	agaa	420
45	gcagaaaa	aac	ttgtaga	aaa	gaaaatt	cac	ccacaaa	caa	tcattgc	ccg	ttggagg	aaa	480
	gcagtag	ata	ttgccaga	aaa	agctctt	tcta	gaaactg	cca	aagaca	acag	ctctgat	tca	540
	gaaaagt	tca	gagaagat	ct	gatgaac	att	gccaga	acta	cactcag	ctc	aaagatt	cctt	600
	tcacaac	ata	aagaatat	ttt	tgccaaa	actg	gcagtag	atg	ctgtgct	gag	attgaa	agggt	660
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	tttttgg	atg	aagggtt	ttttt	attggaca	aaa	aaacctg	ggtg	tacatca	acc	aaagaga	gta	780
50	gaaaatg	caa	aaatcct	gat	agccaac	act	cctatgg	aca	cagataa	aat	caaagt	atttt	840
	ggttctc	caca	ttaagg	taga	ttcaatg	ggt	aaaattg	cag	agctgga	atc	tgcagaa	aag	900
	gaaaaat	ga	aagataa	agt	gaacaaa	att	cttaa	acata	atgcta	atgt	atttatta	aat	960
	agacagt	tga	tttaca	atta	tcctga	acaa	ttgtttg	ctg	atgcagg	agt	tatggct	attt	1020
	gaacatg	cag	attttg	atg	aattgaa	agg	ctagcact	tgt	tcacagg	agg	agagatt	gtc	1080
55	tcaacatt	ttg	accatcc	aga	attggt	aaaa	cttggaa	actt	gtaagct	tatt	tgaacaa	aatc	1140
	atgattg	gag	aagatat	cct	gctccgt	tttc	agtgggt	gttg	ctcttgg				1188

<210> 240

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<211> 25
<212> DNA
<213> *Diabrotica virgifera*

5 <400> 240
ggtgggtgtt gataatcctg ctgct 25

<210> 241
<211> 25
10 <212> DNA
<213> *Diabrotica virgifera*

<400> 241
caagagcaac accactgaaa cggag 25

15 <210> 242
<211> 884
<212> DNA
<213> *Diabrotica virgifera*

20 <400> 242

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	tgaagtagga	gatggcacca	catcagtgc	agtattagca	tctgaactac	ttaaagaagc	120
	agaaaaacct	gtagaacaga	aaattcaccc	acaaacaatc	attgccgggt	ggaggaaagc	180
	agtagatatt	gccagaaaag	ctcttctaga	aactgccaaa	gacaacagct	ctgattcaga	240
	aaagttcaga	gaagatctga	tgaacattgc	cagaactaca	ctcagctcaa	agattctttc	300
	acaacataaa	gaatattttg	ccaaactggc	agtagatgct	gtgctgagat	tgaaagggtac	360
	aggtgattta	caatccatcc	agctgattaa	gaaaactggg	ggtaactttg	aagattcctt	420
30	tttggatgaa	ggttttttat	tggacaaaaa	acctgggtgt	catcaaccaa	agagagtaga	480
	aaatgcaaaa	atcctgatag	ccaacactcc	tatggacaca	gataaaatca	aagtatttgg	540
	ttctcacatt	aaggtagatt	caatggctaa	aattgcagag	ctggaatctg	cagaaaagga	600
	aaaaatgaaa	gataaagtga	acaaaattct	taaacataat	gctaattgtat	ttattaatag	660
	acagttgatt	tacaattatc	ctgaacaatt	gtttgctgat	gcaggagtta	tggtctattga	720
35	acatgcagat	tttgatggaa	ttgaaaggct	agcacttgct	acaggaggag	agattgtctc	780
	aacatttgac	catccagaat	tggtaaaact	tggaaacttg	aagcttattg	aacaaatcat	840

gattggagaa gatatcctgc tccgtttcag tggtgttgc cttg 884

40 <210> 243
<211> 1188
<212> DNA
<213> *Diabrotica virgifera*

45 <400> 243

50

55

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	caagaagccg	aggaagaaaag	ggcagagatt	gcccgactca	gtagttttgt	aggtgctata	180
5	gctataggag	atttggttag	aagcaccttg	ggacccaaaag	gaatggataa	aatttttagta	240
	tccagtggta	gatctgcagg	atcagttgaa	gttactaacg	acggagcaac	tatcctaaaa	300
	tcggtgggtg	ttgataatcc	tgctgctaaa	attttggtgg	atatgtcaaa	agtcaggat	360
	gatgaagtag	gagatggcac	cacatcagtg	acagtattag	catctgaact	acttaaagaa	420
	gcagaaaaac	ttgtagaaca	gaaaattcac	ccacaaaacaa	tcattgccgg	ttggaggaaa	480
	gcagtagata	ttgccagaaa	agctcttcta	gaaactgccca	aagacaacag	ctctgattca	540
10	gaaaagttca	gagaagatct	gatgaacatt	gccagaacta	cactcagctc	aaagattctt	600
	tcacaacata	aagaatattt	tgccaaaactg	gcagtagatg	ctgtgctgag	attgaaagg	660
	acaggtgatt	tacaatccat	ccagctgatt	aagaaaactg	gtggtacttt	ggaagattcc	720
	tttttggtg	aagggttttt	attggacaaa	aaacctgggtg	tacatcaacc	aaagagagta	780
	gaaaatgcaa	aaatcctgat	agccaacact	cctatggaca	cagataaaat	caaagtattt	840
15	ggttctcaca	ttaaggtaga	ttcaatggct	aaaattgcag	agctggaatc	tgcaaaaaag	900
	gaaaaaatga	aagataaagt	gaacaaaatt	cttaaacata	atgctaattg	atttattaat	960
	agacagttga	tttacaatta	tcctgaacaa	ttgtttgctg	atgcaggagt	tatggctatt	1020
	gaacatgcag	attttgatgg	aattgaaagg	ctagcacttg	tcacaggagg	agagattgtc	1080
	tcaacatttg	accatccaga	attggtaaaa	cttggaactt	gtaagcttat	tgaacaaatc	1140
20	atgattggag	aagatattct	gctccgtttc	agtgtgtgtg	ctcttggg		1188

<210> 244

<211> 32

<212> DNA

<213> *Diabrotica virgifera*

<400> 244

ctcactctga tgggtgtaatc actatggaaa tc 32

<210> 245

<211> 31

<212> DNA

<213> *Diabrotica virgifera*

<400> 245

gtcttctaca aatgctgatt tcaaatggtc t 31

<210> 246

<211> 820

<212> DNA

<213> *Diabrotica virgifera*

<400> 246

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	tagaaggaca	aaccagcaca	ccagaacaac	aagaactagc	caacaaatta	ctctattcag	180
	gagacaggaa	gtacattgaa	catcctataa	agccagctcc	aattcctgta	actgtgcgaa	240
	aaccaatacc	ctcatcaaat	cctcacccctc	tacaaccgaa	atctaacaat	cctagcacia	300
	atagtttagc	gcattcttca	tccacactca	gtgttgagga	tgagagacaag	aggacgccta	360
50	ggaaatatgg	tagattagat	tctactggaa	gtccaaatag	atcaagaagc	gcaactaaag	420
	aattagcact	gcctgatgac	tcaacaatgt	acgccccaca	atttaccaaa	aatctcacag	480
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	atcctcaaat	tgtttgagacc	aaaaatggaa	aagccttgag	ttcctctgaa	gttggtgacc	600
55	tcaaatacaa	gaacggaata	gcgaaattac	acataaatga	agtataccct	gaagatgaag	660
	gagaatatgt	gtgcagagca	accaactctg	taggaacctc	tgagaccaaa	tgcaaaactaa	720
	ccattaaacc	aatggccaat	gccaccaacg	gcaagaaaaa	atcctcagaa	gacaaaacccc	780
	caagaatagt	agaccattga	aatcagcatt	tgtagaagac			820

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<210> 247
 <211> 815
 <212> DNA
 <213> *Diabrotica virgifera*

5
 <400> 247

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      gttataccag aaaaagaaga aggtagtctt tcggaagtaa aacaagtgtc gcaggatgtg 60
10    gatactgaag atttgtacac taaatataaa aaacttcaac aacagttgga gttcttggag 120
      gttcaagaag agtacattaa agatgagcaa aggaatctca aaaaggagta tttacatgct 180
      caggaagaag tgaagcgtat ccagtctgtc ccgcttggtt ttggacagtt tttagaagct 240
      gtagatcaaa acactggcat tgttggctca actacagggt caaattatta tgttagaatc 300
      ttatcaacaa ttgatagaga actcttaaaa ccttctgcta gtgttgctct tcataaacac 360
15    agcaatgcct tagtagatgt cctaccacca gaggcagatt cttcaataag catgctccag 420
      gctgatgaaa aaccagatgt tcaatacagt gacattggag gtatggatat gcagaaacaa 480
      gaaattaggg aagctgtaga gttacctttg actcacttcg aattgtataa acagattggt 540
      attgatcccc ccagaggtgt gttgatgtat ggacctcctg gatgcgggaa gactatgttg 600
      gccaaagctg ttgctcatca tactacagct gcctttattc gtgtagtcgg atcagaattc 660
      gtacagaaat atcttgggtga aggtcctcga atggtgagag acgtgttccg tctagcaaaa 720
20    gaaaattctc cagcaatcat ctttattgat gaaattgatg caatcgctac caaacgtttt 780
      gatgcccgaa caggtgctga tcgtgaagtc cagag                                     815
  
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<210> 248
 <211> 28
 <212> DNA
 <213> *Diabrotica virgifera*

<400> 248
 cttcaacaac agttggagtt cttggagg 28

<210> 249
 <211> 25
 <212> DNA
 <213> *Diabrotica virgifera*

<400> 249
 ctctggactt cagcatcagc acctg 25

<210> 250
 <211> 722
 <212> DNA
 <213> *Diabrotica virgifera*

<400> 250

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      cttcaacaac agttggagtt cttggagggt caagaagagt acattaaaga tgagcaaagg 60
50    aatctcaaaa aggagtatct acatgctcag gaagaagtga agcgtatcca gtctgtcccc 120
      cttgttattg gacagttttt agaagctgta gatcaaaaca ctggcattgt tggctcaact 180
      acagggtcaa attattatgt tagaatctta tcaacaattg atagagaact cttaaaacct 240
      tctgctagtg ttgctcttca taaacacagc aatgccttag tagatgtcct accaccagag 300
      gcagattctt caataagcat gctccaggct gatgaaaaac cagatgttca atacagtgac 360
      attggaggta tggatatgca gaaacaagaa attagggaag ctgtagagtt acctttgact 420
      cacttcgaat tgtataaaca gattgggtatt gatcccccca gaggtgtgtt gatgtatgga 480
      cctcctggat gcggaagac tatgttggcc aaagctgttg ctcatcatac tacagctgcc 540
55    tttattcgtg tagtcggatc agaattcgtc cagaaatatc ttggtgaagg tcctcgaatg 600
      gttagagacg tgttcctgtc agcaaaagaa aattctccag caatcatctt tattgatgaa 660
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      ag                                     722
  
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<210> 251
 <211> 1324
 <212> DNA
 <213> *Diabrotica virgifera*

5

<400> 251

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10    tttaaatcgg aaaatggaga agtcgccggt gatatgatgg atctcccat agactgttcc 180
      ttacagcagc tcacgttaat ttgtaatgct ttgttaaaac aggaagaacc agtaccatac 240
      ttatttttacg ttaacgaaaa cgaaataacc catacttttg aaaaagcact aaatataagg 300
      gaattaaata cagaaggtgt tgtagatatc atttatcaac aacaagcagt gtttagggta 360
      cgccctgtaa caaggtgtac cagctcaata ccaggtcatg cagaagcagt tatttcagtt 420
15    agtttttagtc cagacggtaa acatttagca agtggatctg gtgatacaac agtcaggttt 480
      tgggatgttg atacgcaatc tccgttatat acttgtgaag gtcataaaaa ttgggtgttg 540
      tgtatagctt ggtcctctga tagtactaaa ttggcttctg cttgtaaaga tgggaaaatt 600
      atcatatggg atcctttttac aggaaagcaa ataggtaaaa cgttaacggg acataaacag 660
      tggattacta gtttaagctc gggagcctta tcataaaaaac cctgaatgta gatatttggc 720
20    aagttcttca aaagatggag atgtaaggat atgggatact gtactcagca atacattttt 780
      ttgtatatct ggtcatacaa agagtgtaac aatggtgaaa tgggggtggag caggtctcat 840
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25    caagaaaaaa tctcaggact ttgccctcaa acgatactat gaagttacag aatctatttg 1080
      agaaagatta gtatcgggtt ctgatgattt cacattattt ctttggaatc ctgataaaga 1140
      caagaagcct ttagctaggc taacaggtca ccaacaatta gtcaatgacg tgaaattttc 1200
      acctgatggg agaataattag cttcagcatc tttcgataaa tcaatcaaat tgtgggaggc 1260
      aaaacaggaa agttttatttg taccctacgt ggacatgttc aggctgtgta catggtatca 1320
      tttt                                     1324

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30

<210> 252
 <211> 28
 <212> DNA
 <213> *Diabrotica virgifera*

35

<400> 252
 gaaaacgaag gcgaagctgt aacagaac 28

40

<210> 253
 <211> 28
 <212> DNA
 <213> *Diabrotica virgifera*

45

<400> 253
 gctccacccc atttaccat tgttacac 28

50

<210> 254
 <211> 757
 <212> DNA
 <213> *Diabrotica virgifera*

55

<400> 254

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5 gaaaacgaag gcgaagctga acagaacaga agcgtctgtt gtgttggttt aaatcggaaa 60
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 cgттаатттг таатгсттг ттаааасагг аагаассагт ассатаскта тттасгтта 180
 асгаааасга аатаасссат асттгггаа аагсасктаа татаагггаа ттааатасга 240
 ааггтгттгт агататсатт татсаасас аагсасгтгт тагггтасгс ссггтаасас 300
 ггтгтассга ссасатасса ггтсатгсга аагсасгтат тсасгтгагт ттгагтсас 360
 асггтаасас ттгагсасгт ггагтсггтг асасасасгт сасгттггг гатгттгата 420
 ссасатсстс гттататасг тгтгааггтс атааааатгг ггтгттгтгт асасгттггт 480

10 cccctgatag tactaaattg gcttctgctt gtaaagatgg gaaaattatc atatgggagc 540
 cttttacagg aaagcaaata ggtaaaacgt taacgggaca taaacagtggt attactagtt 600
 таагсгггга гссттатсат ааааасссгт аатгтгагата ттггсгаагт тсстсасаагг 660
 атгггагатгт ааггататгг гатасгтсстс тсасгасасас атттттггт ататсгггс 720
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15 <210> 255
 <211> 794
 <212> DNA
 <213> Diabrotica virgifera
 20 <400> 255

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 tgtctgtgat aaatagtaaa aaatattaaa gcgatatttt cgtcgaaact gatatgtatt 180
 aaatttatct tttgtgttat taaagagagt taaacgtagc taaagaagaa aaactattag 240
 tgatttaaac atgagtacga aagatgatga atacgattat ttatttaaag ttgtccttat 300
 tgggtgattct ggtgtaggaa aaagtaactt attgtcaaga ttactagaa atgaattcaa 360
 tttggagtct aaatctacta taggtgtcga attcgctacc agaagtatac aggtggatgg 420
 30 taaaactatt aaagcacaaa tatgggacac ggcaggtcaa gagagatacc gagcaatcac 480
 ggcggcctat tatcgtggtg cagtcggtgc tctactcgtc tacgatatcg ccaaacatct 540
 gacatacgaa aacgttgaac gttggttgcg cgaattgcgc gaccacgcag atcagaacat 600
 tgtgatcatg ttggtcggaa acaaaccga tctgaggcat ttgcgcgcgc tgctgacaga 660
 agaagctaag gctttcgccg aaagaaacgg cctcagcttc atcgagactt cagccctaga 720
 35 ttcgaccaat gtcgataatg ctttcacaaa tatactcaca gagatctata gaattgtttc 780
 ccaaaaacag atca 794

<210> 256
 <211> 28
 40 <212> DNA
 <213> Diabrotica virgifera

<400> 256
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45 <210> 257
 <211> 25
 <212> DNA
 <213> Diabrotica virgifera

50 <400> 257
 cacaatgttc tgatctgctg ggtcg 25

55 <210> 258
 <211> 504
 <212> DNA
 <213> Diabrotica virgifera

<400> 258

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5      ggaacgtatc ggaagtaatg tgtctgtgat aaatagtaaa aaatattaaa gcgatatttt 60
      cgctcgaaact gatatgtatt aaatttatct tttgtgttat taaagagagt taaacgtagc 120
      taaagaagaa aaactattag tgattttaaac atgagtacga aagatgatga atacgattat 180
      ttattttaaag ttgtccttat tgggtgattct ggtgtaggaa aaagtaactt attgtcaaga 240
      tttactagaa atgaattcaa tttggagtct aaatctacta taggtgtcga attcgctacc 300
      agaagtatac aggtggatgg taaaactatt aaagcacaaa tatgggacac ggcaggtcaa 360
      gagagatacc gagcaatcac ggcggcctat tatcgtggtg cagtcggtgc tctactcgtc 420
10     tacgatatcg ccaaacatct gacatacgaa aacgttgaac gttggttgcg cgaattgcgc 480
      gaccacgcag atcagaacat tgtg                                     504

```

<210> 259

<211> 1180

15 <212> DNA

<213> *Diabrotica virgifera*

<400> 259

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20     atttttgggt gtttctttga ttgaacaaaa attacaagcg ttttaaattc actaaatttg 60
      ctttgaaata tacaaatagt taattctagg aaaatatata acctacatac agaatcatgt 120
      cttcccgcaa aaccgtaagc cgccgtggta ccacaaagaa acgtgcccaa agagccacat 180
      ccaatgtatt cgcaatgttt gatcaggctc agattgctga gttcaaagaa gccttcaata 240
      tgatcgacca gaaccatgat ggtttttag ataaagaaga tctgcatgat atgcttgctt 300
25     ccttaggtaa aaacccaact gatgactatc tagatggcat gatgaatgaa gctcctggtc 360
      ccataaactt caccatgttc ttaactctct ttggagaacg tctacaaggc acagaccag 420
      aagacgtaat taaaaacgct tttggctgct ttgacgaaga caacaatggg gtcctcaacg 480
      aagaacgtct cagggagctc ctcacgtcca tgggtgatag attcactgac gatgaagttg 540
      acgagatgta cagggaggct cctattaaga atggcttggt tgattatggt gaattcacc 600
30     gcattttaaa gcacggggct aaggacaagg atgagcaata agagacgaat tgatgatgaa 660
      aggatttgta attaatatgg aaagatgtct tagtttgaat gatttggatt ttcattccat 720
      ttttgtgatt agaaatatat gaaattcatc atactagacc atcaagtctt gtccgttgca 780
      gtatcttctg cacatagaca tgatcatcct gaacaaaact gcaaaaatgg atttgaaaaa 840
      tggtaggttt tgaatgaatt aacagtctaa ttatatagac atcttggtat tgtacttaac 900
35     atctcttgct tgttatttta aagtattcct tgaatgtttt gaatagaaaa cgacattttg 960
      tatattaaaa ctacaaatcc aattgcatgt tatcattata agatcgatat ttttccttca 1020
      aagtattttt agcattgtta gtcagcttat tttgggtttt tacaactttt ggcaacgttt 1080
      tattttattca taagatttat tgtaattata aattttatac ctttatatat catgtaatta 1140
      ttcattaaaa tattgaacca aaaaaaac cacgcgtccg                                     1180

```

40 <210> 260

<211> 26

<212> DNA

<213> *Diabrotica virgifera*

45 <400> 260

gagccacatc caatgtattc gcaatg 26

<210> 261

<211> 30

50 <212> DNA

<213> *Diabrotica virgifera*

<400> 261

caacggacaa gacttgatgg tctagtatga 30

55

<210> 262

<211> 607

<212> DNA

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<213> Diabrotica virgifera

<400> 262

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5      gagccacatc caatgtattc gcaatgtttg atcagggtca gattgctgag ttcaaagaag 60
      ccttcaatat gatcgaccag aaccatgatg gttttgtaga taaagaagat ctgcatgata 120
      tgcttgcttc cttaggtaaa aacccaactg atgactatct agatggcatg atgaatgaag 180
      ctccctgggtcc cataaacttc accatgttct taactctctt tggagaacgt ctacaaggca 240
      cagaccacaga agacgtaatt aaaaacgctt ttgggtgctt tgacgaagac aacaatggtg 300
10     tcctcaacga agaacgtctc agggagctcc tcacgtccat ggggtgataga ttcactgacg 360
      atgaagttga cgagatgtac agggaggctc ctattaagaa tggcttggtt gattatggtg 420
      aattcaccgg catttttaaag cacgggggcta aggacaagga tgagcaataa gagacgagtt 480
      gatgatgaaa ggatttgtaa ttaatatgga acgatgtctt agtttgaatg atttggattt 540
      tcattccatt tttgtgatta gaaatatatg aaattcatca tactagacca tcaagtcttg 600
15     tccgttg      607

```

<210> 263

<211> 966

<212> DNA

20 <213> Diabrotica virgifera

<400> 263

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25     gatctagtga ccagccttga agctatttct acacagagtg gtatagtgtc tgggtgtagtt 60
      gataatctca caagagccat gactcgattg tcggatagtc gtgcttctct catcttatct 120
      gatgggtgata ttggattcgt tgattaccaa acacgaatgg tggactgtgc gaagagtata 180
      gctaaaatcg ccggagaaat tgctagcaaa gctgccactg accctcagaa ggtgggtcaa 240
      ttatctgcag atcttgcgca caaatatgca caactatctg gcgatagtat tggagctgca 300
30     gcagctgcca ctaatgccga agttgcaatc agactaaggg aagttgttca acaactgggt 360
      ggcgcctgcg tagaactcgt ccaaacagga ggccagtgtc tagtccgaaa agatgacgta 420
      ctcttgcgag aagtaggaga ttgctcacgc aacgtaactg agaaagtttc ccgtgttctt 480
      gccacattac aaaacgaatc cagagggtacc caagcttgca tcaatgcagc ttccaccgta 540
      tctggtatca tcggcgattt agaaactacc atcatgtttg ccactgccgg aaatctcaat 600
      cccgaaagcg aacatgaatc gttcgctaata cacagagaga atatatgaa gactgctaag 660
35     gcgttggttag aggatactaa gactttggta gctggcgag cttcatcaca agaacaactg 720
      gctgtagctg ctcaaaattc tgttgcgacc atagtacaat tagccgaagt agtgaaattc 780
      ggagcagcca gcttaggcgt tgacaatcca gattcccaag tgatgcttat caacgcagta 840
      cgtgacgttg ccagtgtctt tgggtgacttg attcaagcta ctaaggctgc tagcgggcaag 900
      cccatcaacg atccggccat ggctcattta aaagacagcg caaagggtgac ggattctgaa 960
40     actgat      966

```

<210> 264

<211> 30

<212> DNA

45 <213> Diabrotica virgifera

<400> 264

ggtgtagttg ataatctcac aagagccatg 30

50 <210> 265

<211> 26

<212> DNA

<213> Diabrotica virgifera

55 <400> 265

cagtttcaga atccgtcacc ttgctg 26

<210> 266

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<211> 913
<212> DNA
<213> *Diabrotica virgifera*

5 <400> 266

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          ggtgtagttg ataatctcac aagagccatg actcgattgt cggatagtcg tgcttctctc 60
          atcttatctg atggtgatat tggattcggt gattaccaa caccgaatggt ggactgtgcg 120
10      aagagtatag ctaaaatcgc cggagaaatt gctagcaaag ctgccactga ccctcagaag 180
          gtggctcaat tatctgcaga tcttgccgac aaatatgcac aactatctgg cgatagtatt 240
          ggagctgcag cagctgccac taatgccgaa gttgcaatca gactaaggga agttgttcaa 300
          caactgggtg gcgcctgcgt agaactcgtc caaacaggag gccagtgcct agtccgaaaa 360
          gatgacgtac tcttgcgaga agtaggagat tgctcacgca acgtaactga gaaagtttcc 420
          cgtgttcttg ccacattaca aaacgaatcc agaggtagcc aagcttgcac caatgcagct 480
15      tccaccgtat ctggtatcat cggcgattta gaaactacca tcatgtttgc cactgccgga 540
          aatctcaatc ccgaaagcga acatgaatcg ttcgctaata acagagagaa tatattgaag 600
          actgctaagg cgttggtaga ggataactaa actttggtag ctggcgagcgc tcatcaca 660
          gaacaactgg ctgtagctgc tcaaaattct gttgcgacca tagtacaatt agccgaagta 720
          gtgaaattcg gagcagccag cttaggcggt gacaatccag attcccaagt gatgcttatt 780
20      aacgcagtac gtgacgttgc cagtgcctct ggtgacttga ttcaagctac taaggctgct 840
          agcggcaagc ccatcaacga tccggccatg gctcatttaa aagacagcgc aaaggtgacg 900
          gattctgaaa ctg                                     913

```

<210> 267
25 <211> 846
<212> DNA
<213> *Diabrotica virgifera*

30 <400> 267

```

          ctctctttga gttgtcgctt ttcgaggtat ttagttgcag gcgtgggtgta tacggtgaaa 60
          tagtgatttt tgttaaaagt gagtaaatat ggcacgcgaa tcaaaaaaag ggtcaacacc 120
          gttagcttca cagcggccgg cgagcccctt aagtcctacc agacattcta gattacagga 180
35      gaagcatgaa cttcagaatc ttaacgaccg tttggcggga tatatagatc gagtaaggta 240
          tttagaaggt gaaaacaaca gattaacgag ggaaatacaa agtaccagag aaacagtaac 300
          aagggaagtt tcaaacatta aatctatgta tgaccatgaa ttatcagatg ctagaaaact 360
          attagacgag acccaccgtg aaaaagcacg tttagagata gatgttaaag gtcttttaga 420
          agagaatgac gaactcaagt ctgagtttagc aaagaagaac aaggatttgg ctctagctga 480
          gaattctgcc aggatatacg agaccagatg taacgagtta cagctcaaag caaatcaagc 540
40      ggctgctgat gctaagaaag ctattgcaga tgctaaggaa cttgagaaag aacgtgataa 600
          gctacgcaa cttcttgata atcatcgtaa acagttagaa gaagaatcat tagcgagagt 660
          ggaagtcgaa aatgccaacc aaagtcttcg agaagagctg tcctttaagg atcagatcca 720
          tcaacaacag ttgacagaaa ctctgactcg tcgtcaagta gaaatcagcg aaatcgacgg 780
          tcgcctggca gaaaaatatg aggctaagct tcaagaggct ctacaagaac tcagagatca 840
45      atatga                                     846

```

<210> 268
50 <211> 31
<212> DNA
<213> *Diabrotica virgifera*

<400> 268
gagaagcatg aactcagaa tcttaacgac c 31

55 <210> 269
<211> 29
<212> DNA
<213> *Diabrotica virgifera*

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<400> 269
gatttcgctg atttctactt gacgacgag 29

<210> 270
<211> 595
<212> DNA
<213> *Diabrotica virgifera*

<400> 270

	gagaagcatg	aacttcagat	cttaacgacc	gtttggcggg	atatatagat	cgagtaaggt	60
	atttagaagg	tgaaaacaac	agattaacga	gggaaacaca	aagtaccag	gaaacagtaa	120
	caagggaggt	ttcaaacatt	aaatctatgt	atgaccatga	attatcagat	gctagaaaac	180
	tattagacga	gacccaccgt	gaaaaagcac	gttttagagat	agatgttaaa	cgtcttttag	240
15	aagagaatga	cgaactcaag	tctgagttag	caaagaagaa	caaggatttg	gctctagctg	300
	agaattctgc	caggatatac	gagaccagat	gtaacgagtt	acagctcaaa	gcaaatacaag	360
	cggtctgctga	tgctaagaaa	gctattgcag	atgctaagga	acttgagaaa	gaacgtgata	420
	agctacgcaa	acttcttgat	aatcatcgta	aacagttaga	agaagaatca	ttggcgagag	480
	tgggaagtcga	aaatgccaac	caaagtcttc	gagaagagct	gtcctttaag	gatcagatcc	540
20	atcaacaaca	gttgacagaa	actcgtactc	gtcgtcaagt	agaaatcagc	gaatc	595

<210> 271
<211> 901
<212> DNA
<213> *Diabrotica virgifera*

<400> 271

	tcaacacgtg	tgaattaaaa	caaattcaaa	aacaaaaatg	tccatccaag	aaaaagtttt	60
	aatgaaaaaa	ataaaaaaga	gggaaaagca	gaaattaaaa	tttgttcaaa	agaaagagtc	120
	tgaaaagagc	aaagaagttt	tagaaacaga	tctaccagag	aaggcaaaag	tgggaaatgg	180
	cttgaaacgc	ttgcagagca	acgatgaagg	accttctaaa	aaaaaaaaaga	agaaaaataa	240
	aaagaagaaa	gagaaaatag	tgaagagga	agatacagac	gaagaacaac	cagaggaaga	300
	tgaaattgag	tctgacattg	aagatcaaga	gattgacaat	ggtgaagaag	atacagatga	360
35	aaaatctgat	ttaggaaaca	aattaccagg	atccagtgtc	acattagaaa	ttctcagtaa	420
	aagtacattt	gactcattga	cggataaagt	atgtgaaaat	actttgaaag	ccattgcaga	480
	tatgggtttt	actactatga	ctgaaattca	agcaaaatct	atacctccac	ttctggaagg	540
	tagagatttg	gttggggctg	caaaaacagg	atctggaaaa	actcttgctt	ttctcattcc	600
	cgctgttgaa	cttattttata	agttaaagtt	tatgccaaga	aatggtactg	gtatcattat	660
40	catttccccc	acacgagaat	tatcaatgca	gacttttgga	gtattaaaag	aactaatgaa	720
	atatcatcac	catacatacg	gtttggttat	gggtggaact	gcaagacaaa	cagaagcaca	780
	aaagctttcc	aaaggtatta	atatcttagt	agcaacgcct	ggtaggcttc	tggatcatct	840
	tcagaatact	cctgacttct	tgtataagaa	tttacaatgt	ttagtcattg	acgaggctga	900
	c						901

<210> 272
<211> 22
<212> DNA
<213> *Diabrotica virgifera*

<400> 272
ggaaatggct tgaacgcgtt gc 22

<210> 273
<211> 27
<212> DNA
<213> *Diabrotica virgifera*

<400> 273

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ctgaagatga tccagaagcc taccagg 27

<210> 274

<211> 672

<212> DNA

<213> *Diabrotica virgifera*

<400> 274

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10      ggaaatggct tgaacgctt gcagagcaac gatgaaggac cttctaaaaa aaaaaagaag 60
      aaaaataaaa agaagaaaga gaaaatagtc gaagaggaag atacagacga agaacaacca 120
      gaggaagatg aaattgagtc tgacattgaa gatcaagaga ttgacaatgg tgaagaagat 180
      acagatgaaa aatctgattt aggaaacaaa ttaccaggat ccagtgtctac attagaaatt 240
      ctcagtaaaa gtacatttga ctcattgacg gataaagtat gtgaaaatac tttgaaagcc 300
15      attgcagata tgggttttac tactatgact gaaattcaag caaaatctat acctccactt 360
      ctggaaggta gagatttggg tggggctgca aaaacaggat ctggaaaaac tcttgctttt 420
      ctcattcccg ctgttgaact tatttataag tttaaagtta tgccaagaaa tgggtactggt 480
      atcattatca tttccccac acgagaatta tcaatgcaga cttttggagt attaaaagaa 540
      ctaatgaaat atcatcacca tacatacggt ttggttatgg gtggaactgc aagacaaaca 600
20      gaagcacaaa agctttccaa aggtattaat atcttagtag caacgcctgg taggcttctg 660
      gatcatcttc ag 672

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<210> 275

<211> 512

<212> DNA

<213> *Diabrotica virgifera*

<220>

<221> modified_base

<222> (370)..(452)

<223> n = a, c, g or t/u

<400> 275

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35      atttagtcca ctgtacaaat gaaccaaatg tttcaattcc acagctagca aatttggttaa 60
      tagaaagatc acagaataca aactgggtag tagtttaciaa ggcattagtt acagttcacc 120
      acatgatgtg ttatggaaat gagagattta ctcagtacct agcatccagt aacagtacat 180
      ttcaacttag caacttctta gataaagggg gacttcaagg atatgacatg tctccattta 240
      ttagaaaata ttcacgatat ctcaatgaga aggccttatc atacagaact acagccttcg 300
40      acttttgcaa agttaaaaga ggggaaggatt gatggcatgt taaggacaat gaacgcagat 360
      aaattattan aaactcttcc cactttaciaa natcaactgg atacctatt ggaantttga 420
      tgttccgcan atgatttnna caacggagtg antaatatgt gtttcatgtt gctttttagg 480
      gatttatacg cttatttttg ctgtataatg at 512

```

<210> 276

<211> 28

<212> DNA

<213> *Diabrotica virgifera*

<400> 276

caaatgaacc aaatgttca attccaca 28

<210> 277

<211> 32

<212> DNA

<213> *Diabrotica virgifera*

<400> 277

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cgataaaatc cctaaaaagc aacatgaaac ac 32

<210> 278

<211> 470

<212> DNA

<213> *Diabrotica virgifera*

<400> 278

```

tgaaccaa at gtttcaattc cacagctagc aaatttggtta atagaaagat cacagaatac 60
aaactgggta gtagttttaca aggcatttagt tacagttcac cacatgatgt gttatggaaa 120
tgagagattt actcagtacc tagcatccag taacagtaca tttcaactta gcaacttctt 180
agataaaggg ggacttcaag gatatgacat gtctccattt attagaaaat attcacgata 240
tctcaatgag aaggccttat catacagaac tacagccttc gacttttgca aagttaaaaag 300
agggaaggat gatggcatgt taaggacaat gaacgcagat aaattattaa aaactcttcc 360
cactttacaa aatcaactgg atatcctatt ggaatttgat tgttccgcaa atgatttaac 420
aaacggagtg ataaatatgt gtttcatgtt gcttttttagg gattttatacg 470

```

<210> 279

<211> 978

<212> DNA

<213> *Diabrotica virgifera*

<220>

<221> modified_base

<222> (918)

<223> n = a, c, g or t/u

<400> 279

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cgcggtggcg cgaacaggcg agaaaagacc tcaaaggact cgaagacact gtcgccaaaag 60
aactacagac tctgcacaac ctgagaaaat tggttcgtgca agatttgcag gcacgtatga 120
agaaaaatct ttcgtcggaa gacaatgagg aagacggcgg ctctctggct caaaaacaga 180
agatatcggt cctcgaaaac aatctcgatc aattgacaaa agtccacaag cagttgggtac 240
gagacaacgc ggatctgcgc tgtgaacttc ccaaactcga aaagagacta cgagctacga 300
tggaagagat caaagcactg gaaactgcac tgaaggaagc caaagaaggc gcgatgagag 360

```

```

accggaagaa ataccaatac gaggttgacc gcattaaaga ggctgtgagg cagaagaacc 420
tcgcaagaag agggccagca gccacaatcg ctaaaccaat cagggcaggg caacacaaca 480
cggttaacgt agctggtaac cccgtcatta gaactggagg catcaacatg gccaacagat 540
cgaccgacga ccagaaacgt aggtctgtta ttgggtggaga taaagattga gtcgccagacc 600
atcttgtcag gtgcttgaga cgtttttagt aagcaaaatc cataaaaactg taataccaaa 660
aatattgccc atacttcgcg cgagtctgtc gccagcagtt tttggaacag acaagaaaaa 720
aaattgctcc tccagactcg ctcttcaatg tgcttacagc ttagatattt ctgtagtata 780
aggtgcactt cattgcattg aaaatgaaac aaattaatcg agtattgtaa cagattgttg 840
gcaaattggt ttaataaaatc gttcattttt tgttttcgat cacttctagc ttctgtgcga 900
attaagtgtt aacactanaa aacaatttgc ttgctgtttt atccttaaaa cgttgcaacg 960
tttacggcga ttttttga
978

```

<210> 280

<211> 26

<212> DNA

<213> *Diabrotica virgifera*

<400> 280

gaacaggcga gaaaagacct caaagg 26

<210> 281

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<211> 26
<212> DNA
<213> *Diabrotica virgifera*

5 <400> 281
cacattgaag agcgagctcg gaggag 26

<210> 282
<211> 741
10 <212> DNA
<213> *Diabrotica virgifera*

<400> 282

15	gaacaggcga	gaaaagacct	caaaggactc	gaagacactg	tcgccaaaga	actacagact	60
	ctgcacaacc	tgagaaaatt	gttcgtgcaa	gattttgcagg	cacgtatgaa	gaaaaatctt	120
	tcgtcgggaag	acaatgagga	agacggcggc	tctctggctc	aaaaacagaa	gatatacgttc	180
	ctcgaaaaca	atctcgatca	attgacaaaa	gtccacaagc	agttgggtacg	agacaacgcg	240
	gatctgcgct	gtgaacttcc	caaactcgaa	aagagactac	gagctacgat	ggaaagagtc	300
20	aaagcactgg	aaactgcacc	gaaggaagcc	aaagaaggcg	cgatgagaga	ccggaaaaga	360
	taccaatacg	aggttgaccg	cattaaagag	gctgtgaggg	agaagaacct	cgcaagaaga	420
	ggcccgacag	ccacaatcgc	caaaccaatc	agggcagggc	aacacaacac	ggttaacgta	480
	gctggtaacc	ccgtcattag	aactggaggc	atcaacgtgg	ccaacagatc	gaccgacgac	540
	cagaaacgta	ggctctgttat	tggtggagat	aaagattgag	tcgccagcca	tcttgtcagg	600
25	tgcttgagac	gttttttagta	agcaaaatcc	ataaaaactgt	aataccaaaa	atattgccga	660
	tacttcgcgc	gagtcctgtcg	ccagcagttt	ttggaacaga	caagaaaaaa	aattgctcct	720
	ccagactcgc	tcttcaatgt	g				741

<210> 283
30 <211> 876
<212> DNA
<213> *Diabrotica virgifera*

<400> 283

35	ggaaaactgg	tcccttctgt	ttttctgatg	tctcaaattt	tctgtcctaa	cttctaacac	60
	ttgttttaaaa	tccgttgaca	tacttgctaa	tttggatgga	gtgctaagac	aatgctactc	120
	gtgtgtgatt	gtagatgttt	cccacttgat	ccctgcttct	gtttcctaga	tacatcttgt	180
	aattgggcta	tttgttgatt	caagttgcta	agatcacctt	ttatgatata	tgtgagttct	240
40	tggattttctg	atgttttctg	gtcaaataaa	gatttttctg	ttgccaacaa	tgtcaacttt	300
	tccaatttag	cataagtgtc	agctatatgc	cgtccacat	tcttcgcaat	tagcataaac	360
	tcgctatgac	tttgtataac	cctcgatttc	ttcgggtccc	tagcagctac	tgccctagca	420
	atgttcctgc	cttgtaaatgt	ctgtatagta	tttaciaaatt	cactagttct	gtctctggca	480
45	gtcatgacta	attctgggtc	agtgtagtct	tcgatataat	cttcctctaa	atagtagtca	540
	gatgtaacat	tgtttgata	caccgtgtgt	gactgattcg	ttttaggctg	agggttagtc	600
	caataattat	cgttacctac	tataacttgg	ggctcagttt	cagagccagc	tcgacgacgt	660
	ctaggaagca	ttgcattctt	aagaggctac	aaagttaatt	ttgaaagtag	cacaaccata	720
	tttaaagcac	tagaatttca	ctttatatta	tattttttatc	acctactgta	gtatatatca	780
50	tgactaattg	tttaattggg	tttaatatgt	ttaattacaa	ttaataatga	acttttacttt	840
	ttcttttgaa	agtacacgtc	tatttgcccg	gacgcg			876

<210> 284
<211> 32
55 <212> DNA
<213> *Diabrotica virgifera*

<400> 284

EP 2 431 473 B1

ggttgctgcta ctttcaaaat taactttgta gc 32

<210> 285

<211> 29

<212> DNA

<213> *Diabrotica virgifera*

<400> 285

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<210> 286

<211> 645

<212> DNA

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<211> 883

<212> DNA

<213> *Diabrotica virgifera*

<400> 287

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<211> 28

<212> DNA

<213> *Diabrotica virgifera*

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<210> 289
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<213> *Diabrotica virgifera*

<400> 289
gactgacaga cagcaaaat acgatagc 28

<210> 290
<211> 586
<212> DNA
<213> *Diabrotica virgifera*

<400> 290

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<212> DNA
<213> *Diabrotica virgifera*

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<210> 292
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<213> *Diabrotica virgifera*

<400> 292
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<210> 293
 <211> 27
 <212> DNA
 <213> *Diabrotica virgifera*

5

<400> 293
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<210> 294
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 <212> DNA
 <213> *Diabrotica virgifera*

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<400> 294

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30 <210> 306
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10      <210> 308
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      <210> 309
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<400> 313
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15 <210> 314
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taaacgacac agatactcct aattcttttag agatggatga aggagacaca attgaagtat 360

30 atcaacaaca gacagggtgg ttcttctatc ggtttctatt c 401

<210> 315
<211> 822
35 <212> DNA
<213> *Diabrotica virgifera*

<400> 315

40 aaacgacgat tcagtgcacc gacgcaacgt acgccagcca attgtcccta gagaatccca 60
aaggattttc tagagatgct tttggaaggc agagtatgtc agagaagagg catgcgacgt 120
tggatgccaa gaataccgac acatatcaga aatcgaagaa gattagggag gagaggaaga 180
tgaaagaaat aaatgctgat aaattaggcc aattaggacc aagtttaggc atgaagaaat 240
45 cttcaagctt ggaatcgtaa cagacaatgg tacaagagat tcaaagcaa gaagaaggcg 300
accagctta tagttataga ggacccaatg gagcttttaa agtaatcagg gggaaaggct 360
gtgaagaaag ctttagggca gctgtagtgg atccaaatca ccgaagtggat atcggagcca 420
aaaagcattg gttgcttgac ggtccaatgg aaaacgaacg agaagtggat ggcttcagca 480
atgctcgagg aggtcctagg caatcttctc tgaatgcagc tattgatata aagaataaat 540
cagcaaagaa gaaacctggt atatttaaag gcattgggtc gatgttcagg tttggcaaac 600
50 atcgtaaaact ggacttccaa acagcagagg ctgcccaaca ctatcatcat acaaacgaat 660
tcgattcaaa tgccaacgta cctcaacaac acaccgcaga taccgaaaac cgaacgcaaa 720
gtagtcaaac agaacggacg caagagcatt cacaaaaagt acctctaaat agcaaccccc 780
agaacaaaaa cacttcccaa ggatctcacc accagacgca ag 822

55 <210> 316
<211> 32
<212> DNA
<213> *Diabrotica virgifera*

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<400> 316
gatgccaaga ataccgacac atatcagaaa tc 32

<210> 317
<211> 25
<212> DNA
<213> Diabrotica virgifera

<400> 317
cttgctctg gtggtgagat ccttg 25

<210> 318
<211> 700
<212> DNA
<213> Diabrotica virgifera

<400> 318

gatgccaaga	ataccgacac	atatcagaaa	tcgaagaaga	ttagggagga	gaggaagatg	60
aaagaaataa	atgctgataa	attaggccaa	ttaggaccaa	gtttaggcat	gaagaaatct	120
tcaagcttgg	aatcgttaca	gacaatggta	caagagattc	aaatgcaaga	agaaggcgac	180
ccagcttata	gttatagagg	acccaatgga	gctttaaaag	taatcagggg	gaaaggctgt	240
gaagaaagct	ttagggcagc	tgtagtggat	ccaaatcacc	gaagtgagat	cggagccaaa	300
aagcattggt	tgcttgacgg	tccaatggaa	aacgaacgag	aagtggatgg	cttcagcaat	360
gctcgaggag	gtcctaggca	atcttctctg	aatgcagcta	ttgatataaa	gaataaatca	420
gcaaagaaga	aacctggtat	atttaaaggc	attggttcga	tggttcagggt	tggtcaaact	480
cgtaaaactg	acttccaaac	agcagaggct	gccaacact	atcatcatac	aaacgaattc	540
gattcaaatg	ccaacgtacc	tcaacaacac	accgcagata	ccgaaaaccg	aacgcaaagt	600
agtcaaccag	aacggacgca	agagcattca	caaaaagtac	ctcaaaatag	caacccccag	660
aaccaaaca	cttccaag	atctcaccac	cagacgcaag			700

<210> 319
<211> 1321
<212> DNA
<213> Diabrotica virgifera

<400> 319

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      ttagccaagc ggcattggaag taaagaccca aaggagctct gttttcattg taatgcctat 60
      cgaaattata attttaagaag ttataaaatt gatctccagt aagaatggtg gaacatgagt 120
      caaccatggc acaacctggt aaatactcat cattttcagg atcttctctt ctatctagtt 180
5      cgtaagtac  catttcccat actgcatgtg atcttggttg gcaatttttg aggtttccgt 240
      gacatctgtg tggcattcta aaatacatag tatagggcca tagtggtggg ttattttaagg 300
      gtgcggtgat agtggagtcg tataagaagg cttcttcttc catcatagta aattggttgt 360
      tacctcctac tcttagataa ggggctctta ctctactac gctgttatcg gtaatattgg 420
      cgaatttctc agtgatgact cgcataacct ccatttcttt aaccagtc aattcgtgac 480
      cgttggacca gaagttttcg tcatcattgt gcgatattga atgtactgcg atttcgtgac 540
10      cttttctatg catttcttgg actgccgagt agttggtgta cttgtgagac acgaagaatg 600
      tagccttgat atgacaaccg ttggggtttt tccgttcacc gttgaaaatg ttcttgtata 660
      gaccgatgtt gttattatgt atggcgctcg caaatgtgac agttatcatt tgaggtagat 720
      ctttggtggtg taaatcattg ggaatgcctg taccgtcctc tgagcagaaa caatcaggga 780
      gaacgcatac tgcggggtcg caggggtggg cactattggg gtcactatcg atatcgagg 840
15      tagtttcatc agacccatcc tggcaatcct tttccccgtt acaaaagagc cctctttcta 900
      tacactgacc atctccgcag gccaatcac cttcgttaca tacgggtttg tccgtaaaca 960
      acatgggttt tacccgccgc tctttgtttt tcaatttgca gtttttaact gagtccttcc 1020
      agtcgcatgt ttgcttttcg atgtcgaaat atagaccggc tggacaacga atggcttgca 1080
      ggcccgaaga tgtacattga atgacgtctc gacagggtgc cccctcccct cccactaaac 1140
      gaaaccactc gcccgcgctc ttgtctttgc atatttcggc ctcgaaactc tcctctttct 1200
20      tcggttcatc gtctttggcc tgctgtgtg ccaaaccgct tgaggctacc aacgcaacca 1260
      agaaaaatcgt cgttgcgaag tacgccatga cacttaaaca actgaaagta ccggacgcac 1320
      a

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<210> 320

<211> 29

<212> DNA

<213> *Diabrotica virgifera*

<400> 320

cagttgttta agtgtcatgg cgtacttcg 29

<210> 321

<211> 25

<212> DNA

<213> *Diabrotica virgifera*

<400> 321

ggaggttcc gtgacatctg tgtgg 25

<210> 322

<211> 1075

<212> DNA

<213> *Diabrotica virgifera*

<400> 322

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      cagttgttta agtgtcatgg cgtacttcgc aacgacgatt ttcttggttg cgttggttagc 60
      ctcaagcggg ttggcacaac agcaggccaa agacgatgaa ccgaagaaag aggagagttt 120
50      cgaggccgaa atatgcaaag acaaagacgc gggcgagtgg ttctgtttag tgggagggga 180
      gggggacacc tgtcgagacg tcattcaatg tacatcttcg ggctgcaag ccattcgttg 240
      tccagccggg ctatatcttc acatcgaaaa gcaaacatgc gactggaagg actcagttta 300
      aaactgcaaa ttgaaaaaca aagagcggcg ggtaaaaccc atgttggtta cggacaaacc 360
      cgtatgtaac gaaggtgaat tggcctgcgg agatggtcag tgtatagaaa gagggctctt 420
      ttgtaacggg gaaaaggatt gccaggatgg gtctgatgaa actacctgcg atatcgatag 480
55      tgaccccaat agtgcctcac cctgcgaccc cgcagtatgc gttctccctg attggttctg 540
      ctgagaggac ggtacaggca ttcccaatga tttaccagcc aaagatgtac ctcaaagat 600
      aactgtcaca tttgacgacg ccataaataa taacaacatc ggtctatata agaacatttt 660
      caacggtgaa cggaaaaacc ccaacgggtt tcatatcaag gctacattct tcgtgtctca 720

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caagtacacc	aactactctg	cagtccaaga	aatgcataga	aaaggtcacg	aaatcgcagt	780
acattcaata	tcgcacaatg	atgacgaaaa	cttctggtcc	aacgccagtg	taaagtactg	840
gggttaaagaa	atgggaggta	tgcgagtcac	cactgagaaa	ttcgcaaata	ttaccgataa	900
cagcgtagta	ggagtaagag	ccccttatct	aagagtagga	ggtaacaacc	aattttactat	960
gatggaagaa	gaagccttct	tatacgactc	cactatcacc	gcaccattaa	ataaccacc	1020
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<210> 323

<211> 1703

<212> DNA

<213> *Diabrotica virgifera*

<220>

<221> modified_base

<222> (1641)

<223> n = a, c, g or t/u

<400> 323

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gcacttgat	aaataaaacg	aaagtctgag	atcacttctt	ggctagtgtg	tgaattttca	120
gcatggctga	caaaaagacta	tggctgtgtt	gtttttttatt	attgacaatt	gcttacgctc	180
aagatgaaga	tgatgacgat	tcaggggaac	cacagatcga	ccagctgtgt	gaaaacaggc	240
ctgctgatga	atatttttagg	ttaagcactg	atggagactg	cagagaagtt	gtaaggtgtg	300
atctcaattc	agatcttaag	ggcgttactc	gattggcagc	ggtaaaatgt	ccgacaggac	360
ttgcttttga	tcttttccga	caaacttgag	attggaaaag	caatgtcaaa	aattgtgata	420
tcgtagaaaa	accaagaaaa	gtccttccaa	ttttgaaaac	cgacgaacca	agatgtccag	480
aaggaaaagct	gatgtgtggt	aatgaagaat	gtatcgacaa	agatcttttc	tgtaatggaa	540
agccagactg	taaagatgaa	tcagacgaga	atgcatgcga	tgttgatagt	gatcccaacc	600
gtgcacctga	ctgtgaccca	actcaatgtg	taattccgga	ctgtttctgc	tcagcggacg	660
gaactagaat	tcctggcgcg	ctagaaccag	caaagtgtac	acaaatgata	accatttcgt	720
tcaatggtgc	cgtaaatgta	gataacatcg	atctatatga	agaaatcttt	tcaggcacta	780
gacttaaatcc	aaatggttgc	caaattaaag	gaaatttctt	cgtttctcac	aaatacacaa	840
actactcagc	agtacaggac	ctacacagac	gtggtcatga	aatcgcggtg	ttttcattga	900
ctcataaaga	ggatccaaac	tactggtccc	aggggttctta	tgacgactgg	ttggctgaaa	960
tggctggagc	tagattgatt	attgaaagat	ttgccaacat	taccgatgga	tcaataattg	1020
gagtgaagag	tccataacct	agagtaggag	gaaacagaca	atttgaaatg	atgacagatc	1080
aatcttttat	ttatgattca	tcaattacag	cctctcttgg	acgtgtccca	atctggcctt	1140
atactttata	cttcaggatg	ccacataagt	gcaacggaaa	tgcccacaac	tgtcccagca	1200
gaagccatcc	cgtttgggaa	atagtcatga	acgaattgga	cagacgtgat	gatcctactt	1260
ttgacgaatc	actacctggt	tgccacatgg	tagactcctg	ttctaattgt	caaactggag	1320
atcaattttgc	aagactactc	agacacaatt	tcaacagaca	tttgaattca	aaccgagctc	1380
cgttgggtct	taacttccat	gcctcatggt	taaagagtaa	gaaagaattc	aaagaagaac	1440
ttattaaatt	cattgaagat	atgttggccc	gaaatgatgt	ttatttcgta	acaaacagtc	1500
aagtcaccca	atgggttcag	aatcccacag	aactcagtg	attaagagac	ttccaagaat	1560
ggaaagaaaa	gtgtgacatt	aaaggtcaac	cttactgttc	attgcccaat	tcattgtccat	1620
tacataccag	agaactgcca	nggtgaactc	tacgattgtt	tacctgtatg	gaatgtccca	1680
acaattatcc	atggattttg	gat				1703

<210> 324

<211> 28

<212> DNA

<213> *Diabrotica virgifera*

<400> 324

gacgaacca gatgtccaga aggaagc 28

<210> 325

<211> 30

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<212> DNA
<213> *Diabrotica virgifera*

<400> 325
gttgggacat tccatacagg taaacaatcg 30

<210> 326
<211> 1221
<212> DNA
<213> *Diabrotica virgifera*

<220>
<221> modified_base
<222> (271)..(358)
<223> n = a, c, g or t/u

<400> 326

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gacgaaccaa gatgtccaga aggaaagctg atgtgtggta atgaagaatg tatcgacaaa 60
gatcttttct gtaatggaaa gccagactgt aaagatgaat cagacgagaa tgcattgcat 120
gttgatagtg atcccaaccg tgcacctgac tgtgacccaa ctcaatgtgt aattccggac 180
tgtttctgct cagcggacgg aactagaatt cctggcgcgc tagaaccagc aaatgtacca 240
caaatagataa ccatttcgtt caatgggtgcc ngttaatgta gataacatcg atctatatga 300
agaaatcttt tcaggcacta gacttaatcc aaatgggtgc caaattaaag gaaatttnc 360
tcgtttctca caaatacaca aactactcag cagtacagga cctacacaga cgtgggtcatg 420
aaatcgcggt gttttcattg actcataaag aggggtccaa ctactgggtcc cagggttctt 480
atgacgactg gttggctgaa atggctggag ctagattgat tattgaaaga tttgccaaca 540
ttaccgatgg atcaataatt ggagtggag ctccatacct cagagtagga ggaaacagac 600
aatttgaaat gatgacagat caattcttta tttatgattc atcaattaca gcctctcttg 660
gacgtgtccc aatctggcct tatactttat acttcaggat gccacataag tgcaacggaa 720
atgccacaaa ctgtcccagc agaagccgtc ccgtttggga aatagtcattg aacgaattgg 780
acagacgtga tgatcctact tttgacgaat cactacctgg ttgccacatg gtagactcct 840
gttctaattg tcaaactgga gatcaatttg caagactact cagacacaa ttcaacagac 900
atgtgaattc aaaccgagct ccgttgggtc tcaacttcca tgcctcatgg ttaaagagta 960
agaaagaatt caaagaagaa cttattaaat tcattgaaga tatgttggcc cgaaatgatg 1020
tttatttcgt aacaaacagt caagtcatcc aatgggttca gaatcccaca gaactcagt 1080
gattaagaga cttccaagaa tggaaagaaa agtgtgacat taaagggtcaa ccttactgtt 1140
cattgcccaa ttcattgtcca ttacatacca gagaactgcc aggtgaaact ctacgattgt 1200
ttacctgtat ggaatgtccc a 1221

```

<210> 327
<211> 826
<212> DNA
<213> *Diabrotica virgifera*

<220>
<221> modified_base
<222> (658)..(683)
<223> n = a, c, g or t/u

<400> 327

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```

    caaattgttt attacaagtt tattaccatg agagtgtata taatattatt tagcgtcttt 60
    tgcttgagcc attgcgctcc acaggaaaac aaaaataaat ttccagaaca ataccaaggt 120
    caacacatac caattgtaag gcaagaacaa gaagtgaatt atgatggcac ctacgaatac 180
    aactttgaaa ctggaaatgg catagtccaa gaagaaaaag gatttttgaa aaacgccggt 240
5   acaaagggaag aagctcaagt cgctcaaggt ttttcctcat atacttcccc cgaaggagta 300
    aaaatagaac tccggtacat cgcagacgaa aacggtttcc agccaatcgg agaccaccta 360
    ccgactccgc caccaatccc tgaggctatt ttacgagcgc taagtgtact gaaacagttg 420
    ggtaattttga atgaagacca agaagaaaat aacaacatta gatgaagaga gagtgtgata 480
    aaatcgttat tttggataag tcccttcata tttcaaaatg gtaccatact aactatgaaa 540
10  tacttcaaaag aattaagatc tttttaaaat acgtcaacac tttagagtag gaaacagcgg 600
    tggaaacctcg caaaatgtac acaagttcgg ttttattttt ttgcaggaaa atcaaggngt 660
    gcttataatg aaactaacat ttttctaaaa aatttcgccc ctgaaccccc ctttttatcc 720
    ctttgaagggt ggggtatttgt ggtttttgct aaacgaagcc cttcctgtat acgtttttaca 780
    aaagaatgta ctaaatagta aatgaagag gactataatt tgctac 826

```

15

<210> 328

<211> 29

<212> DNA

<213> *Diabrotica virgifera*

20

<400> 328

ccagaacaat accaaggtca acacatacc 29

25

<210> 329

<211> 25

<212> DNA

<213> *Diabrotica virgifera*

30

<400> 329

gaggttccac cgctgtttcc tactc 25

35

<210> 330

<211> 505

<212> DNA

<213> *Diabrotica virgifera*

<400> 330

40

```

    agaacaatac caaggtcaac acataccaat tgtaaggcaa gaacaagaag tgaattatga 60
    tggcacctac gaatacaact ttgaaactgg aaatggcata gtccaagaag aaaaaggatt 120
    tttgaaaaac gccggtacaa aggaagaagc tcaagtcgct caaggttttt cctcatatac 180
    ttcccccgaa ggagtaaaaa tagaactccg gtacatcgca gacgaaaacg gtttccagcc 240
    aatcgggagac cacctaccga ctccgccacc aatccctgag gctatttttac gagcgctaag 300
    tgtactgaaa cagttgggta atttgaatga agaccaagaa gaaaataaca acattagatg 360
45  aagagagagt gtgatcaaat cgttattttg gataagtccc ttcataattc aaaatgggtac 420
    catactaact atgaaatact tcaaagaact aagatctttt taaaatacgt caacacttta 480
    gagtaggaaa cagcgggtgga acctc 505

```

50

<210> 331

<211> 731

<212> DNA

<213> *Diabrotica virgifera*

55

<400> 331

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```

5      ttggtaaaagt ttgttgtagt ttcagtgatc ttcattttga actctttttt tttttcaata 60
      tgcgaactac gtactttaca ttagttgtaa tattagctgt agctgtacaa gaacatgcat 120
      ctcaacaatt accagtaacg caagcttgct tgggatgtat atgtgaagct atttccaact 180
      gtaatgtaac tagcggttgt tctggtgagg tttgtggacc atttcggatc acctgggcat 240
      attgggcaga tgctggaaag cccaccgtga aaggagtatc accagaagac aataatgcat 300
      atggatcttg tgctactgat acgtattgtt ctgcattagc tgttcaagga tatatgaata 360
      aatttcaaca ggattgcaat ggtgatggta aaatagactg tgacgattat gcaagtattc 420
      acacgcatgg tggatatggc tgcaaaggaa ctaatctacc acaacctttt ggaaatcgat 480
      attatcaatg taaagagata gttggacgta gaccagagta atgttggagt aaccccagga 540
10     ttgagaacag gaagattgat agaaacgcat ttactactct atgaattttg ttggatgatt 600
      attgcaactt aatgtaattc aatatgttta agggctgtaa ttacaattaa ataaaaataa 660
      ctgacatcat agaatacact attgtaacaa ctattttttt aggtatagta ttttaagtaa 720
      actctttttt t                                     731

```

```

15     <210> 332
      <211> 29
      <212> DNA
      <213> Diabrotica virgifera

```

```

20     <400> 332
      gcatctcaac aattaccagt aacgcaagc 29

```

```

      <210> 333
      <211> 32
25     <212> DNA
      <213> Diabrotica virgifera

```

```

      <400> 333
      gtttctatca atcttctgt tctcaatcct gg 32

```

```

30     <210> 334
      <211> 450
      <212> DNA
      <213> Diabrotica virgifera

```

```

35     <400> 334

```

```

40     gcatctcaac aattaccagt aacgcaagct tgcttgggat gtatatgtga agctattttcc 60
      aactgtaatg taactagcgg ttgttctggt gaggtttgtg gaccatttcg gatcacctgg 120
      gcatattggg cagatgctgg aaagcccacc gtgaaaggag tatcaccaga agacaataat 180
      gcatatggat cttgtgctac tgatacgtat tgttctgcat tagctgttca aggatatatg 240
      aataaatttc aacaggattg caatggtgat ggtaaaatag actgtgacga ttatgcaagt 300
      attcacacgc atggtggata tggctgcaaa ggaactaatc taccacaacc ttttggaaat 360
      cgatattatc aatgtaaaga gatagttgga cgtagaccag agtaatgttg gagtaacccc 420
45     aggattgaga acaggaagat tgatagaaac                                     450

```

```

      <210> 335
      <211> 878
      <212> DNA
50     <213> Diabrotica virgifera

```

```

      <400> 335

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```

55

```

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gtgattgtgg tgttttatcg gtgttaagac aggatgggtt tcggtcaaaa aattctagtc 60
cctctagtc ttatagaaat gtccctactg gttacatcca gaataatata tgaccatcag 120
caagaagata atcacgaagg gcaacaagtt caatacacca attactatgg tcacgaagag 180
tctgccacaa cagcacattt ccaacaaccc gtccagtttc ccgaggaaca tagccaaggt 240
5 ttgcacaaaag aggaacacat cgattattac gcaccagcca agtattcctt caaatatgga 300
gtcaacgact accacactgg cgatataaaa agccaacacg aatccagaga cggagatact 360
gtcaaaggcc aatacacact tgtagaaccc gacggatcta tcagaactgt agactacact 420
gctgacaaac acagtggatt taacgcagta gtgcgcaaat cagggtccac aaaacacata 480
gaaggaaggc atctggaaca ccaaccgaa gaagagcaac atatacctca gcatcatttg 540
10 gcagaagatc atgttttacc gcagtatcaa ctggaacacc aacaggcttt ggaagaagat 600
gttgaagaag gacatctgga agctgaagat gctagtcaat atgaagaaga agagcattag 660
gtgttatatt aagttaaagg acgtaatggg ttgtaaataa gcgaactcaa agattaaagt 720
agtatctttt aaaattattg gagaaaataa gaatttttgt ttgtaagaaa aagtatcatc 780
atcaactata tttttttata acacttttaa catttttgga acgtaaatatt cgaatttata 840
15 cactcacaga caaaaatctt gcatattttg aaattatg 878

```

<210> 336

<211> 27

<212> DNA

<213> *Diabrotica virgifera*

<400> 336

ggtgttaaga caggatgggt ttcggtc 27

<210> 337

<211> 28

<212> DNA

<213> *Diabrotica virgifera*

<400> 337

ggtgttcag ttgatactgc ggtaaaac 28

<210> 338

<211> 560

<212> DNA

<213> *Diabrotica virgifera*

<400> 338

```

ggtgttaaga caggatgggt ttcggtcaaa aaattctagt ccctctagtc cttatagaaa 60
tgtccctact ggttacatcc agaataatat atgaccatca gcaagaagat aatcacgaag 120
ggcaacaagt tcaatacacc aattactatg gtcacgaaga gtctgccaca acagcacatt 180
tccaacaacc cgtccagttt cccgaggaac atagccaagg tttgcacaaa gaggaacaca 240
tcgattatta cgcaccagcc aagtattcct tcaaatatgg agtcaacgac taccacactg 300
45 gcgatataaa aagccaacac gaatccagag acggagatac tgtcaaaggc caatacacac 360
ttgtagaacc cgacggatct atcagaactg tagactacac tgctgacaaa cacagtggat 420
ttaacgcagt agtgcgcaa tcaggtccca caaacacat agaaggaagg catctggaac 480
accaaccgga agaagagcaa catatacctc agcatcattt ggcagaagat catgttttac 540
50 cgcagtatca actgaacacc 560

```

<210> 339

<211> 831

<212> DNA

<213> *Diabrotica virgifera*

<220>

<221> modified_base

<222> (807)

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<223> n = a, c, g or t/u

<400> 339

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      caggctgaac aagacacaaa cgtcccacaa aactaccaag ataactcaga tcaataccaa 180
      cagaattctg tccaacaaaa cccaccgcaa catcaggaaa aatcgcaata tgaaccacga 240
10     gtaaaagaaa ctatcaaatt cataccaatt atcagattcg ataaagaaca aggagaagcc 300
      ggtaattaca aagctgcata tgaaacccgga aacaacatta tcgctgaaga agaaggttac 360
      ttgaaggaaac tcggtccaga tccagaccag caaggacaag ttatcaaata gcaagtacaa 420
      cagggtcact tcacatatat atcccctgaa ggagtagtta ttgaaactaa atatactgct 480
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15     gaacaaagat taaaagatca cccagaagaa agagacagac ctgaaaatta cgacgatggt 660
      caataccgac cggcacaaca ggagtaattt tactctttat ttatagttaa gcaccatcat 720
      tctgtgattt tgtcgtcatt tctatagaat atcttctgta cagactgaat aagattgata 780
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20 <210> 340

<211> 24

<212> DNA

<213> *Diabrotica virgifera*

25 <400> 340

gattgtgcc gcattggtgt ttgg 24

<210> 341

<211> 27

30 <212> DNA

<213> *Diabrotica virgifera*

<400> 341

gacgacaaaa tcacagaatg atggtgc 27

35 <210> 342

<211> 690

<212> DNA

<213> *Diabrotica virgifera*

40 <400> 342

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      agatcaatac caacagaatt ctgtccaaca aaaccaccg caacatcagg aaaaatcgca 180
      atatgaacca cgagtaaaag aaactatcaa attcatacca attatcagat tcgataaaga 240
      acaaggagaa gccggtaatt acaaagctgc atatgaaacc ggaaacaaca ttatcgctga 300
      agaaggaggt tacttgaagg aactcgggtc agatccagac tagcaaggac aagttatcaa 360
      atcgcaagta caacagggtc acttcacata tacatcccct gaaggagtag ttattgaaac 420
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      accagttagc gccgaagtac aaaagggatt ggaccttatt tttgctggta tcagagctca 540
      acaggaggcg ttagaacaaa gattaaaaga taccacagaa gaaagagaca gacctgaaaa 600
      ttacgacgat ggtcaatacc gaccggcaca acaggagtaa ttttactctt tatttatagt 660
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55 <210> 343

<211> 633

<212> DNA

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<213> Diabrotica virgifera

<400> 343

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      agaacatgga catggatatt cagctccagt ttttaagtcac gcacatgctg cacctggttc 180
      tcacggatat tctgctcctg ttctcgccca cggacattcc gcacatcacg atgtagatta 240
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      tgttggtgaa aaatctggac acccagttca cccagctcca gctcatggac acggaaaagt 480
      actcctagct gctcccgtg tccaccacgc tccattgtac catcattaaa acctgaaaga 540
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<210> 344

<211> 27

<212> DNA

20 <213> Diabrotica virgifera

<400> 344

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25 <210> 345

<211> 30

<212> DNA

<213> Diabrotica virgifera

30 <400> 345

cagggtttaa tgatggtaca atggagcgtg 30

<210> 346

<211> 421

35 <212> DNA

<213> Diabrotica virgifera

<400> 346

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40     ctaggtggtt cagaacatgg acatggatat tcagctccag ttttaagtca cgcacatgct 60
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      gatgtagatt acaacgctta tcccaaatac gaattcaact acggagttca agatggccac 180
      actggagacc acaaaactca acacgaagtc cgtgatggtg acgtagtcaa aggttcctac 240

45     acagtagctg aacctgacgg tactcttcgt actgtccact acactgctga tgaccacaac 300
      ggtttcaatg ctgttggtga aaaatctgga caccagttc acccagctcc agctcatgga 360
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50 <210> 347

<211> 698

<212> DNA

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55 <220>

<221> modified_base

<222> (14)

<223> n = a, c, g or t/u

<400> 347

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      tactcagccg ctccagctgt atcatactca agtgtgtcat cacctgtagc ttacgcagca 180
      ccagctgttg ctaaattagc tgcacctgta tcttatgtctg caccagcttt atcttacgct 240
      gcaccagtcg ctaaagttgc ctactcatca gctccagctg tctcttactc cagtgtatcc 300
      gcaccagtag cctacgccgc tgccccagcc tacgccaaag tagctgctcc agtatcgtac 360
      gcagctccag ctgtttccta cgcgctcca gctctctcct atgccgcccc agcccttaaa 420
10     gtagctgccc cagtagctta tgccgctcct gttgccaaag cagtttacgc cgaaccatca 480
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      agccaacaag aatctcgcca cggatgatgt gtacatggaa gctattccct tattgaagcc 600
      gatggcagca aacgtaccgt agaatacacc gctgatgaac acaatgggtt taatgcagtt 660
      gtacacaagg aaccagccac agttgcggtt aaagcagt 698

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<210> 348

<211> 25

<212> DNA

<213> *Diabrotica virgifera*

<400> 348

gctcgtgctg gtgtcatcgg agaag 25

<210> 349

<211> 26

<212> DNA

<213> *Diabrotica virgifera*

<400> 349

gcaactgtgg ctggttcctt gtgtac 26

<210> 350

<211> 641

<212> DNA

<213> *Diabrotica virgifera*

<400> 350

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      gtagcttacg cagcaccagc tggttgctaaa ttagctgcac ctgtatctta tgctgcacca 180
      gctttatctt acgctgcacc agtcgctaaa gttgcctact catcagctcc agctgtctct 240
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45     gccccagccc ttaaagtagc tgccccagta gcttatgccg ctctgttgcc caaagcagtt 420
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      accggagata gcaaaagcca acaagaatct cgccacgggtg atgttggtaca tgggaagctat 540
      tcccttattg aagccgatgg catcaaactg accgtagaat acaccgctga tgaacacaaat 600

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50 ggttttaatg cagttgtaca caaggaacca gccacagttg c 641

<210> 351

<211> 977

<212> DNA

<213> *Diabrotica virgifera*

<400> 351

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15 caggggtagc ggcgccgtat tggtaaacc cggccgtgta ctaaattattg actgactata 900
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<210> 352

<211> 32

<212> DNA

<213> *Diabrotica virgifera*

<400> 352

caagattacc ttcagcatcc ttatagcagt tc 32

<210> 353

<211> 30

<212> DNA

<213> *Diabrotica virgifera*

<400> 353

gtcactaaac tctcaaacc tgaaggcaag 30

<210> 354

<211> 777

<212> DNA

<213> *Diabrotica virgifera*

<400> 354

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tgctgatgac gtgcaggatg ccctaacagg agattcaaaa ggacaagttg aaagcagagc 240
45 caacggcggt gtaagaggac aatatcaagt agcagatcca gacggtagca gaagaattgt 300
agattattac gccgatcctg tgcatggatt caatgctgtg gtcagaagag ttctcttagg 360
tggtgcagtt gctcctgtcg tagccaaagc tgtagctcct gttgctccaa tcgctcccgt 420
cgctagatca ttagtccttc ctgctccagg gcttccagtt gctgccgctc ctgtaccagt 480
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tgctgcagct ccagctatatt ctccatactt aaccagagct ggattcttcc cagctccagc 660
tccagccgta gttcctgctg ctccaggtcc tgcatacttg cctgctgctc catcaagatt 720
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<210> 355

<211> 1176

<212> DNA

<213> *Diabrotica virgifera*

<400> 355

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      ccttttttaa gtctgcaggt gtaaggctca caactggctc catcgggcgc gtcagcagtt 180
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      aagctggtgt cagtttgctc aaaccagtat gagttgatca tcaaatttat gggagttcta 360
      gatttacttc taattccttc aatttgatca tccaaatatt tggcgatttc atcaacacta 420
10     ccttctattc cacaagtagc cagtgaattg cattctgtac catttggtga agttaaatcg 480
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      cattgttctg ttgattgata atccaatgta tagggaaata atcttcttga tggcaaagag 600
      ggccatgaac tatcatatgc caattctgat gctatatagg cctcaatgga agtgtttctt 660
      gcaagttgta gttggggagt tctgactcca ataatagctt cagctggtat gttggcataa 720
15     gtacttataa tttgcttttg gcctttaaat tcttttgta gtgtgtctag agttgcatat 780
      ctccagtaat tttgtctaaa atccttcgta attgagtgca caccaatttc aaatccaaag 840
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      ctaattggct tatcatctgg attatatata tttccgagca atgtaatcca actgttgtcg 960
      tagatgtgtt gtgtaacagc ttcacaaat gttaaactaa tcagctgagg atactctgtg 1020
      agatctccac ctagaggtga cacttgacta gaacatctac aattgttgcc gatcgtacaa 1080
20     gaatcagact cacacggttt tgctacatca tttgcaatcg cactatcgaa tgctaaagta 1140
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<210> 356

<211> 27

25 <212> DNA

<213> *Diabrotica virgifera*

<400> 356

30 gcaaatgatg tagcaaaacc gtgtgag 27

<210> 357

<211> 27

35 <212> DNA

<213> *Diabrotica virgifera*

<400> 357

ggattcgtc tggacaagga acacacg 27

<210> 358

40 <211> 1043

<212> DNA

<213> *Diabrotica virgifera*

<400> 358

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      attttaacgg gattttttat aaaatctagg acctgttttt gtgagacgaa gaaggatatct 180
      tttgcttcac gtgcaactgt gttttccaag aattttcgaa gcccatcgaa gctggtgtca 240
      gtttgttcaa accagtatga gttgatcatc aaatttatgg gagttctaga tttacttcta 300
      attccttcaa tttgatcatc caaatatttg gcgatttcat caacactacc ttctattcca 360
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      atccaataac ctgggaaagc ttcgttagga cattctgcgc ccaaaagaca ttgttctgtt 480
      gattgataat ccaatgtata gggaaataat cttcttgatg gcaaagaggg ccatgaacta 540
55     tcatatgcca attctgatgc tatataggcc tcaatggaag tgtttcctgc aagttgtagt 600
      tggggagttc tgactccaat aatagcttca gctggtatgt tggcataagt acttataatt 660

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5
 10
 15
 20
 25
 30
 35
 40
 45
 50
 55

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ttaa	gatag	atact	ggtaca	atggt	aattgg	840
tcat	tatat	tccgag	gtaat	tgttg	gatgt	900
gtaac	catcaa	taaact	agctg	actct	atctcc	960
agagg	cttgac	acatct	ttgttg	tcgtac	atcagac	1020
cacgg	ctacat	tgc				1043

<210> 359

<211> 649

<212> DNA

<213> *Diabrotica virgifera*

<400> 359

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 45
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tatgc	ttgtg	tatat	tggt	tgatg	cttg	180
gccgt	tgga	tgatt	acacg	cttcc	gggtg	240
cattt	aattc	aattt	gaata	caa	agg	300
cacta	aaatg	catgt	aata	cgcc	ctttg	360
aagt	atcg	gtata	tta	tga	agtag	420
gatg	tta	tacga	ttt	tcag	tcttag	480
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aac	cgat	caaga	gtg	tgg	gacca	600
ctc	gaaa	gtc	tata	tct		649

<210> 360

<211> 32

<212> DNA

<213> *Diabrotica virgifera*

<400> 360

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<210> 361

<211> 30

<212> DNA

<213> *Diabrotica virgifera*

<400> 361

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<210> 362

<211> 547

<212> DNA

<213> *Diabrotica virgifera*

<400> 362

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 gccgtcatta tggacaattt tgattattta acacgtgatc cttccatatt ggggtgctcat 240
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 cactacagcg aaatgtacga catgttgaaa atatggatcc gccactaggc tttggaaaca 360
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 atgggaaagt taattttact acgacattct ttgctctcgt cagagaaaat cttagcatta 480
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<210> 363

<211> 677

<212> DNA

15 <213> Diabrotica virgifera

<400> 363

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 30 gttgctctct agtattt 677

<210> 364

<211> 27

<212> DNA

35 <213> Diabrotica virgifera

<400> 364

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40 <210> 365

<211> 24

<212> DNA

<213> Diabrotica virgifera

45 <400> 365

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<210> 366

<211> 587

50 <212> DNA

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<400> 366

55

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ttggtatcag aatgaactac cgaaaaggat caaaagtcgt ggcaaagatg cccacttagt 180
acacgaggag ttggtacaat gcatgaaatg gaaacagacc agggggaagt tcttcccca 240
5 attatcgtat ttggtaaagg ttaacactcc tagagctgtt atggcagaaa cgaagagagc 300
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<210> 367

<211> 882

<212> DNA

15 <213> *Diabrotica virgifera*

<220>

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<222> (792)..(853)

20 <223> n = a, c, g or t/u

<400> 367

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ggctttcaga tcctttgacg aaaacggcac cattgacgga gacagattcc gtcattgccct 480
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acatctaagt gtggtgtgtt tcttatataa ttccaatgaa cacataagaa aagggtgtact 780
tatatgtgta tnttattatg tatttgtttt taagttttatt tttattcagt tgctttacca 840
tcacgcgact canaagaaat aatatattat tttttgtttc at 882

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<210> 368

<211> 28

<212> DNA

<213> *Diabrotica virgifera*

<400> 368

ggcggataaa gaaaagaagg tcaagaag 28

<210> 369

<211> 31

50 <212> DNA

<213> *Diabrotica virgifera*

<400> 369

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55 <210> 370

<211> 711

<212> DNA

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<213> *Diabrotica virgifera*

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<223> n = a, c, g or t/u

<400> 370

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      ccaggcactt atcaccctct taacagcagc cgagaaggaa gaaggtgaag aaggcgaagc 600
20      agcataaaca ccatcataac ttacaactga nagtcaatgt aaatcttcac ggctaccgtg 660
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<210> 371

<211> 2918

25 <212> DNA

<213> *Diabrotica virgifera*

<400> 371

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 aactaaacga taacttctgt ttatactgtt gtttttatcg tttacaatg gctctcttc 180
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<210> 372

<211> 26

50 <212> DNA

<213> *Diabrotica virgifera*

<400> 372

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<210> 373

<211> 30

<212> DNA

<213> *Diabrotica virgifera*

<400> 373

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<210> 374

<211> 1036

<212> DNA

<213> *Diabrotica virgifera*

<400> 374

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gacagacaga aagggaattc caaacacttt taaattatca aaataaagaa tatgtcagga 240
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<210> 375

<211> 620

<212> DNA

<213> *Diabrotica virgifera*

<400> 375

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aatatgacgc cataggcaaa agttttgtcc aacaatatta tatgcttttc gatgatccaa 180
accaaaggcc taatttggtt aacatgtata atgtagaaca ttcattttatg acctttgaag 240
gcaagcaatt acaaggatct gcaaagataa tggagaaatt aaattcctta ggattccaaa 300
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<210> 376

<211> 34

<212> DNA

<213> *Diabrotica virgifera*

<400> 376

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<210> 377
<211> 32
<212> DNA
<213> Diabrotica virgifera

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<400> 377
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<210> 378
<211> 429
<212> DNA
<213> Diabrotica virgifera

15

<400> 378

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tgacctttga	aggcaagcaa	ttacaaggat	ctgcaaagat	aatggagaaa	ttaaattcct	180
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atacacaagt	ttttgtttta	aaaccattaa	atggatcatt	ttttgttcaa	catgacattt	360
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<210> 379
<211> 846
<212> DNA
<213> Diabrotica virgifera

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<400> 379

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cccagcaaca	ggtgaatgaa	gttgtgggta	ttatgagagt	aaacgtcgag	aaagttctag	240
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<210> 380
<211> 35
<212> DNA
<213> Diabrotica virgifera

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<400> 380
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<210> 381
<211> 26
<212> DNA

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<213> Diabrotica virgifera

<400> 381

cacattgaac atttgacag gcgaca 26

<210> 382

<211> 656

<212> DNA

<213> Diabrotica virgifera

<400> 382

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gagagtaaac gtcgagaaag ttctagagag ggaccagaaa ctttcagagc tcgatagtcg 180
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aatatgggtg ttctgtttaa aaagtgaaca cctatcagtt gtgtaagtat tgagaatttg 600
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<210> 383

<211> 841

<212> DNA

<213> Diabrotica virgifera

<400> 383

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ccaaggagaa tacagagaat cgttttggca acctttatat tttccgttct acatatattt 180
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ttcagaatat gtaaagaacc tcttaatgga gttagtccac tttttaataa aaaaaaaatc 780
ttgtttataa tgatttaaat gaggatgaaa aattattttc aggttatgta tttccatccc 840
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<210> 384

<211> 28

<212> DNA

<213> Diabrotica virgifera

<400> 384

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<210> 385

<211> 36

<212> DNA

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<213> Diabrotica virgifera

<400> 385

ggactaactc cattaagagg ttctttacat attctg 36

<210> 386

<211> 636

<212> DNA

<213> Diabrotica virgifera

<400> 386

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<210> 387

<211> 2158

<212> DNA

<213> Diabrotica virgifera

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<210> 388

<211> 33

<212> DNA

<213> *Diabrotica virgifera*

<400> 388

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<210> 389

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<212> DNA

<213> *Diabrotica virgifera*

<400> 389

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<210> 390

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<212> DNA

<213> *Diabrotica virgifera*

<400> 390

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cgtgtgtatc acttaacgtg aagagcccct tggtttccga cacagaaata ggaatgggta 300
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<210> 391

<211> 2158

<212> DNA

<213> *Diabrotica virgifera*

<400> 391

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25 <210> 394
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<212> DNA

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<222> (833)..(8938)

<223> n = a, c, g or t/u

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<210> 397

<211> 32

<212> DNA

<213> *Diabrotica virgifera*

<400> 397

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<210> 398

<211> 826

<212> DNA

<213> *Diabrotica virgifera*

<400> 398

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<211> 1057

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<211> 23

<212> DNA

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<400> 400

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<210> 401

<211> 29

<212> DNA

<213> *Diabrotica virgifera*

<400> 401

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<210> 402

<211> 511
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      gtgcttcaca atttgaacag caagcgggaa aactaaagag aaaattttgg ttacagaatt 300
      taaagatgat gataataatg ggtgttattg gtcttgtaat ctttaataatc atagtcatga 360
      acttcattga actcatgggc caaaaattcg ttogaataat tggcatatac agaaaatcta 420
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25

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 <213> *Diabrotica virgifera*

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<210> 405
 <211> 26
 <212> DNA
 <213> *Diabrotica virgifera*

55

<400> 405

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<210> 406

<211> 763

5 <212> DNA

<213> *Diabrotica virgifera*

<400> 406

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<210> 409

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<211> 29
<212> DNA
<213> *Diabrotica virgifera*

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<210> 410
<211> 1125
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<213> *Diabrotica virgifera*

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35 <211> 1844
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<400> 411

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<210> 413

<211> 29

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<213> *Diabrotica virgifera*

45

<400> 413

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<210> 414

50 <211> 948

<212> DNA

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30     <400> 415

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<213>	Diabrotica virgifera

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<210> 418
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<212> DNA
<213> *Diabrotica virgifera*

<400> 418

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20 <400> 419

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<210> 421
 <211> 23
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 <213> *Diabrotica virgifera*

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<210> 422
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<400> 423

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<210> 424

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<212> DNA

<213> *Diabrotica virgifera*

<400> 424

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<210> 425

<211> 26

<212> DNA

<213> *Diabrotica virgifera*

<400> 425

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<210> 426

<211> 453

<212> DNA

<213> *Diabrotica virgifera*

<400> 426

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 <211> 1529
 <212> DNA
 <213> *Diabrotica virgifera*

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 <223> n = a, c, g or t/u

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25

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35

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tttgacagaca actggacgat acaagggatc taataacttt tagcaattga taaattgaac 960
gaaaaaatca caatgtttta tcaaaagctc aaacacaaga acacaaagtt tttatgatgt 1020
taaataaatg aagactttct accgttcaca cgaaaggcgc ttatcctgat ctggttacat 1080
tttcttaaga taaaaccgtg ggtacataat atacacaatc aaacttatat ggaatcacca 1140
tgtattttcaa accaatattt atttcttttg aaaaaaactt gttaccaggc gcggatacag 1200
gggaggggtca aggggtctat agacccccct attgtattta gtctataaga atttttttat 1260
tattttattat ttttttctgt caactctaaa ctttaagcca ccagtagaac actaaaatta 1320
aacgacaacc acttccaaag aattattgaa agaagcaata aaatctaata aaaccgagcc 1380
ttttctgaaa aataaattga agccgcattt gtttggttac cgatggagcc gtaacaact 1440
```

```
gaaatatttt tctcaattca aagaataacg gaaatgatat cttaaaatgc aaatactttt 1500
cgtgaggtaa ggtttatacc cgtgtgaat 1529
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40

<210> 428
 <211> 30
 <212> DNA
 <213> *Diabrotica virgifera*

45

<400> 428
 gtcaaaagac catgactatc acagatgtgg 30

50

<210> 429
 <211> 31
 <212> DNA
 <213> *Diabrotica virgifera*

55

<400> 429
 cgtccagttg tctgcaaaact atgtacttac c 31

<210> 430
 <211> 731

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<212> DNA

<213> *Diabrotica virgifera*

<400> 430

5

10

15

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gtcaaaagac catgactatc acagatgtgg attagtagca cttcaaattt gtttaataaaa 60
catagaattt atagaatagt ttccccgttt tataccgcat atgcgacttt aggattatag 120
caggctgtca tctctagggc tacgggtatac aagaaagata acagggccag tgctacgctt 180
caaccgccta ttattacccc tgggttttagc caaggaactc attttattca ggctgagtcg 240
acctggggcc tatttaaaaa tgtctagttg ttcttgccgg cgctgggtct cgaaccagg 300
tctaccagca agcgagtcag acatcctacc gctgaactac gccggcccat acgtagagtt 360
tataattatc ttatatataa taaaggaatt tgattaaaaa aggtaaaaat acattgtatt 420
gggttgctta ggcctaaata catatctctt cctattagta agttacaaaa tggtgagatt 480
cgatcatttt tgtgggatat gtagttgatg aattaagtag taagtagtag ttgaatacac 540
gttacatttt ctcaacattg attaatacat ttattttttt ccaaataaag aaaaatttag 600
ctactaaaaa aatataatgct aaatattgtt tatcatcagc taaaagttag gagatctgtt 660
aaatcctata aaatatgaaa acaatgaaat gtgttgtttc ggtaagtaca tagtttgtag 720
acaactggac g 731
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20

<210> 431

<211> 1208

<212> DNA

<213> *Diabrotica virgifera*

25

<400> 431

30

35

40

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taaactgtta tttttgataa cagtaatat ggtatccctt tgcgccatcca gtgcagacaa 120
ttataacaaa tgcctgaaa ccagccatat acgatcccta atttaccaga atacattgaa 180
ggggagagtt atacatgtac gcattccagg cacaggtttc tttgaagctc caatcacttg 240
tcttcaggtt accgatataa atgaaagttt cagtagacca gttgtagaag aaggtggata 300
tggaaggagag tacgtagttt tacgtattga cccagttgaa tcaggagaac agttacaata 360
cgatgttcag atttatattg acgaagctgt tacagcctat cctcaataaa tgttcggtat 420
aaatgtttta gaaattcgag tagccccttt aaagataagc agttgctggt attttaacag 480
cattactgat tgtaagttaa tcatttcaga ccttcacgta aactatgttg ttacaaaaaac 540
gcatattagg acaataatcc aaattattag acaataaata ttaggcaaga gaaattaaac 600
gagtttctag ttttaagtac aaacaagtga agttcatcag caaaacagaa ttcagaatta 660
ttctacgtat tatattaaaa gcactatttg gttaaaagtt atcatttttg ggggtaaaag 720
aatctattaa tttgtcttga gtaaaggtag tatttgttta aatttgccga ccgatgatag 780
gtagattggg ccaagtacag tgggtgatca tattattaga gccacctaata atgttcagtg 840
ttttggagga atgtttacaa tgttttgtaa tttaatgttt acaatgttta gaatgtttac 900
attaaattac aaaaacgcat attaggacaa taatccaaat tattagacaa taaatattag 960
```

45

```
gcaagagaaa ttaaacgagt ttctagtttt aagtacaaac aagtgaagtt catcagcaaa 1020
acagaattca gaattattct acgtattata ttaaaagcac tatttggtta aaagttatca 1080
tttttggggg taaaagaatc tattaatttg tcttgagtaa aggtagtatt tgtttaaatt 1140
tgccgaccga tgataggtag attgggccaa gtacagtggg tgatcatatt attagagcca 1200
cctaatat 1208
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50

<210> 432

<211> 23

<212> DNA

<213> *Diabrotica virgifera*

55

<400> 432

ccttcgccca tccagtgcag aca 23

<210> 433

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<211> 30
<212> DNA
<213> *Diabrotica virgifera*

5 <400> 433
ctccaaaaca ctgaacatat taggtggctc 30

<210> 434
<211> 752
10 <212> DNA
<213> *Diabrotica virgifera*

<400> 434

15 ccttttcgcca tccagtgcag acaattataa caaatgtcct gaaaccagcc atatacgatc 60
cctaattttac cagaatacat tgaaggggag agttatacat gtacgcattc caggcacagg 120
tttcttttgaa gctccaatca cttgtcttca ggttaccgat ataaatgaaa gtttcagtac 180
accagttgta gaagaagggtg gatatggaag ggagtacgta gttttacgta ttgacccagt 240
tgaatcagga gaacagttac aatacgatgt tcagatttat attgacgaag ctgttacagc 300
20 ctatcctcaa taaatgttcg gtataaatgt ttaagaaatt cgagtagccc ctttaaagat 360
aagcagttgc tgggtatttta acagcattac tgattgtaag ctaatcattt cagaccttca 420
cgtaaactat gttgttacia aaacgcataat taggacaata atccaaatta ttagacaata 480
aatattagga aagagaaatt aaacgagttt ctagttttaa gtacaaacaa gtgaagttca 540
tcagcaaaac agaattcaga attattctac gtattatatt aaaagcacta tttgggttaa 600
25 agttatcatt tttgggggta aaagaatcta ttaatttgtc ttgagtaaag gtagtatttg 660
tttaaatttg ccgaccgatg ataggttagat tgggccaagt acagtgggtg atcatattat 720
tagagccacc taatatgttc agtgtttttg ag 752

<210> 435
30 <211> 1290
<212> DNA
<213> *Diabrotica virgifera*

<400> 435

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aaaaccgggtg tatattattg tgaataaatg tgtcaaataat aggatataata cctgaaacag 120
attaaactgca cttgttttaaat aaaaggcact actacttact aacacaagat gtccgtattg 180
40 ggaatgggtat cagccgtagc gggcctttgtc aaagtccgct acttgggtga taaagctcta 240
atcgacaata tgggtgtttag agccactat agagtcacgt cggccatatt gtttttatgc 300
tgtatcatcg ttactgcgaa taatctaatt ggtgacccca ttcagtgcac caacgacagg 360
gggtgttccag gtcattgtaaat aaatacgttt tgctgggataa cgcatacttt tacgtttacca 420
catgaacaag gaaaacgcgt cgggacagaa gttgctcatc ctggtcttgg taacgaaaat 480
caggataaga gataccacag ctactaccaaa tgggttccat tcggttttatt cttccagggc 540
45 gtcctctttt acatccctca ttgggttgtgg aaaaattggg aacaaggaaa aattcgtatg 600
atcaccgaag gtatgagagg atcgatggtc ggagttggggg aaaaggcaga gagagaacat 660
agacagaata gactcgtaca atatcttatac gaaacgatgc acatgcacac ttcctatgca 720
ttcggataact ttatttgtga agctctaaac ttcgttaatg tgatggtaaa catattcatg 780

50 actgacaaat tcctcgggtg agcgttccta acctacggca ctgacgtagt ttcctttttcg 840
aacatgaatc aagaaaaatcg cacggatccc atggtagcca tctttccaag ggtaacaaaa 900
tgtacattcc acaaattcgg tccttcagga tcaattcaga agcatgacgc cctctgcgtg 960
ttagccttga acatttctcaa cgagaagatt tacattttcc tatgggtctg gtttattatt 1020
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55 acaagagaaa cgatttttgaa gaggagattc agattcaagg tacccaatgc tggtgagact 1140
attgtcagaa aaacacaggt tgggtatttc cttttgattc acttactggg acaaaacaca 1200
aaccaattgg tatttggcga aattttggac gaattcgtaa gaagactgaa tttcggtagt 1260
aacagcaact taccgtctgc tcccagcacg 1290

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<210> 436
<211> 29
<212> DNA
<213> Diabrotica virgifera

5

<400> 436
cacaagatgt ccgtattggg aatggatc 29

10

<210> 437
<211> 31
<212> DNA
<213> Diabrotica virgifera

15

<400> 437
gtaagtgaat caaaaggaaa tcaccaacct g 31

20

<210> 438
<211> 1023
<212> DNA
<213> Diabrotica virgifera

<400> 438

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cacaagatgt	ccgtattggg	aatggatc	gccgtagcgg	gctttgtcaa	agtccgctac	60
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gccatattgt	ttttatgctg	tatcatcgtt	actgcgaata	atctaattgg	tgacccatt	180
cagtgcataca	acgacagggg	tgttccaggt	catgtaataa	atacgttttg	ctggataacg	240
catacttttta	cgttaccaca	tgaacaagga	aaacgcgtcg	ggacagaagt	tgctcatcct	300
ggctcttggt	acgaaaatca	ggataagaga	taccacagct	actaccaatg	ggttccattc	360
gtttttattct	tccagggcgt	cctctttttac	atccctcatt	ggttgtggaa	aaattgggaa	420
caaggaaaaa	ttcgtatgat	caccgaaggt	atgagaggat	cgatggtcgg	agttggggaa	480
aaggcagaga	gagaacatag	acagaataga	ctcgtacaat	atcttatcga	aacgatgcac	540
atgcacactt	cctatgcatt	cggatacttt	atttgtgaag	ctctaaactt	cgtaaagtgt	600
attgtaaaca	tattcatgac	tgacaaattc	ctcgggtggag	cgttcctaac	ctacggcact	660
gacgtagttt	ccttttcgaa	catgaatcaa	gaaaatcgca	cggatcccat	ggtagccatc	720
tttccaaggg	taacaaaatg	tacattccac	aaattcggtc	cttcaggatc	aattcagaag	780
catgacgccc	tctgcgtgtt	agccttgaac	attctcaacg	agaagattta	cattttccta	840
tggttctggg	ttattatttt	agctatactg	tccggtttgg	ctatttgtga	ttcggcagct	900
gttgtattac	tacctagtac	aagagaaacg	atttgaagag	gagattcaga	ttcaaggtac	960
ccaatgctgt	tgagactatt	gtcagaaaaa	cacagggttg	tgatttcctt	ttgattcact	1020
tac						1023

40

<210> 439
<211> 845
<212> DNA
<213> Diabrotica virgifera

45

<400> 439

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catatgtttc	gtgttaaagt	gcagtgtgag	tgaagttaca	actttgcggg	gcacgccta	120
aaagtcattg	ctcttgtagc	cagctcctgg	cgagagacat	ccttaggtta	cccggtgagc	180
ctgaactctt	tgcccaacgg	tttgaatcct	ttacctcaga	ctagtacttt	aactccttta	240

55

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```

cccaccaaca ttaatcctat taatcttgaa acatccgata cttcgctgat caatcgacaa 300
acgccgtcac aaaactcaca aaatagtaat aacagtgtag ataagaacca gaacattgag 360
tgtgttgtgt gtggggacaa agtttctggt aaacactacg gacaattcac atgcgaagga 420
5  tgcaaatcat tttttaaaag gagtgttaga agaaatttaa cgtactcatg tgcgaggagc 480
cgaaattgtc cgatagatca acatcataga aaccagtgcc aatattgtcg tttaaaaaaa 540
tgtatgaaaa tgggcatgcg gagagaagct gtgcagcgtg gcagagtacc accgtcgcag 600
ccttcgcttc caggtttacc aaatcagttc cttaactcaa cagactcgat gaatacatct 660
ctaagcaacc acacgtacct cagtagttac atatcactat tattaagagc agagccgtac 720
cctacgagtc gatatggtca atgtctgcaa agtaataaca ttatgggcat tgacaatata 780
10  tgcgagttag cagcgcggct gctattctca gcagtagaat gggcaaggaa tataccgttc 840
tttcc 845

```

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<210> 440
<211> 25
15  <212> DNA
    <213> Diabrotica virgifera

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<400> 440
gctcctggcg agagacatcc ttagg 25
20

```

```

<210> 441
<211> 28
<212> DNA
25  <213> Diabrotica virgifera

```

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<400> 441
gcagacattg accatatcga ctgtagg 28

```

```

<210> 442
30  <211> 606
    <212> DNA
    <213> Diabrotica virgifera

```

```

<400> 442
35

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tgaatccttt acctcagact agtactttta ctcctttacc caccaacatt aatcctatta 120
atcttgaaac atccgatcct tcgctgatca atcgacaaac gccgtcacia aactcacaaa 180
40  atagtaataa cagtgtagat aagaaccaga acattgagtg tgttgttgtt ggggacaaaa 240
gttctggtaa acactacgga caattcacat gcgaaggatg caaatcattt tttaaaagga 300
gtgttagaag aaatttaacg tactcatgtc gagggagccg aaattgtccg atagatcaac 360
atcatagaaa ccagtgccaa tattgtcgtt taaaaaatg tatgaaaatg ggcattgcgga 420
gagaagctgt gcagcgtggc agagtaccac cgtcgcagcc ttcgcttcca ggtttaccaa 480
atcagttcct taactcaaca gactcgatga atacatctct aagcaaccat acgtacctca 540
45  gtagttacat atcactatta ttaagagcag agccgtaccc tacgagtcga tatggtcaat 600
gtctgc 606

```

```

<210> 443
<211> 932
50  <212> DNA
    <213> Diabrotica virgifera

```

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<220>
<221> modified_base
55  <222> (650)..(836)
    <223> n = a, c, g or t/u

```

```

<400> 443

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 aaagagtatg tgggtgtttaa tgttatttcg agtgggatta tctatcttat ttttctttca 60
 tacaacatta gctcttcctg atgaatgtag ttctatttcg cctgtaagaa gttgtttact 120
 gaggacaaac tacatagata tacggctgtg gagatattac gctggctatt tttgctacat 180
 ttatacaaat gaagccaggt tggatatcaa atataattcc actagttaca acataacatg 240

10
 tggcggtgaa aacgcaacga ttcccgtagc aaggggtggag gagaacataa tagctagtta 300
 tgattatata gataaagaag atgtccagca tatcagaaaa tcgtttaaga ctgacgaggt 360
 ttttaaaaat tatatatctt gttgccaaag agctataagg tgttgcaatg atcacatgga 420
 cgaggaaaat gttattccaa cgcaatcaca atgtcctgta atatgggatg cctgggtcttg 480
 ttttccacaa actaaagtta atactacagc caagctacca tgtagtagcc aagcatacca 540
 atctcccgat gaagtctgta ctttagaaaag cgaaaaaacac tgcattctgga acggaacaaa 600
 tcaaaaagca caatggatcc aacaaactga ctacacaacg tgtgccatan gcgccggttt 660
 acgaacgaag atacaacttc catattatat ttctggggag tctgtatcgg cttttgtata 720
 ccggcaatat ctatatTTTT ctttttcgaa aaacttcgaa agaccatcag agttattctg 780
 15 cataggaacc ttttgatagc ccattgtgng tcaggaatgt cttgacaatt atgtgncaag 840
 aactagtgtc gctagacgtt ttaaaagctt cggctctaag tcatcgtagc atggacaaca 900
 atggagtccc atggtcggat attggctttt at 932

20
 <210> 444
 <211> 31
 <212> DNA
 <213> Diabrotica virgifera

25
 <400> 444
 gctcttctg atgaatgtag ttctatttcg c 31

30
 <210> 445
 <211> 26
 <212> DNA
 <213> Diabrotica virgifera

<400> 445
 cgtacgatga cttagagccg aagctt 26

35
 <210> 446
 <211> 817
 <212> DNA
 <213> Diabrotica virgifera

40
 <220>
 <221> modified_base
 <222> (627)
 <223> n = a, c, g or t/u

45
 <400> 446

50

55

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tacatagata tacggctgtg gagatattac gctggctatt tttgctacat ttatacaaat 120
gaagccaggt tggatatcaa atataattcc actagttaca acataacatg tggcgggtgaa 180
aacgcaacga ttcccgtagc aagggtggag gagaacataa tagctagtta tgattataca 240
5 gataaagaag atgtccagca tatcagaaaa tcgtttaaga ctgacgaggt ttttaaaaaat 300
tatatatctt gttgccaaag agctataagg tgttgcaatg atcacatgga cgaggaaaaat 360
gttattccaa cgcaatcaca atgtcctgta atatgggatg cctggctcttg ttttccacaa 420
actaaagtta atactacagc caagctacca tgtagtagcc aagcatacca atctcccgat 480
gaagtctgta ctttagaaaag cgaaaaacac tgcctctgga acggaacaaa tcaaaaagca 540
10 caatggatcc aacaaactga ctacacaacg tgtgccatag cgccgggtta cgaacgaaga 600
tacaacttcc atattatatt tctgggnagt ctgtatcggc ttttgtatac cggcaatatc 660
tatatttttc ttttctgaaa aacttctgaaa gaccatcaga gttattctgc ataggaaacct 720
tttgatagcc attgtggtca ggaatgtctt gacaattatg tgcaaagaac tagtgctgct 780
agacgcttta aaagcttcgg ctctaagtca tcgtacg 817

```

<210> 447

<211> 880

<212> DNA

<213> *Diabrotica virgifera*

<220>

<221> modified_base

<222> (737)..(851)

<223> n = a, c, g or t/u

<400> 447

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ttgaaagtag tgaaaaaatc aggtgaaact ggatattggg tgatcaatac taaggtaggc 180
aaaggacaga tagtatttaa tggaaaagac aagccagatg ttactttcat tgtaaaggaa 240
gaggatgttt tagaattatt gtctggcaaa attccaccac agaaggcatt tttccaaggc 300
aaagtataaaa ttcaagggaa tatgggtgta gccatgcgat taatagaatt acagaaaaca 360
gccgctgcca aaattgaggt acttagggct aagttataaa ttacgtttat aggtaatttt 420
35 ctttatcttt ctgtattgtg tacactaagg ttttgtttta tctttttggg agtatatatt 480
atataagtga caaacatac tttcttggtt tacacatcac ttctgtaaa aatattgtac 540
acgctgtaca atgagtcctt tatgtaaaca aatatgtaag tataaatact tgctctgtta 600
tctccttttt attacatatt tttgttgata acttcagaat ctattgacct tttgtgaaat 660
actttcaata ttttgtaaac agttgaagac cagtgttaatt tttcctgaga tactaaattc 720
40 aatatatttt gtttcanaca agtttggtcc gtaaataaac tagacatgta tatcattgta 780
tattattaat aatatgaaac cttgatgtct gtaggtaaat ggtcttaatg atttaatggt 840
ttttcataat ncatagtcn aagtcacaaa atagcatata 880

```

<210> 448

<211> 30

<212> DNA

<213> *Diabrotica virgifera*

<400> 448

ggcaatgaat gaagatgaag aaggattagt 30

<210> 449

<211> 34

<212> DNA

<213> *Diabrotica virgifera*

<400> 449

ccattaaatc attagacca ttacctaca gaca 34

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<210> 450
 <211> 774
 <212> DNA
 <213> *Diabrotica virgifera*

5
 <400> 450

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10    agtagtgaaa aaatcaggtg aaactggata ttgggtgatc aatactaagg taggcaatgg 120
      acagatagtg tttaatggaa aagacaagcc agatgttact ttcattgtta aggaagagga 180
      tgttttagaa ttattgtctg gcaaaattcc accacagaag gcatttttcc aaggcaaagt 240
      aaaaattcaa gggaatatgg gtgtagccat gcgattaata gaattacaga aaacagccgc 300
      tgccaaaatt gaggtactta gggctaagtt ataaattacg tttataggta attttcttta 360
      tctttctgta ttgtgtacac taagggtttt ttttatcttt ttgggagtat atattatata 420
15    agtgacaaaa catactttct tgttttacac atcacttcct gtaaaaatat tgtacacgct 480
      gtacaatgag tcctttatgt aaacaaatat gtaagtataa atacttgctc tgttatctcc 540
      tttttattac atatttttgt tgataacttc ggaatctatt gaccttttgt gaaatacttt 600
      caatattttg ttaacagttg aagaccagtg taatttttcc tgagatacta aattcaaata 660
      tttttgtttc aaacaagttt gttccgtaaa taaactagac atgtatatca ttgtatatta 720
20    ttaataatat gcaaccttga tgtctgtagg taaatggtct taatgattta atgg      774
  
```

<210> 451
 <211> 576
 <212> DNA
 <213> *Diabrotica virgifera*

25
 <400> 451

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      aaattatcgg catatattat gcaggataac caactacatg ctaatctaag agtggatgaa 60
30    gctatggctg tcgcagctgc acttaaaatt ggcgccaaaa gtccaaaaga tcgagaagat 120
      atcattaacg aaatcctaga cacacttgga ctgctggatc ataagaaaac aatgacaagc 180
      gggttgtcgg ggggccaaaa gaagagattg tcaatcgctc tagaattagt tagtaatcct 240
      ccagttatgt ttttcgatga acctactagt ggattggatt cttcatcatg ttttcaatgt 300
      atatcactgt tgaaaacctt agctaaaggt ggaagaacta taatatgtac tattcaccaa 360
35    ccttcagcta gactgtttga aatgttcgac caactttata cactcgctga tgggtcaatgt 420
      gtttaccaag gttctacgac attcttggtg cccttttttg caagtctgca gttacagtgt 480
      ccttcatacc acaatccagc ctccctatatt atagaagtag catgtgggga atatggagat 540
      cacacgagaa cgttagttaa cgctatagaa aatggt      576
  
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<210> 452
 <211> 34
 <212> DNA
 <213> *Diabrotica virgifera*

40
 <400> 452
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<210> 453
 <211> 26
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 <213> *Diabrotica virgifera*

50
 <400> 453
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<210> 454
 <211> 482
 <212> DNA

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<213> Diabrotica virgifera

<400> 454

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      cacttggact gctggatcat aagaaaacaa tgacaagcgg gttgtcgggg ggccaaaaga 180
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      ctactagtgg attggattct tcatcatgtt ttcaatgtat atcactgttg aaaaccttag 300
10     ctaaagggtg aagaactata atatgtacta ttcaccaacc ttcagctaga ctgtttgaaa 360
      tgttcgacca actttatata ctcgctgatg gtcaatgtgt ttaccaaggt tctacgacat 420
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<210> 455

<211> 759

<212> DNA

<213> Diabrotica virgifera

<400> 455

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      atatatggga attgtgcaat gttttttatt ctggacaggt aaaaagcgc tctgttcttc 180
25     aaagaatggt tggcaacatt aaaactgcag taatcttaaa agatgtgtcc atgttggtac 240
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      atgttatttc aagacgagca caaggcccta taagaggaca gatatatctg aacaaccatc 360
      cagtcagtat gggtttattc cagcagaaat gtgcatatgt tacacataaa tgtgatttta 420
      taccaggact aaatgttgaa cagacgttgt attatactcc gactaagttc actggctatt 480
30     taaaaatgtc taaagtaaag caagtgatag cagatttagc attgtcacia gtcgctaaaa 540

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      tcaaaaaccc agtggtagta ttactagacg aaccacactg ggatctggac ccactaaaca 660
      catacctaata aatttcaata ctttcaaatg cagctaaaaa gtatggaact gctataatct 720
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<210> 456

<211> 32

<212> DNA

<213> Diabrotica virgifera

<400> 456

ggtactgctt tagttgttt ttgacagatt cg 32

<210> 457

<211> 31

<212> DNA

<213> Diabrotica virgifera

<400> 457

gcttccat cgtcaagatt atagcagttc c 31

<210> 458

<211> 710

<212> DNA

<213> Diabrotica virgifera

<400> 458

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<210> 459

15 <211> 837

<212> DNA

<213> *Diabrotica virgifera*

<400> 459

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 aataaagaga tgttacggtc catcgctgaa cagagtattg gcccacattg ttattggtct 180
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 tgtatatttg tatggtactc ttttactcac agtatatact ggtaaaatgc ccgtaaacttt 300
 atcatttcct ctagaaatga agatactctc tagagagcat ttttaaccgtt ggtataagct 360
 aactccatat ttattgtctg tgatattagt tgaaattcct ttccaagtta tatgtacatg 420
 gatgtacata gcagtatctt attcggttaac gaaccagcca ttagacttta gggtattctt 480
 gtttgtcatt tttgtaacag cgtgttctct ctgtggccaa tccatgggat attttatagg 540
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35 <210> 460

<211> 28

<212> DNA

<213> *Diabrotica virgifera*

40 <400> 460

ggtctctatt ccgacgaaac gaaagcag 28

45 <210> 461

<211> 31

<212> DNA

<213> *Diabrotica virgifera*

50 <400> 461

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<210> 462

<211> 673

<212> DNA

55 <213> *Diabrotica virgifera*

<400> 462

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 ttggccacaca ttgttattgg tctgatcttt ggctatttgt atagaaacgt tggagtgcc 180
 gcgataacag ttttagcaaa ttatgtatat ttgtatggta ctcttttact cacagtatat 240
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 cattttaacc gttgggtataa gctaactcca tatttattgt ctgtgatatt agttgaaatt 360
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 10 ccagtgttag cctgcttctt atcagtcctc gggttttgca tcagagcaat agacacctct 600
 accatgttca aaccgatctt cttcatcagt tacttttagag cagcattcca aagcgtcggt 660
 tatagtattt acg 673

<210> 463

15 <211> 660

<212> DNA

<213> *Diabrotica virgifera*

<400> 463

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 atcagagtca aaactttaga tgctagtcat aatcgtaata ccgaaatttc tcctatgtct 180
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 aatttagatt taaattctct gagaatcgct ccagttcatt cgaaccgttc cttaccagaa 360
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<210> 464

<211> 31

35 <212> DNA

<213> *Diabrotica virgifera*

<400> 464

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40
 <210> 465
 <211> 26

<212> DNA

<213> *Diabrotica virgifera*

45
 <400> 465

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<210> 466

50 <211> 543

<212> DNA

<213> *Diabrotica virgifera*

<400> 466

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 gaaattttctc ctatgtctat tcctaataagt atagaactttt tatttattaa taacaatttt 180
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 aaccgttcct taccagaaat atatcttggg ggcaatacct ttcattgtga ctgtactatg 360
 gagtggctac agcttatcaa caacatgtca gcatccaggc agtatcctcg tgtaatggac 420
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<210> 467

<211> 894

<212> DNA

15 <213> *Diabrotica virgifera*

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<400> 467

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 gatcccatct ggaaacaaac tagcagattt tttgcccccg aaaactgttt atgatgccat 180
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 30 ggacgtatct tccatttag gaatatctac actagacctt agcctcaatc agatatcaac 420
 aatccatcca caggcctttg acaacatgcc ggatctctta aacattcaac ttgctgacaa 480
 ttttataacg caatggaatc cagaatggct caagaataca ccgctattga ccaggatctc 540
 gcttcagaat aattccatag aaaagctacc agcccatgca tttaaaaaca tggtaggaga 600
 taaaaagtat ggaaaaatag acctcactat taatctggta tttagtcata ataaaataag 660
 35 tgagatagat cctgaagctt tcgcggatct cagcagaatt aacaacttgt ggtagataa 720
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 aacgaacaca tagattcgaa tcgcgcgact gtaattgctt gagaagatca agga 894

40 <210> 468

<211> 26

<212> DNA

<213> *Diabrotica virgifera*

45 <400> 468

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<210> 469

<211> 32

50 <212> DNA

<213> *Diabrotica virgifera*

<400> 469

ctaaccacaa gttgttaatt ctgctgagat cc 32

55 <210> 470

<211> 544

<212> DNA

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<213> Diabrotica virgifera

<400> 470

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      attgcaaagg atgtattttc ccatttagga atatctacac tagaccttag cctcaatcag 240
      atatcaacaa tccatccaca ggcctttgac aacatgccgg atctcttaaa cattcaactt 300
10     gctgacaatt tcataacgca atggaatcca gaatggctca agaatacacc gctattgacc 360
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      gtaggtgata aaaagtatgg aaaaatagac ctactatta atctggtatt tagtcataat 480
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<210> 471

<211> 210

<212> DNA

<213> Diabrotica virgifera

<400> 471

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25     atgccaaata caaacacggg ctctttgccc gcaaaagact tcttcctcac tgaagatatc 180
      ttgtaagttc ttcctctttt caaacgggcg

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<210> 472

<211> 25

<212> DNA

<213> Diabrotica virgifera

<400> 472

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<210> 473

<211> 33

<212> DNA

<213> Diabrotica virgifera

<400> 473

ccgttgaaa agaggaagaa cttacaagat atc 33

<210> 474

<211> 203

<212> DNA

<213> Diabrotica virgifera

<400> 474

gctgacataa ccaaaaagcg caagcgccac cacacaaaaa accgtcttca ttttcttgag 60

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      caaatacaaa cacgggctct ttgccggcaa aagacttctt cctcactgaa gatattctgt 180
      aagttcttcc tcttttcaaa cgg

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<210> 475
 <211> 1139
 <212> DNA
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<400> 475

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	caagaaaatg	gaactcggct	agggccggttc	tgthtaaaagg	cgcttgactg	attggcgctg	180
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	tgggtcgagc	tctccgtggg	taataataat	tattgggttca	aaaggatcca	aacttgtcac	360
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	tctttagaag	actacaacag	ttcacacagt	tctttaaacc	atcaattctg	cgaagcttcg	1080
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<210> 476
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 <212> DNA
 <213> *Diabrotica virgifera*

30

<400> 476
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35

<210> 477
 <211> 31
 <212> DNA
 <213> *Diabrotica virgifera*

40

<400> 477
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<210> 478
 <211> 444
 <212> DNA
 <213> *Diabrotica virgifera*

45

<400> 478

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<210> 479
 <211> 851
 <212> DNA
 <213> *Diabrotica virgifera*

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<210> 480
 <211> 27
 <212> DNA
 <213> *Diabrotica virgifera*

<400> 480
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<210> 481
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 <213> *Diabrotica virgifera*

<400> 481
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<210> 482
 <211> 797
 <212> DNA
 <213> *Diabrotica virgifera*

<400> 482

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55

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<210> 483

<211> 1612

<212> DNA

<213> *Diabrotica virgifera*

<400> 483

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 cgagctgtga taaattaccg gaaaatatcc acaatggtgc caaaagcaac attttggaca 660
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 35 ttaatgatag ggcttgtcca gatagatcca tttatatctg ttcgaacagt caagcacctc 780
 taaaggctct ggaagcaccg aagcaagtca gctctaagtt gattcttgaa tgcaagatag 840
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<400> 493
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 g c g a t g g a t c a g a t g a a g a a t g c t t a c c t a a c a a a t g t c c c c a a g a a g c t t t t a g t t g c a 480
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<400> 502

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 g c t g a t t c a t c t t c a a a a t g c a t a g a a g g a a t t t g c g a c t g t a t t a t t c g g a c a a a t g g c 240
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 t c a g a t g a a g a a t g c t t a c c t a a c a a a t g t c c c c a a g a a g c t t t t a g t t g c a a a t c a t c a 420
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<213> Diabrotica virgifera

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<211> 31

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31

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<210> 513
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 <213> *Diabrotica virgifera*

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<400> 515

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	attatctaata	caatcacatt	ttacactaat	attctcaaaa	tcacatttag	attttaataa	420
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<212> DNA

<213> *Diabrotica virgifera*

<400> 519

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<212> DNA

<213> *Diabrotica virgifera*

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<213> *Diabrotica virgifera*

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<212> DNA

<213> *Diabrotica virgifera*

<400> 522

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<212> DNA

<213> *Diabrotica virgifera*

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<212> DNA

<213> Diabrotica virgifera

<400> 524

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<210> 525

<211> 33

<212> DNA

10 <213> Diabrotica virgifera

<400> 525

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<210> 526

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<212> DNA

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<400> 526

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<213> Diabrotica virgifera

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25 <213> Diabrotica virgifera

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<211> 36

<212> DNA

<213> Diabrotica virgifera

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<210> 530

<211> 947

40 <212> DNA

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<400> 530

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<212> DNA

<213> *Diabrotica virgifera*

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taaccacact ccaccagtc cgaatatttc ttgaggagaa atattcggcc tacttactaa 1140

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<210> 532

<211> 29

<212> DNA

<213> *Diabrotica virgifera*

<400> 532

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<213> *Diabrotica virgifera*

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<400> 533
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<213> *Diabrotica virgifera*

<400> 534

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    gcagcgtgga aactatcaat gagtaggaga cagttcataa cggctcttcta cccgacagtt 240
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    agtcatgggg ttttatggta ttattttctat acatggtttt gaataatgta agtctcgtca 480
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    ctgggttgggt cttgcagact attaaaaaga agtagttttt aatagctgat ggacaaaaca 720
    ggcacaaaata tgcacaaaatt gcacagtagt gagggtccaa aagccttagt aattaggaac 780
    aaaatcttta aatagctctt taataaaatg ttttatactt acatgaaaag gttgcagcca 840
    cccatccttg gaatagttga tgaaagagaa agaatttaat gaagggtgaa atgaaacatg 900
    atatgaacca gatgagatgt gataggaatg tggatttggg aacgaaggac tatggatatt 960
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<400> 535

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    caatgggtta atgtatataa acgtcctata aaaatgctaa ataactatat ccgtgttact 480
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<213> Diabrotica virgifera

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<210> 537

<211> 31

<212> DNA

<213> Diabrotica virgifera

<400> 537

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<210> 538

<211> 917

<212> DNA

<213> Diabrotica virgifera

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<212> DNA

<213> Diabrotica virgifera

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25 <213> *Diabrotica virgifera*

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<213> *Diabrotica virgifera*

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<212> DNA

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<400> 552

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<213> *Diabrotica virgifera*

<400> 556

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<213> *Diabrotica virgifera*

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<210> 558

<211> 725

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<212> DNA

<213> *Diabrotica virgifera*

<400> 558

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10 gattaagatt ccaatcaaag tttttggcct aggtgaactg tagttttata gaaaaatctc 240
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15 agataaaaaga ttttgttttg tgagaatatc gctaaatatt atatdddttga tacattaata 600
aatatacaga ttgggcaagc tagtttttga ataacatatt gacattdttat tatcggtattc 660
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<210> 559

<211> 874

<212> DNA

<213> *Diabrotica virgifera*

<400> 559

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25 atttgattaa attatttaaag ttttgtattdt tgataatgat ttccaagttg gaaattgaaa 180
cgtcaaataa attdtaattta aaacttaaac tgtggccttg tcccctgtca caagaaaaaa 240
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caatgattca cagtgttcaa ggaattdgtt caacttagcc gcccgtaa atgacccata 420
gaccggaggt atattgttac cgaggcaaat tttatgaaat catcttcctt tttcccttat 480
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gagagagaac aaatgattga gtaaatttagt aaaaaaacat taatttagtag tcatcttaat 660
tataaatcaa attaataata aaaatatccc aactaaaata ttttactaaa cgtcataaccg 720
ttggtcatat taaacgtcat acatatttdt acctaattat gacagaagtc aacaagcact 780
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<210> 560

<211> 24

<212> DNA

<213> *Diabrotica virgifera*

<400> 560

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<210> 561

<211> 32

<212> DNA

<213> *Diabrotica virgifera*

<400> 561

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gagatcaaac ttgtagaggt ggaaaattgt cg 32

<210> 562

<211> 658

<212> DNA

<213> *Diabrotica virgifera*

<400> 562

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      tatagaccag cgaagtattg ataaggttac caatgattca cagtgttcaa ggaatttggt 180
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      cctaattatg acagaagtca acaagcactt aagataacgt ctaaatgtga gaaactacta 600
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<210> 563

<211> 849

<212> DNA

<213> *Diabrotica virgifera*

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<221> modified_base

<222> (765)

<223> n = a, c, g or t/u

<400> 563

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      ttcagttttt ttaagtctgc ttattttacat agaattgtgt gccagtgtgg agtgcagtgc 180
      attctatgta aatggcgtac ttaaacaagg ttgaggtttt ggacttctca ctgttgcttt 240
      gatgtatcga tataagctac atagtagata catagaggaa atcttgtgct ttattctttt 300
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      accttcattg acatatatcc aaatctatat tgccagggtg ttggaaataa taccctggat 480
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      ctattgaaga atattaagaa gctacagggt acttttcatt tttccaaaat atcatttgta 600
      tttttcagtt ctattctgtc acaactaaat tttattccac tttaccacga gagtaatctg 660
45      ttttttcgta actaaaagag gatcgatggg tagccaagaa gttgagaaac agtaagattt 720
      caaatattgc aaaacgttgc aaatattttt aagaatgtat tttanaatgt taaatggata 780

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50      gaaaacatc 849

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<210> 564

<211> 28

<212> DNA

<213> *Diabrotica virgifera*

<400> 564

cattcagtgg accaaaggat acatatcg 28

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<210> 565
<211> 35
<212> DNA
<213> *Diabrotica virgifera*

5

<400> 565
gactgcttc tgattagttc atgtatccat ttaac 35

10

<210> 566
<211> 655
<212> DNA
<213> *Diabrotica virgifera*

15

<400> 566

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acatagagga	aatcttgtgc	tttattcttt	tttagaattt	caatgggtta	tatattagat	180
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gtacacaaac	tactagtcta	aagaaacacc	gactattgaa	gaatattaag	aagctacagg	420
ttacttttca	tttttccaaa	atatcatttg	tatttttccag	ttctattctg	tcacaactaa	480
atTTTtattcc	actttaccac	gagagtaatc	tgTTTTttcgc	taactaaaag	aggatcgatg	540
ggtagccaag	aagttaagaa	acagtaagat	ttcaaataat	gcaaaacgct	gcaaataattt	600
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<210> 567
<211> 848
<212> DNA
<213> *Diabrotica virgifera*

30

<400> 567

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acgcccagat	ggatcgccgt	caccgggtgcg	atatatgtgt	caaggggtcat	aattggaaaag	180
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<210> 568
<211> 24
<212> DNA
<213> *Diabrotica virgifera*

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<400> 568
cgattacgtc atcacgccca gatg 24

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<210> 569
<211> 31
<212> DNA
<213> *Diabrotica virgifera*

5

<400> 569
ctttacaaag atcgaagata gaaagcatcc a 31

10

<210> 570
<211> 610
<212> DNA
<213> *Diabrotica virgifera*

15

<400> 570

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gtttacaagg	gggtcaaaat	atgggtgaatg	gccctgtaca	ttcattgggg	ccgaccgatc	180
ggctctgtcc	cgtcatacag	ctgaccgact	gtaataactt	ttattttatat	tcgattttaga	240
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tttttagcgc	tttatattgg	aaaattaaca	tttttcaata	taaaccgtcc	actatattaa	480
tagatacaaa	attaggagct	gtagcagaaa	agtatctcaa	ctgactcaat	ttattttatt	540
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tcttgtaaaag						610

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<210> 571
<211> 828
<212> DNA
<213> *Diabrotica virgifera*

<400> 571

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at ttttttaag	at ttttgctaa	tcatttttgac	gttctattga	caaaatatga	at tttcttact	480
tcggatactt	tcacaattat	cgtgtagatg	gcgctaagat	taatggatta	atagattaat	540
agaacattaa	aaaaacttaa	attcagtatt	taaaacgtaa	gcatatttaa	ggtaaaaata	600
tataccacag	ctttgactaa	ctaataatttt	ttataattaa	tg tttttta	tttaatttta	660
aattaatcac	tttgacattt	atgtcaaatt	tccggtaaa	gtttacagac	ttgtcactaa	720
tggcgttcgc	gaatttgtaa	atatcccctc	tacgtacgag	ctcacagcgt	ataactgaac	780
gacaacgaac	gaacgaacac	gaacactgaa	cacagattca	cagatagc		828

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<210> 572
<211> 29
<212> DNA
<213> *Diabrotica virgifera*

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<400> 572
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<210> 573

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<211> 29
<212> DNA
<213> *Diabrotica virgifera*

5 <400> 573
gctatctgtg aatctgtgtt cagtgttcg 29

<210> 574
<211> 609
10 <212> DNA
<213> *Diabrotica virgifera*

<400> 574

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	aaagtaatta	aattgtaatg	gatttttttaa	gatttttgcta	atcatttttga	cgtcctattg	240
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	agcatattta	aggtaaaaaat	atataccaca	gctttgacta	actaatattt	tttataatta	420
	atgttttttaa	ttttaattttt	aaattaatca	ctttgacatt	tatgtcaaatt	ttccggtaaa	480
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<210> 575
<211> 824
<212> DNA
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<222> (785)
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<400> 575

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	acctcgatcg	acttcggcga	gagtggtggag	ctcacataac	atTTTTTcat	agagagtaat	180
	aatgtaacag	tttgtagttt	ctaccagttg	tgatgtaaca	ggcgtaacgc	tatgttattt	240
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	taaacctTTg	taaaacatgt	accattaatg	ttgcccttct	actcctTTtat	aaaaataatt	600
	gttaaaataa	cttataaaat	taatcttTgt	taatgactcg	aaatataaat	tttaattTTc	660
50	gtataagggt	cagattttaca	gtattagtta	tattataatt	tacagaaatt	tttcaattTTc	720
	ttttctaata	actacacata	cagcaaaaag	tatgcctggg	ggtaacgttc	attaaattaa	780
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55 <211> 23
<212> DNA
<213> *Diabrotica virgifera*

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<400> 576
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<210> 577
<211> 27
<212> DNA
<213> Diabrotica virgifera

10
<400> 577
cacaagtffc aagcaacgac aatcttc 27

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<211> 804
<212> DNA
<213> Diabrotica virgifera

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<220>
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<222> (27) (165)
<223> n = a, c, g or t/u

<400> 578

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cctcgatcga cttcggcgag agtgtggagc tcacataaca tttnttcata gagagtaata 180
atgtaacagt ttgtagtttc taccagttgt gatgtaacag gcgtaacgct atgttatttc 240
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tataaggttc agattttacag tattagttat attataaatt acagaaattt ttcaattttct 720
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<210> 579
<211> 812
<212> DNA
<213> Diabrotica virgifera

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<400> 579

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      catgtacaag tatgcatgca caatgcgcca ttttaaactt gaacatcagt agttgaagca 180
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      tgtaagggtta ggtcgaacac gttgaccatt cgcaaaatta aattccaaca gagggcgctc 480
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10     agtttctaaa cgttacatta aaatcattta caggagtgtt ttgccaaagt aaccactaag 600
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      cattcattaa aatttgatgc taactactga tttgttttta cttttttttc ataaaaaaat 720
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15

<210> 580

<211> 24

<212> DNA

<213> Diabrotica virgifera

20

<400> 580

ggagacgagt catttgcgga catg 24

25

<210> 581

<211> 30

<212> DNA

<213> Diabrotica virgifera

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<400> 581

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<210> 582

<211> 599

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<400> 582

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      ccagtatcgt atgtctacac gaatgggtcaa aactcaactg tattaaactt tgtacaagtc 240
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      aaatttcaaa gatggacgac aactctagga aaacaattca ttttgtcatt tgaattcaca 540
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<210> 583

<211> 802

<212> DNA

<213> Diabrotica virgifera

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<400> 583

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 tatctattttc taatcgaatc aacaaaatat gatcttactg aacagaatat gatgcaagct 180
 aatattaaat gcaactcgtat tgtttttatta tatcctaaac caaagactta ttcattcttga 240
 aggtgactgt gtgccgtcat ctctttttatt gagacaatta ggacgttttt cgttctcagc 300
 ggcttctcgg aaatccctgg cttacagaaa cggatggtga ctatagtcac ggaactgtca 360
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 caggaactgg aaagaagtat atgccctcag tttgttatct ttctctagat gatgggagga 480
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 aatggctttt ggtgtggaca atagttatag aactttcaaa accaattttg tgtcctgtct 660
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<210> 584

<211> 33

<212> DNA

<213> *Diabrotica virgifera*

<400> 584

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<210> 585

<211> 35

<212> DNA

<213> *Diabrotica virgifera*

<400> 585

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<210> 586

<211> 737

<212> DNA

<213> *Diabrotica virgifera*

<400> 586

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 atggcttttg gtgtggacaa tagttataga actttcaaaa ccaattttgt gtctgtcta 660
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<210> 587

<211> 778

<212> DNA

<213> *Diabrotica virgifera*

<400> 587

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30 <210> 590
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35 <400> 590

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	tgagataaaa	tgaacttcca	tcaagtaacg	gtcgaatcca	tcaattacat	tgattttcaa	600
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55 <400> 591

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	agaataggag	atattatttt	tagaggatat	tttgaggggtg	aatttatattc	aatagatgtt	660
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 <213> Diabrotica virgifera

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<210> 593
 <211> 29
 25 <212> DNA
 <213> Diabrotica virgifera

<400> 593
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30 <210> 594
 <211> 726
 <212> DNA
 <213> Diabrotica virgifera

35 <400> 594

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 <212> DNA
 55 <213> Diabrotica virgifera

<400> 595

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      gatggatatg agctattacc tccgatttcg ttgaacgaaa aatcgtcaca attgccgtta 720
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15 <210> 596
 <211> 34
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<210> 597
 <211> 31
 25 <212> DNA
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<400> 597
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30 <210> 598
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35 <400> 598

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      gtcatatgat gtacttttcc attttaaaaa aattaaagtt gtgcctgtca cctgaagagg 240
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      gcgagcagtg agtgateccac agttgcgctt taatattttt tctgcgggtga atacactgtt 600
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50      tc

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<210> 599
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 <212> DNA
 55 <213> Diabrotica virgifera

<220>
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<222> (525) (705)

<223> n = a, c, g or t/u

<400> 599

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20 <211> 27

<212> DNA

<213> Diabrotica virgifera

<400> 600

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<210> 601

<211> 32

<212> DNA

30 <213> Diabrotica virgifera

<400> 601

cgattttagt tggagacatt cttctgaaa tc 32

35 <210> 602

<211> 395

<212> DNA

<213> Diabrotica virgifera

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50 <210> 603

<211> 699

<212> DNA

<213> Diabrotica virgifera

55 <400> 603

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5 gttactgttt aaattttatgt cttacgtttt aacctaacta cctgagggtat tagatttaaat 240
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10 gattaaagac aatcacagggt aagatatcag tcattgaaag atagtatagg agtatagcat 600
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<210> 605
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25 <213> Diabrotica virgifera

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<400> 605
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30 <210> 606
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35 <400> 606

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<400> 607

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5
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15
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25
30
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45
50
55

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688

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<210> 608

<211> 32

<212> DNA

<213> *Diabrotica virgifera*

<400> 608

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<210> 609

<211> 32

<212> DNA

<213> *Diabrotica virgifera*

<400> 609

ccagaagtat tattttaacg gcatcggaat ag 32

<210> 610

<211> 550

<212> DNA

<213> *Diabrotica virgifera*

<400> 610

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50
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<211> 973

<212> DNA

<213> *Diabrotica virgifera*

<220>

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<222> (943)

<223> n = a, c, g or t/u

<400> 611

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10 tttattttata agttgaagta actacggtaa agagttgggtg gctaaatatt tatccgctgt 420
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<210> 613
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<400> 613
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40

<210> 614
<211> 867
<212> DNA
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<222> (771)
<223> n = a, c, g or t/u

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<400> 614

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gatacacttg tatagtaata taggtcaatc atgtttatga taaacaacgc gtattcgttt 660
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gaaaatatta ccagtgaatt gtatttttat caaaatatac tgcaaaaaaa cccatcattt 840
15 atgactctat agtggacgca catatcc 867

<210> 615

<211> 967

<212> DNA

20 <213> Diabrotica virgifera

<220>

<221> modified_base

<222> (784) (895)

25 <223> n = a, c, g or t/u

<400> 615

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gacgtatagc aggtttttaca aagcttcggg aattggacac atatttgaca ttaatcagtc 180
aactgtcata caacatactc atttttattt caaggaaata atcttagaat aagtattttt 240
tgcgtaaaaca tgttatatga cgtataatag ataatatgat gtatattcca tagacatata 300
35 tattattatc atagactgag cctaccctcc gcgcttccctg gcgacaagat ctcttggaca 360
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cactgagcca caaaaaaaaa gatggtgtcg tcaactcgcg caacatgaca ctctatgata 540
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agtagcttat atttggctcc aggcaattct gtttgtgatg ttaagcactc atagggaatt 660
40 ttttaatttat tgtttatgtg gtttgtgtga caaaataaga cttttcattt gggatatttag 720
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45 atttgac 967

<210> 616

<211> 25

<212> DNA

50 <213> Diabrotica virgifera

<400> 616

gcaagagttg ttcattccact gcatg 25

55 <210> 617

<211> 28

<212> DNA

<213> Diabrotica virgifera

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<400> 617

gtgcggcaaa ataagactcc atttaggt 28

<210> 618

<211> 846

<212> DNA

<213> *Diabrotica virgifera*

<400> 618

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caagagttgt tcatccactg catggacttt tgggtaaaaag acgtatagca gggttttaca 60
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tttttatttc aaggaaataa tcttagaata agtattttttt gcgtaaacad gttatatgac 180
gtataataga taatatgatg tatattccat agacatgtat attattatca tagactgagc 240
ctaccctccg cgcttcctgg cgacaagatc tcttggacag gtttgcggtg tctctttcta 300
gcacattgta tgcagaaaact aacatgaaac tgagtggggg tataggcacg gaaagggagg 360
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atgggtgtcg cacttcgcgc aacatgacac tctatgataa tgtatgtgtc tatggtatat 480
cccagtgagc atcctgagtc ttgacgtcac aaagtggga gtagcttata tttggctcca 540
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gagattttta ttcgtttttg cccaggtgag ttaatttaaa taaatgatta gaatgtaaac 720
agtttttgag ttatgtttat tttccatcac taaggaataa aaaccacctg agcaggaacg 780
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<210> 619

<211> 967

<212> DNA

<213> *Diabrotica virgifera*

<400> 619

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tcgagttatt aagccttgaa aatggccatt ttcgcgtttt tcaaatttga aattgcatgt 180
aactcggaac cagtcaattt tatagaaaaa tcacaagata ccttttttgc tcagcttgat 240
ccagaaaaatc taaaacaagt ttgtccgaag tgaaaaaatt gattttttga attcgtttaa 300
aaaaatgtgt agaacaactt tccgaccgag gtactgcctg gcacctgtg aatttggtat 360
aaggacctgt ttttgagtaa gtttgtgcaa aaaaattaat cggaataatt tacctaaccg 420
gacaagcata cagcgtggac tatttgcat atgagccaaa cgtaaatggg ttgtaaaata 480
cactaaacac aaaaaaaaaa agcagccatc gccaaaaaaa gttatacgtc cctattaaaa 540
aacaacaaaa atgaggttat aatatgtaca ctcgaccttc gggccgtaaa aaatggatgt 600
tctgtaaaag cctcagctgt gcgtgtgaat tttttgtaaa ttataattta ataattacta 660
actgttctaa atacgaaatg agccacagtt tggctaaaaa atgatttttt ctacaaccgt 720
gttaaaaatg caatttttag cactccatac gtgcgttaaa aatgctactt taagacacta 780
gtgcttttaa atatttttaa ggcactgcag ttcgtattga ccgtatagac aattttgatg 840
taatgtcaaa aaaatataaa aatggaatgt cagtcacgtt caaagtaaaa gttttgtaga 900
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aggcact 967

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<210> 620

<211> 31

<212> DNA

<213> *Diabrotica virgifera*

<400> 620

gctcagcttg atccagaaaa tctaaaacaa g 31

<210> 621
 <211> 32
 <212> DNA
 <213> *Diabrotica virgifera*

5

<400> 621
 ctgtggctca ttctgtattt agaacagtta gt 32

10

<210> 622
 <211> 458
 <212> DNA
 <213> *Diabrotica virgifera*

15

<400> 622

20

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gaattcgttt aagaaaatgg ttaaaacaac ttcccgaccg cgggtactgaa tggcaccttg 120
tgaatttggtt ataaggacct gtttttgagt aagtttgtgc aaaaaaatta atcggacaag 180
cggattaacg ggacaagcat acagcgtgga ctatttgcac tatgagccaa acgtagatgg 240
tttgtaaaat acactaaaca caaaaaaatt agcagccatc gccaaaaaag ttatacgtac 300
ctattaaaaa acaaaaaaaaa atgagggttat aatatgtaca ctcgaccctc ggggtccacaa 360
aaatagatgt tctgtaaaag cctcagctgt gcgtgtgaat tttttgtaat ttataattta 420
ataattacta actgttctaa atacgaaatg agccacag 458

```

25

<210> 623
 <211> 1376
 <212> DNA
 <213> *Diabrotica virgifera*

30

<400> 623

35

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atagttttatt tgaaataatc agaaatttcc ataattagtg gttagtatta ttagttgcgg 180
ttttattaat aagtggtcaac tgtcatttgc caaaatgtca actgtcattt gtcaaaatgt 240
catctgttat ttgtcaaaat gacagatgac aataactcaa ctgtcagttg tcaaaaagat 300
ggcgtaaaaa tatataaatt agttctgtag agtataaaag tcctttatgt aattcttact 360
ttcaaataaa ctcttgcaact gacaaattaa atgtaatttt gacagtttct gaaaggtttg 420
actaaatgta aatgtcagaa ttatatatct gttgattttt atacaggcac atcaaacata 480
ttaacataca caattgaaga tcgttgtaac tgatatctgc agtcaacaat ttggaaattg 540
cttcacagct aactcaaat agaaagtatg tttcacaact gcataaaata attgtaaca 600
ggatcaatat tttattgttt atattagttt ttgtaaagat atgtttcact agtacttaaa 660
tatcgatcag agacacaaac tgtgttagaa aaggtccatg gaatgtatca atatgatttt 720
atTTTTtata tcaccttcat ttgtgcattc cggctcfaat aattaatgta aaacgtcaaa 780
ttttcgtttc aggcgacaat tactgatact gcctacaaat agtggataaa ggcttttcat 840
cgattgtcat ttgtttcgag cttcttctgt catctagcag gcaagaccgc ctaaatgcgg 900
tataatttct agctatttca gctatgttta ggtatgcagc atgcaaacct gcctttggctc 960
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tcaaaagata tcaagctttg aattttttcca ttgaaaataa aattggcctg ctagagggat 1080
aatctgtgta taatattaat atacacggat tataccacat attatgacag aagctcgaaa 1140
taaagtactg aatgaaaagc cctatggagc gagacttgct agaacatgtt ttgggttcac 1200
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ccactgtctt ttttatgaat aacaattact gttttaccta aaaacaatta aaaaacatgt 1320
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55

<210> 624
 <211> 26
 <212> DNA
 <213> *Diabrotica virgifera*

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<400> 624
ggataacagt catggcggttc gtcacc 26

<210> 625
<211> 28
<212> DNA
<213> Diabrotica virgifera

<400> 625
catgttctga caagtctcgc tccatagg 28

<210> 626
<211> 1148
<212> DNA
<213> Diabrotica virgifera

<400> 626

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ggataacagt catggcggttc gtcaccaacg ctttcgagtg atggcgacca caaaacatta 60
tcacaaatgt acttgaagca atagttttatt tgaaataatc agaaatttcc ataattagtg 120
gttagtatta ttagttgcgg ttttattaat aagtgtcaac tgtcatttgt caaaatgtca 180
actgtcattt gtcaaaatgt catctgttat ttgtcaaaat gacagatgac aataactcaa 240
ctgtcagttg tcaaaaagat ggcgtaaaga tatataaatt agttctgtag agtataaaaag 300
tcctttatgt aattcttact ttcaaataaa ctcttgcact gacaaattaa atgtaatttt 360
gacagtttct gaaagggttg actaaatgta aatgtcagaa ttatatatct gttgattttt 420
atacaggcac atcaaacata ttaacatata caattgaaga tcgttgtaac tgatatctgc 480
agtcaacaat ttggaaattg cttcacagct aactcaaatt agaagttatg tttcacaact 540
gcataaaata attgttaaca ggatcaatat tttattgttt atattagttt ttgtaaagat 600
atgttttact agtacttaaa tatcgatcag agacacaaac tgtgttagaa aagggtccatg 660
gaatgtatca atatgatttt attttttata tcaccttcat ttgtgcattc cggctctcaat 720
aattaatgta aaacgtaaaa ttttcgtttc aggcgacaat tactgatact gcctacaaat 780
agtgggtataa ggcttttcat cgattgtcat ttgtttcgag cttcttctgt catctagcag 840
gcaagaccgc ctaaattgcgg tataatttct agctatttca gctatgttta ggtatgcagc 900
atgcaaacct gcttttggtc gtatactact aagtgtactt gtaaataattt ggttaacgct 960

```

```

aattgattgg ctctattaag tcaaaaagata tcaagctttg aatttttcca ttgaaaataa 1020
aattggcctg ctagagggat aatctgtgta taatattaat atacacggat tataccacat 1080
attatgacag aagctcgaaa taaatgactg aatgaaaagc cctatggagc gagacttgctc 1140
agaacatg 1148

```

<210> 627
<211> 1142
<212> DNA
<213> Diabrotica virgifera

<400> 627

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    tttattgtat taatgtataa tgtgcagtat cattcagacc tagtatttaa agaatttatt 60
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    tagataagat aggtagatgt taagtcatgt ttgttctcat tttttgtaac ttcggcttgt 180
    aatatttgtg gaagttaaaa agtagattgt ttcattttct attagtacaa aaatgttgaa 240
5   caacaattca atattttaca aaagtcaagt ggttttaatg tatctttggt ttatttaaca 300
    aaaaaattta attgtagaga aattgcatat attctgaaaa ccatgctata actgccagat 360
    ttgtgaacaa acaatagcaa gttcctaaga agaacttccg tagcagctat acaaatttaa 420
    acctctgttt aaaaaatctg aattaagagt atatgatata ggcacataaa agtgatgtcg 480
    aaattaggag tacaaaatgt taatttttaa taattaattt ggcatatgag actaactgaa 540
10  ggcaaacaaa acttaataac atcataaaat cattgcaata aaaaactgaa aactttttgt 600
    cttccatgtt tttatgtggc gcagaaggta caaaaacgta aatctgtaat ttaaaacaat 660
    tactgttttt ttatacgtag ttctggcaaa gttttacatt tgcatttttag aaaaatgtgt 720
    ttcatgttgt gtagtaaagc caaatttagt taactgtaaa aataaattac aaatttattt 780
    tggttgtgaa ttggcccgaa aatttttttt atatctacat ttattcagtt ttgccaaact 840
15  actaacagat acgtattttc gaatatcctt ttgattttta caaagagcat tgattatttt 900
    aagcttctag atgtgaaata aacggtcaac cacaaaaaaa aaaaaaaagg gcggccgccc 960
    tttttttttt tttttaacat aatagtgaag tctttatttt aatacatatt atagtgcac 1020
    attataaagc caatacatta acggcttata acgcatttgt cgttactcga tccatctact 1080
    tgtgacagtt ggaagctgac gaagatatcc gcagcttgtc cttcaagtgg gtcaatatca 1140
    tt                                     1142

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20
    <210> 628
    <211> 28
    <212> DNA
    <213> Diabrotica virgifera
25
    <400> 628
    ccatgctata actgccagat ttgtgaac      28

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30
    <210> 629
    <211> 31
    <212> DNA
    <213> Diabrotica virgifera
    <400> 629
35  gtggtgacc gtttattca catctagaag c      31

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```

    <210> 630
    <211> 593
    <212> DNA
40  <213> Diabrotica virgifera
    <400> 630

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45  ccatgctata actgccagat ttgtgaacaa acaatagcaa gttcctaaga agaacttccg 60
    tagcagctat acaaatttaa acctctgttt aaaaaatctg aattaagagt atatgatata 120
    ggcacataaa agtgatgtcg aaattaggag tacaaaatgt taatttttaa taattaattt 180
    ggcatatgag actaactgaa ggcaaacaaa acttaataac atcataaaat cattgcaata 240
    aaaaactgaa aactttttgt cttccatgtt tttatgtggc gcagaaggta caaaaacgta 300
50  aatctgtaat ttaaaacaat tactgttttt ttatacgtag ttctggcaaa gttttacatt 360
    tgcatttttag aaaaatgtgt ttcatgttgt gtagtaaagc caaatttagt taactgtaaa 420

    aataaattac aaatttattt tggttgtgaa ttggcccgaa aatttttttt atatctacat 480
    ttattcagtt ttgccaaact actaacagat acgtattttc gaatatcctt ttgattttta 540
55  caaagagcat tgattatttt aagcttctag atgtgaaata aacggtcaac cac          593

```

```

    <210> 631
    <211> 1137

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<212> DNA
 <213> *Diabrotica virgifera*

<220>

<221> modified_base

<222> (1128)

<223> n = a, c, g or t/u

<400> 631

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tcaaaaaaatt atttccattt attactattg ataaaaattga ctagcttatt atttactatt 120
gaactgggtta tatgcattat gtgataatag gctggcatta ataatatctg tccattagaa 180
aaactgttaa gtgctcctgt tagcgatccg atttttagct aggtttaaag tataggtaac 240
tctgtcgcct gattcctcct cggcacatcg gtcctacatc cgacaatatt ttacggagtg 300
tttcataaca taacacggat atattgatta acaaatatta taaatagttt ctgtgtttaa 360
taagagttgt acaacatcta cagttttgca tcgagctgac ctagttttaa aaaggatcgt 420
taacaagaga tgtaaagacg cagatatata cgactatcgt ccagatattt gtatatacag 480
cgtcttaaga tgtatcattt aacgaaatat acagttttta caagaagaaa agataatata 540
gtatggtaac cttatcatca aattaacatc gcataaaaaac cgttcaagaa acacagagat 600
attgaggaaa agaaaagcac aacattaatt taatcaaaaa tatttctgtt ttacaatata 660
tctcactaag aaacatttct gatttataat atttttagata tgtttagagg gagttataga 720
ccaggggcgca tctgtaaaaa tattagtaca tttggacggt gagagggtgac tcaaatttct 780
ttgcagaaat tgcacgaaaa caactcaaac aacaataatt gagtcaatca tcccactcaa 840
aaagggtccgg gaacattgcc taattaatca aaatgtcaaa aactgaagga aaatttcgat 900
tttttccttg gtcttttgat tataacttta aaactattca tttctgagaa aagttgtacc 960
gacatagaag ttgcgtaact aaatttcaca cattatagaa ttgggtcaaaa attcaaaaaa 1020
tagtcacccc tgttgcaaaa cagcaataat tgcgaaaaaa ccatacaaaa acaagtattc 1080
gcatttttacg cttttcaacc atttatgcta cacttaggac ccttttcngg acgcgtg 1137

```

<210> 632

<211> 28

<212> DNA

<213> *Diabrotica virgifera*

<400> 632

gtgctcctgt tagcgatccg atttttag 28

<210> 633

<211> 31

<212> DNA

<213> *Diabrotica virgifera*

<400> 633

gcaacttcta tgcggtaca acttttctca g 31

<210> 634

<211> 781

<212> DNA

<213> *Diabrotica virgifera*

<220>

<221> modified_base

<222> (100) (880)

<223> n = a, c, g or t/u

<400> 634

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attcctcctc ggcacatcgg tcctacatcc gacaatattn tacggagtgt ttcataacat 120
aacacggata tattgattaa caaatattat aaatagtttc tgtgttaa atagagttgt 180
cacaacatct acagttttgc atcgagctga cctagtttaa aaaaggatcg ttaacaagag 240
atgtaaagac gcagatatac tagactatcg tccagatatt tgtatatata gcgtcttaag 300
atgtatcatt taacgaaata tacagttttt acaagaagaa aagataatat agtatggtaa 360
ccttatcatc aaattaacat cgcataaaaa ccgttcaaga aacacagaga tattgaggaa 420
aagaaaagca caacattaat ttaatcaaaa atatttctgt tttacaatat atctcactaa 480
gaaacatttc tgatttataa ttttttagat atgttttagag ggagttatag accagggcgc 540
atctgtaaaa atattagtag atttggacgt tgagagggtta ctcaaatttc cttgcagaaa 600
ttgcccga aaactcaaa caacaatatt tgagttatcc tccctttcaa aaaggtccgg 660
aacattgttc aaacaatcaa aatgtcaaaa ataaaggaaa aactcgattt tttcttcgtc 720
tcttgactac aacttcaaaa gtattcattt ctgagaaaag ttgtaccgac atagaagttg 780
c

```

<210> 635
 <211> 1142
 <212> DNA
 <213> *Diabrotica virgifera*

<400> 635

```

tttattgtat taatgtataa tgtgcagtat cattcagacc tagtatttaa agaatttatt 60
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tagataagat aggtagatgt taagtcagtg ttgttctcat tttttgtaac ttcggcttgt 180
aatatttgtg gaagttaaaa agtagattgt ttcatttttct attagtacaa aaatggtgaa 240
caacaattca atattttaca aaagtcaagt ggttttaatg tatcttttgt ttatttaaca 300
aaaaaattta attggataga aattgcatat attctgaaaa ccatgctata actgccagat 360
ttgtgaacaa acaatagcaa gttcctaaga agaacttccg tagcagctat acaaatttaa 420
acctctgttt aaaaaatctg aattaagagt atatgatata ggcacataaa agtgatgtcg 480
aaattaggag tacaaaatgt taatttttaa taattaattt ggcatatgag actaactgaa 540
ggcaaacaaa acttaataac atcataaaat cattgcaata aaaaactgaa aactttttgt 600
cttccatggt tttatgtggc gcagaaggta caaaaacgta aatctgtaat ttaaaacaat 660
tactgttttt ttatacgtag ttctggcaaa gttttacatt tgcatttttag aaaaatgtgt 720
ttcatgttgt gtagtaaacg caaatttagt taactgtaaa aataaattac aaatttattt 780
tggttgtgaa ttggcccgaa aatttttttt atatctacat ttattcagtt ttgccaaact 840
actaacagat acgtattttc gaatatcctt ttgattttta caaagagcat tgattatttt 900
aagcttctag atgtgaaata aacggtcaac cacaaaaaaa aaaaaaaagg gcggccgccc 960
tttttttttt tttttaacat aatagtga aaactttatt aatacatatt atagtgcac 1020
attataaagc caatacatata acggcttata acgcatttgt cgttactcga tccatctact 1080
tgtgacagtt ggaagctgac gaagatattc gcagcttgct cttcaagtgg gtcaatatca 1140
tt

```

<210> 636
 <211> 27
 <212> DNA
 <213> *Diabrotica virgifera*

<400> 636

ggaacgtaca caaaagtttg ggagggt 27

<210> 637
 <211> 25
 <212> DNA
 <213> *Diabrotica virgifera*

<400> 637

gaacagcaac cagcctgata cgacg 25

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<210> 638
 <211> 582
 <212> DNA
 <213> *Diabrotica virgifera*

5
 <400> 638

```

      ggaacgtaca caaaagtttg ggagggttta agggaacaaa acccccttaa aatttttatg 60
10    ggggtggacaa atttcactat aattttgttt aaagatgggt ctgccatgag aatgatacat 120
      gtccattttc aataaaaagt atctaatagt ttctgatata ttgaaaaaga tcgattttca 180
      ttttgtaact tcaaggggct gtaactttta tgatgagcac atttgtacca aggtaagtta 240
      gattcaatca aactattttt gaccccagaa tgtgtgggtat aatttgtgac caatcttttc 300
      gggacaccct gtatacaata tatgttcctt atgtccagct gaacgattta cgtagggttag 360
      atcgactaat atagtaaacy acaattataa tacgttttgt cgacaattat aatacgtttt 420
15    gtcgtcatat tttaaaagac tcacatttta atgactgacg ttaaataatac acacttctcc 480
      atcaattcga taccatgatg ttgaaatagc atatcaaaat gtaaaagagg cacaaactga 540
      atgcagacgt tcagtgcgct cgtatcaggc tggttgctgt tc 582
  
```

<210> 639
 <211> 1039
 <212> DNA
 <213> *Diabrotica virgifera*

20
 <220>
 <221> modified_base
 <222> (748) (896)
 <223> n = a, c, g or t/u

30
 <400> 639

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      atatttgaat aataataatt gatgtaaggc gtacaattaa taaaaagtta tttattgttt 120
      atatattatt tatggaaaat ccaagtattt caagtcatta aagttcaaata aaaagtatta 180
      ttttataaga gtttgttccg ataaccgtaa ataggtagca gtttagctat aaagtaaagt 240
35    gaccgtgggtg gcataaaaat tagtaaatgc taatgcttca agcacgtact acattttttga 300
      agatttcact acacttaaaa agcatatttg cttttctccg tagtatttgc tactattttac 360
      cagcctacat agaagaatgt actacgcttt ttaaataatgt gcttgtttag tactatttgg 420
      cttcagttta agtgaagtgt gtgggtggac gttttcggcg taggtatttt tttgttacaa 480
      tatggcagca tttatgaatg tatgtcatag aaaaatttac aaactacgaa gaagattcct 540
40    aatttttggg gtcattcttt tatcaaataa aatttaataa ttgtgaagaa gattaacaaa 600
      taacaattgt ttattttttat ccttgcgtaa ctctttggtc gcttcggatc tgagtcactc 660
      atttttactc atgtacaatt ctaataattt ggtacgtaaa atgtgaattc acaaatcaaa 720
      agcacatgga aaactaattc catcacgnat ggtgtaatgc agacaccgct ggcgctacgc 780
      tttgtagtag atacttctgg tcagtagtag gtactttctg tgtgtactaa gntctcaaca 840
      aaagcaccta ctttttatgt aaaagaaaat gctacaaagt aatgactatt tactgnagca 900
45    ataacatcta ctacgtttat gcattccgcc catttcttga gtgaattatt aaatgtgact 960
      tctattttat aaaaaaaatt ttaggggttt aaattaaagg ttccctttta ccgaaagt 1020
      taacaaattt ttttttttc 1039
  
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<210> 640
 <211> 29
 <212> DNA
 <213> *Diabrotica virgifera*

55
 <400> 640
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<210> 641
 <211> 34

<212> DNA

<213> *Diabrotica virgifera*

<400> 641

5 ctactgacca gaagtatcta ctacaaagcg tagc 34

<210> 642

<211> 798

<212> DNA

10 <213> *Diabrotica virgifera*

<400> 642

15 cgccccgtgat aacaaaatca atcaaagagt tgtttatttaa atagtattga tagtgtatttt 60
 gaaaaataat aattttattta aggcgtacaa ttaataaaaaa gttattttatt gtttatatat 120
 tttttatgga aaatccaagt atttcaagtc attaaaattc aaataaaagt attattttat 180
 aagagtttgt tccgataacc gtaaataaggt atgagtttag ttataaaagta aagtgcccat 240
 ggtgtcataa aatgtagtaa atgctaagtc ttcaagtacg tactacattt ttgaagattt 300
 cactgcactt aaaaagcatt tgcctttctc cgcagtattt gctactattt accagcctac 360
 20 atagaagaat gtactacgct tttgaagtat atgcttggtt agtagtattt tgcttcagtt 420
 taagtgaagt tgggtgggtgg tcgtcttcgg cgtaggtatt tttttgttac aatatggcag 480
 cttttatgaa tgtgtgtcat agaaaaattt acaaaactaag aagaagattc ttaatttttg 540
 gggtcattct tttatcaaat aaaatttaat aattgttaag aagattaaca aataacaata 600
 attgttcatt tttatcctcg cgtaactctt tgtcgttcg gatctgagtc actcattttt 660
 25 actcatgtac aatttctaata atttggtacg taaaaatgtg aatttacaata tcacaagcac 720
 atggaaaact aattccatca cgattggtgt aatgcagaca cggctggcac tacgctttgt 780
 agtagatact tctggtca 798

<210> 643

30 <211> 1035

<212> DNA

<213> *Diabrotica virgifera*

<220>

35 <221> modified_base

<222> (790) (857)

<223> n = a, c, g or t/u

<400> 643

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 aagagactgg tagagatgct aaatttagtg ataaaagcct atgaacttgc attctacttg 120
 gtgtttccca ccttttagaca tatcagagct atatgtcaac taaaactgtc actgtcacag 180
 45 tgtcagttta caaacaagtc caatatgtct aaagggtggga aacagcagat agaattgtgga 240
 tttataggtt ttatcactgg atttcgcacc tctactagtt taattccttt ttatctcaca 300
 acttaatatg ttattagcat gctcatcact gtatactgac taactttttt tgttttttaa 360
 cctcaccaaaa cctttttttat tcgtatctgt atattttatcg aagttcaaat gtattttttt 420
 tattcttcca aatgagccag aaacttgaca aaaaaacaat tttctgaatc cttcgaata 480
 aaattccttt taagtttatc tcatcggaat aaaaaatacc ttttctctct tggtaatttt 540
 50 tcgaaaaatg cttccttttc acgttggttg ctattttttg ttaaagaaat gccttaatta 600
 gcgatttttg ggattttttc ccaaaaacta ctcaatgaat tataattcta caaaaggctt 660
 tataatcctt aaaccctcaa gtataagtaa gaatttttg acaaggacac atgggtttata 720
 tctcgctgaa aacatggagt caaaaattca tctaaaatag gcccttcaga cagtctaccg 780
 ctgccatgtn gcctaagtn tggacagtgg gttgcagaaa aacgggcaca tgtcacataa 840
 55 atatttgtat aaatttnaaa ctatcgtttg agcaagatag aagccactta tccttgtcaa 900
 atattaataa taaggtttta agatataaag tttttatata ctacatttca tttagttgtt 960
 tcttagaaaa aaatcgcaat aactcaaaat tcgtccctga aaattttttac taaatgattc 1020
 cgaaaaatgt ttttt 1035

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<210> 644
 <211> 31
 <212> DNA
 <213> Diabrotica virgifera

5

<400> 644
 gttgtgagat aaggggaaaa gagactggta g 31

10

<210> 645
 <211> 30
 <212> DNA
 <213> Diabrotica virgifera

15

<400> 645
 gacaaggata agtggcttct atcttgctca 30

20

<210> 646
 <211> 853
 <212> DNA
 <213> Diabrotica virgifera

<400> 646

25

gttgtgagat	aaggggaaaa	gagactggta	gggatgctaa	atttagtgat	aaaaacctat	60
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aaactgtcac	tgtcacagt	tcagttaaca	aacaagtcca	atatgtctaa	aggtgggaaa	180
caacagatag	aatgtgaatt	tatagggttt	atcactaaat	ttcgcacctc	tactagttta	240
attccttttt	atctcacaac	ttaatatgtt	attagcatgc	tcactactgt	atactgacta	300
attttttttg	tttttttagc	tcaccaaact	ttttttattc	gtatctgtat	atztatcgaa	360
gttcaaagt	atttttttta	ttcttccaag	tgagccagaa	acttgacaaa	aaaacaattt	420
tctgaatccc	ttcgaataaa	attcttttta	agtttatctc	atcggaataa	ataatacctt	480
ttctctcttg	gtaatttttc	gaaaaatgct	tccttttcac	gttgtttgct	attttttggt	540
aaagaaatgc	cttaattagc	gatttttggg	attttttccc	aaaaactact	caatgaattg	600
taattctaca	aaaagcttta	taatccttaa	accctcaagt	ataagtaaga	atattttgac	660
agggacacat	ggtttatatc	tcgctgaaaa	catggagtca	aaaattcatc	taaaataggc	720
ccttcagaca	gtctaccgct	gccatgtgcc	taagtgtgga	cagtgggtgc	agaaaaacgg	780
gcacatgtca	cataaatatt	tgtataaatt	taaaactatc	gtttgagcaa	gatagaagcc	840
acttatecct	gtc					853

30

35

40

<210> 647
 <211> 1017
 <212> DNA
 <213> Diabrotica virgifera

45

<400> 647

50

55

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 ctgtatatga gatacaaatg aatcgcgatg attttttcta actagcgatt tcggtatatg 120
 aatctgaatc ctgacagatg taaacataga ctaaataaac tacactcaga gaaaaaatg 180
 atgtgaaata aaattattcg gaggtagata agtgaacgaa cagtaggaaa 240
 ttaaaggcct tggggaaatg tggataaggt ctgaaatgac aggctgcgtt ctgttgatag 300
 gtttgctctt atttaaaaaa tgtgaaaaat tcattattac atcagcaatt tatccctttc 360
 ttgagtttat ggaacttatc agtttttcta aattaagcgt ttcaaatacaa attttttagg 420
 aagtgttttt aaagggacga ttattcttta gtttttaaaa tgcgtttttat ccaatgttgc 480
 10 ctacttctta aatgtatata acaataaaaag caataccatt ttggatgta cataggttgt 540
 taataaacag atgaaaagggt gtgtttgtct aagaacagggt atatatattgc aatgatatag 600
 agattactgt agttaaaagaa actatgcaaa agattagagg tgatagtgga tacagttgat 660
 agctaataaaa tcaataattc tatacattta tcttcgatta aataattatg ttattgtggt 720
 tttcatggaa actattaaac tatttttaatt aatgacgaag gtagaataacc ttaaaacttc 780
 tccatggctc tgtcagaaga tatgaagtgt tcattttatta ataagtttcc tagttggaag 840
 15 ggattttctaa ctttgttaatt ataaaaaatt ttttaaaaaa tttcttctta tttatctgga 900
 ggggtttttt aatccaccgc tggtagcatt attttttaac aaataaatgg taaaaacaaa 960
 aattttatgg gaaaattttt ttacgggggg ggctttcaca ccaggaaatt tgttttt 1017

20 <210> 648
 <211> 28
 <212> DNA
 <213> Diabrotica virgifera

25 <400> 648
 ggtccagaa tgtgtgattt agtttgtg 28

30 <210> 649
 <211> 30
 <212> DNA
 <213> Diabrotica virgifera

<400> 649
 gaacacttca tatcttctga cagagccatg 30

35 <210> 650
 <211> 806
 <212> DNA
 <213> Diabrotica virgifera

40 <400> 650

45 gtccagaat gtgtgattta gtttgtgacc tgtatttttg ttacaccctg tatatgagat 60
 acaaatgaat cgcgatgatt ttttctaact agcgatttcg gtatatgaat ctgaatcctg 120
 acatatgtaa acatagacta aataaactac actcagagaa aaaaatgatg tgaaataaaa 180
 ttattcggag gtagataagt gaaaaaatac gaacgaacag taggaaatta aaggccttgg 240
 ggaaatgtgg ataaggctctg aaatgacagg ctgcgctctg ttgatagggt tgctcttatt 300
 taaaaaatgt gaaaaattca ttattacatc agcaatttat ctctgggccc tttcttgagt 360
 ttatggaact tatcagtttt tctaaattaa gcgtttcaaa tcaaattttt taggaagtgt 420
 50 ttttaaaggg acgattattc tttagttttt aaaatgcgtt ttatccaatg ttgcctactt 480
 cttaaatgta tataacaata aaagcaatac catttttggt gttacatagg ttgttaataa 540
 acagatgaaa aggcgtgttt gtctaagaac aggtatatat ttgcaatgat atagagatta 600
 ctgtagttaa agaaactatg caaaagatta gaggtgatag tggatacagt tgatagctaa 660
 taaatcaata attctatata tttatcttcg attaaataat tatgttattg tggtttcaat 720
 55 ggaaactatt aaactatttt aattaatgac gaaggtagaa taccttaaaa cttctccatg 780
 gctctgtcag aagatatgaa gtgttc 806

<210> 651
 <211> 1013

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<212> DNA
<213> *Diabrotica virgifera*

<220>
<221> modified_base
<222> (657)
<223> n = a, c, g or t/u

<400> 651

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aaaacaactg ctagacgacc aaaaaaatga aatagataaa aattatataa aatttaattg 180
tctccatttt tgtataggta catttttgtc gtaaaactaa taataaacgc gataactcaa 240
taattctgct gttacttttt tccccatta ctcgaaaaat atcgaccgca caaaaaattt 300
gtaataaaaag acattataga aaatcatatt ttcaacaatt tcagtcgctcg cactttttgt 360
cgaaaagtgt aaaatgacgg agatattgag caaaaacggc tctcctttaa attcaacatg 420
gcggctaacg taacggcgga attcactcgc gatattaaat ttacactact attgacaccc 480
gtaaagatta gaaaaattaa attttggaca tctcggcatg caaggtcaaa gctaaagtcc 540
tgtatttttg ctatctgtag gaaaacatca aaataactta ttataatgct gtttaatgac 600
atttttgagc cccttatgtt gaaacattat tttttttaat tgatactttc tgataanata 660
tacaaattta ttaaaaataaa caccaaatca ctgtgaaatt gctacaaatg atatttataa 720
cattttttat gttgcgcaga agctatgcac caagtttttt ggatccaaat tgagtgggtt 780
gaaatgaatc gcccataaat atttgagttt attgtcattg gaaactataa gcaagtatta 840
caatacgctt aatttttaat tttaaatagg gatttggact gactatgaat ctgatcaata 900
ttttttaaat aattgtaaaa tttgatgagt cattatccct gtgtgggtct gattgttttt 960
aatagaaact ttttttaaac agtgtaatat ttctagtaaa ataattttca acc 1013

```

<210> 652
<211> 31
<212> DNA
<213> *Diabrotica virgifera*

<400> 652

gatattgaac aaaaacaact gctagacgac c 31

<210> 653
<211> 29
<212> DNA
<213> *Diabrotica virgifera*

<400> 653

gatcagattc atagtcagtc caaatccct 29

<210> 654
<211> 789
<212> DNA
<213> *Diabrotica virgifera*

<400> 654

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```

gatattgaac aaaaacaact gctagacgac caaaaaaatg aaatagataa aaattatata 60
aaatttaatt gtctccattt ttgtataggt acatTTTTgt cgtaaaacta ataataaacg 120
cgataactca ataattctgc tgttactttt tccccccatt actcggaaaa tatcgaccgc 180
5 acaaaaaatt tgtaataaaa gacattatag aaaatcatat tttcaacaat ttcagtcgtc 240
gcactTTTTg tcgaaaagtt gaaaatgacg gagatattga gcaaaaacgg ctctccttta 300
aattcaacat ggcgggtaac gtaacggcgg aattcactcg cgatattaaa tttacactac 360
tattgacacc cgtaaagatt agaaaaatta aattttggac atctcggcat gcaagggtcaa 420
agctaaagtc ctgtattttg gctatctgta ggaaaacatc aaaataactt attataatgc 480
10 tgtttaatga cattttttgag ccccttatgt tgaaacatta ttttttttaa ttgatacttt 540
ctgataaaa atacaaattt attaaaataa acaccaaatac actgtgaaat tgctacaaat 600
gatattttaa acatttttta tgttgcgag aagctatgca ccaagttttt tggatccaaa 660
attgagtggg ttgaaatgaa atcgcccata aatatttgag tttattgtca ttggaaacta 720
taagcaagta ttacaatacg ctttaattttt aatttttaaat agggatttgg actgactatg 780
aatctgatc 789

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15 <210> 655
    <211> 1012
    <212> DNA
    <213> Diabrotica virgifera

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20 <220>
    <221> modified_base
    <222> (929) (949)
    <223> n = a, c, g or t/u

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25 <400> 655

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tttcaacagt gcaatgtaac acacaagtcg cctgctgaat cgcaaaataa attatgttat 120
30 ctaatgtatt gtttgaaaga ccactaagta ccgattcggc attccagatt gtaaggaaaa 180
atgcaataag tgcaataatg agttttacca tgaaaccgaa attcacaatc ttggaaggaa 240
aaattcacta agtgcaataa tacgttttaa tgagttttgc cctgaaacca aaattcacia 300
taatgcactt agtgaattgt accataaatt atctcagcaa ttagaagggt tagagtccca 360
gggtgacttct ccagagctgg gcagtaccgt atcgagttca aattaataaa aatgtcaata 420
35 tctcaaaaaa gtgcacttag ttagttttac ctctaatagg acgatttgtc ttgtttttatc 480
cattatgata cattcacttc attatgtaca agcttatcga tatttgaggta agtgtcgact 540
aggcagagtc agttcaatta ctatttcttc cttgagtgtt atgcttccat catcagccaa 600
gttaatgttg tataagtatc atactccata tcatagacaa atattcttca gtcacaaaat 660
atggctcagt aatagaagaa gagaagatag aaggactgga tggcagagaa cttgagaaag 720
40 tgaaatacac actacaaaaa ctttcaatgc cagtcttttg agatacatat ttggtcatta 780
gggtgatattc agattttgag atattacata ttgtaggact ggtatgggag gagattctac 840
aggcaaaaga ccactcggac gtcccagaat gtgatggaga gatacatcca agcagatctc 900
cgaaaaatga acatcccatt tgaccctang ntgatggaag accaacaant tgggaagaaag 960
tgtacagtca gccaggaccc accccagggt gtagecgctac gtgatgatga tg 1012

```

```

45 <210> 656
    <211> 28
    <212> DNA
    <213> Diabrotica virgifera

```

```

50 <400> 656
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```

```

55 <210> 657
    <211> 27
    <212> DNA
    <213> Diabrotica virgifera

```

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<400> 657

tgtatctctc catcacattc tgggacg 27

<210> 658

<211> 825

<212> DNA

<213> *Diabrotica virgifera*

<400> 658

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tcaacagtgc aatgtaacac acaagtcgcc ttctgaatcg caaaataaat tatgttatcc 60
aatgtattgt ttgaaagacc actaagtacc gattcggcat tccagattgt aaggaaaaat 120
gcaataagtg caataatgag ttttaccatg aaaccgaaat tcacaatctt ggaaggaaaa 180
attcactaag tgcaataata cgttttaatg agttttgcc tgaacccaaa attcacaata 240
atgcacttag tgaattgtac cataaattat ctcagcaatt agaagggtta gagtcccagg 300
tgacttctcc agagctgggc agtaccgtat cgagttcaaa ttaataaaaa tgtcaatatc 360
tcaaaaaagt gcacttagtt agttttacct ctaataggac gatttgtctt gttttatcca 420
ttatgataca ttcaattcat tatgtacaag cttatcgata tttgggtaag tgtcgactag 480
gcagagtcag ttcaattact atttcttctc tgagtgttat gcttccatca tcagccaagt 540
taatgttgta taagtatcat actccatate atagacaaat attcttcagt cacaaaatat 600
ggctcagtaa tagaagaaga gaagatagaa ggactggatg gcagagaact tgagaaagtg 660
aaatacacac taaaaaaact ttcaatgcca gtcttttgag atacatatat gggtcattagg 720
tgatattcag atttttgcgat attacatat gtaggactgg tatgggagga gattcctaca 780
ggcaaaagac cactcggacg tcccagaatg tgatggagag ataca 825
```

<210> 659

<211> 990

<212> DNA

<213> *Diabrotica virgifera*

<400> 659

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tgatctgtta aaatctagac gtcacacgaa gaactggaat tttccaagag tatcgaacaa 120
caaaatatcc aaatgtaacc tcaaaatagt atcattcgct tatacaaaac aatgctataa 180
tatgatcctt gctacataaa ctcactaatc acagtttaagg ggggaggggt atggtttgac 240
atcagcattt cgagcacatt tttgtgaatt ttttgaatct atattagaat tattttttaa 300
ttaaataaat agattcagta gagataggcg ttacctcacg aaatatctaa agaaagtctg 360
caaaatttca ggtggatcgg taaaatagtt ttggagttac aatatccacc acctttgaaa 420
aaagcagttt tgagaaaaat gcgttcaaag ttttgaaaac tttattttca attttatttt 480
tgttttgtcaa atcgtaaagt aatgcacacc gaaatatgtt tttgcacgc ggagtaattt 540
acaaaagggg aacagctgtt gaacgtttct aactacgctc aagcacgctg tagcgaagct 600
gccgcaaagc gagtcgaagg tagggatatt tacttgctgt atctctggta attttactcc 660
aatcaatctg aaattttcgg agagtagtct tgaagttaat tttaaaattt caaacggtt 720
caacctcccc ccttaatcac aaaaccttca actgtgttat tcacttcact tcaaatcgag 780
ttatacctat aacactctac tggaaagatt catactctat gtgttgtcac gttctagtat 840
ttcataaata ttattaaaag cgcttaaaaa ttcagctaga tggacgaaat ttactttttt 900
agatccctag tttttcaaat tttacgtgct atattttttc tgcgtacgat atacctcctc 960
gcacattata ggtactggag ggaaagggtta 990
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<210> 660

<211> 32

<212> DNA

<213> *Diabrotica virgifera*

<400> 660

agagcattcc acagtgtct gttaaaatct ag 32

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<210> 661
<211> 31
<212> DNA
<213> *Diabrotica virgifera*

5

<400> 661
cgattgaag tgaagtgaat aacacagttg a 31

10

<210> 662
<211> 688
<212> DNA
<213> *Diabrotica virgifera*

15

<400> 662

20

agagcattcc	acagtgatct	gttaaaatct	agatgtcaca	cgaagaactg	gaattttcca	60
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gaacaatgct	ataatatgat	ccttgctaca	taaactcact	aattacagtt	aaggggggaa	180
gggtatgggt	tgaaatcaac	atttcgagcc	cattttttgtg	aattatttag	agttagtgtt	240
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ttttgaaaaa	tttattttca	attttatttt	tgtytgtyaa	atcgtaaagt	ratgcacacc	420
gaaatatggt	tttgmactgc	ggagtaattt	acaaaagggg	aacagctggt	gaacgtttct	480
aactacgctc	aagcacgctg	tagcgaagct	gccgcaawgc	gagtcgaagg	tagggatatt	540
yacttrctkt	atctctggta	attttactcc	aatcaatctg	aaattttcrg	agagtagtct	600
traagttaat	tttaaaattt	caaaccgttt	caacctcccc	ccttaatcac	aaaascttca	660
actgtgttat	tcacttcact	tcaaactcg				688

25

<210> 663
<211> 997
<212> DNA
<213> *Diabrotica virgifera*

30

<400> 663

35

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tatattccac	ttatacagat	taaacgaaac	aagttagggg	atatttcctt	atatttaaat	180
taatagaat	ctttcaatat	tatttctacg	cgtatataat	aaaatatgtc	tagtggctgt	240
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gtgtgacgtc	acgtgctata	acgcggatga	cgtgcaacgg	tgtctatatt	gtacggactg	360
tattgaatgt	gttaagtgtg	tttaatat	aatattccga	taactaatcg	aataaaggat	420
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gatatccgat	aagaacttag	cctctccgcc	ctagtgcgtc	actattgcaa	gggatataata	780
ccatcgtata	atacattctt	gtagaccgcc	tatgtcaaaa	tctgagccaa	atcgggactt	840
gtaatttttt	taattttatta	agaaaaacat	acaatcccca	tccacccccg	cagggttatt	900
aaaaggagta	gtaacgtacc	caaaaattcc	gttttaataa	taataaaaaa	gagggaatat	960
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<210> 664
<211> 28
<212> DNA
<213> *Diabrotica virgifera*

55

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5 <210> 665
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 <213> Diabrotica virgifera

10 <400> 665
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15 <210> 666
 <211> 848
 <212> DNA
 <213> Diabrotica virgifera

20 <400> 666
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 ctttcaatat tatttctacg cgtatataat aaaatatgtc tagtggctgt aattccagtg 180
 taccctgcta aacgattcta aaaaggaaca cacctacgac ttaaataatc gtgtgacgtc 240
 acgtgctata acgcggtatga cgtgcaacgg tgtctatatt gtacggactg tattgaatgt 300
 gttaagtgtg ttttaatat taaatattccga taactaatcg aataaaggat tacagattac 360
 25 ggtaaatatt tattaaacat atatgattac aaacttttgt acatgtttta ttttagaccg 420
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 acatttatga ttagttaact agtaatttgt tatgttgaat ttggttatgc gatatccgat 660
 30 aagaacttag cctctccgcc ctagtgcgtc actattgcaa gggaaatata ccatcgtata 720
 atacattctt gtagaccgcc tatgtcaaaa tctgagccaa atcggacttg taattttttt 780
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35 <210> 667
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 <212> DNA
 <213> Diabrotica virgifera

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 <223> n = a, c, g or t/u

45 <400> 667

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 aacgatttcc ataaacttaa ttacaattta cgccgttatt aatcaaaaact catagttggc 180
 5 gcaacgattt gaaattgttc taatttcgag gcgaatcatg taaattttat tgcgtttgag 240
 tgacattgta ttttccataa tatgcgtgag gtgtccttta cattgcaaac tatttgtatt 300
 tgagtagtat cggttaaattt cgagaggtaa aatattgaat agctgggtata ataattaaaa 360
 gtacaataga ttaacaatac tttctacctg taccggaaac ttaccacacc attcaaatac 420
 aaatgactgt aagcttaaaa tttttctgga atattttaat ggcaactata agtagtttcc 480
 gcggtgaaac accttgtatg catttaaattg gtttcggctc acgtcagcaa tgaaagatgc 540
 10 tcattctttt cagtataaaa tccaaaacta atttgagact gaatcgagtt ggggtgataaa 600
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 caaattgtgc agtatttaaat gtaagatcat ccattcttcc gtatcttcca aaacttttta 720
 aatatactac gtttaaaact ctanagttga ttttagtttc cccaaaacag caatactcgc 780
 ggttttagttg agttgaaagt gtgatagaca ggttttagtt actatataaa tatttttttt 840
 15 acgatttgta ttagttgtaa tatacaatga aagacggaat tgtttttcgt tgtgtataaa 900
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gagaagtatc tcggttgaa ttgttcctt ttttt 996

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 <212> DNA
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25 <400> 668
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30 <210> 669
 <211> 25
 <212> DNA
 <213> Diabrotica virgifera

35 <400> 669
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40 <210> 670
 <211> 949
 <212> DNA
 <213> Diabrotica virgifera

<400> 670

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 caatttacgc cgttattaat caaaactcat agttggcgca acgatttgaa attgttctaa 180
 tttcgaggcg aatcatgtaa attttgttgc atttgggtga cattatattt tccataatat 240
 gcgtgcagtg tcctttacat tgcaaaactat ttgtatttga gtagtatcgt taaatttcga 300
 gaggtaaaaa tattgaatag ctggtataat aattaaaagt acaatagatt aacaatactt 360
 50 tctacctgta ccggaaactt accacaccat tcaaatacaa atgactgtaa taagcttaaa 420
 atttttttct ggaatatttt aatggcaact ataagtagtt tccgcgggtga aacaccttgt 480
 atgcatttaa atggtttcgg ctcacgtcag caatgaaaga tgctcattct tttcagtata 540
 aaatccaaaa ctaatttgag actgaatcga gttgggtgat aaagtgtgaa tacggtgcga 600
 tatggagtct ggcgtaagat tttttgtaca cgctgtatcg acacaaattg tgcagtattt 660
 aatgtaagat catccattct tccgtatctt ccaaaacttt ttaaataaac tacgttttaa 720
 55 actctaaagt tgatttttagt ttccccaaaa cagcaatact cgcggttttag ttgagttgaa 780
 gttgtgatag acaggtttta gttactatat aaatattttt ttacagattt gtattagttg 840
 taatatacaa tgaaagacgg aattgttttc cggtgtgtat aaaacttgtg ttgacttttt 900
 gaaatgtaca tagttctagt ataagtttgt tgtgctgagc cacgagaag 949

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<210> 671
 <211> 991
 <212> DNA
 <213> *Diabrotica virgifera*

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<220>
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 <222> (906) (921)
 <223> n = a, c, g or t/u

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<400> 671

15

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aacactatac aaaccttatt tattagatat ttaataaaca caaacattat gctgtttttc 180
tattactggt atcagtatgt tatcaatgta tattatgcct atgatcgatg attcatgata 240
gttgagttac agtaaaatta ttttagcaca gaaggaacgc agcgctgccg gctgtatttg 300
cttttctgtg gacattaatc aaatgcatta aaattaataa attatttttt tgaaaacggg 360
tgacttaaca aaaaaaattt attagacttt tttgctctaa atgggtgcact tagcccatat 420
cttgaggagg cgcactatgt tccgggacac cctgtatagt ttaaaaatta ttttctgttg 480
ctcaatcggg cattcgttcg tggaagtaga tacatcatgc attaattgaa agatctatcc 540
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20

25

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tccaagttct tacgagcttt gctgttgctg cctgctccta cgtcaaagtc tgaatttgca 720
tgaacactga accttacttt ccaaggaata tattaaataa tatcatttat ttaatacttt 780
tcgtagcaag ctaagtaatg ttaacgaaga gaattatgac tttgcttagc aaatacagag 840
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gagagcagag gtgtataaat aaatttttgg t 991
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<210> 672
 <211> 28
 <212> DNA
 <213> *Diabrotica virgifera*

35

<400> 672
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40

<210> 673
 <211> 30
 <212> DNA
 <213> *Diabrotica virgifera*

45

<400> 673
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50

<210> 674
 <211> 733
 <212> DNA
 <213> *Diabrotica virgifera*

<400> 674

55

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 tacaaacctt atttattaga tttttaataa acacaaacat tatgctgttt ttctattact 180
 gttatcagta ttttatcaat gtatattatg cctatgatcg atgattcatg atagttgagt 240
 tacagtaaaa ttatttttagc acagaaggaa cgcagcgctg ccggctgtat ttgcttttct 300
 gtggacatta atcaaatgca ttaaaattaa taaattattt ttttgaaaac gggtgactta 360
 acaaaaaagt ttattagact tttttgctct aaatgggtgca cttagcccat accttggagg 420
 ggcgcactgt tttcagggac accctgtata gtttaaaaaat ttttttctgt tgctcaatcg 480
 gtcattcggt cgtggaagta gatacatcat gcattaattg aaagatctat ccactgggtg 540
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 tccaatattt tttgttcacg tttggtacaa atatttttta gaagggtatg cgtccaagtt 660
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 gaaccttact ttc 733

15 <210> 675
 <211> 990
 <212> DNA
 <213> *Diabrotica virgifera*

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 <223> n = a, c, g or t/u

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 ataattttaa atctatatat ttttttctgt tttctggcct tgggttagaa gaacccttag 180
 ccaatgtaaa atagttcaaa ctatcaaaaa cgcttgtgac gttacattac tgtattttct 240
 actgacgttt atagtgtcta attttaaatt atatacaatt ttgtttactt tgttggtgca 300

35 gaatgtacat gcacaactat atgacgtcaa tatgcgtttt ggaccacctg ttttaatttg 360
 aatttttaat cgtcttttagg ggccaaacga aagacaaaca aaactttttt tatctttgat 420
 acatgtttta aattatgttc tgttgtgatt tataacattt ttttcgaatt taaaaattta 480
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 gggttatgact ataaatatct gaaaaatata tacatacttg taaagtaaac accactctta 720
 40 ccattttcta atattatcta agtattgact ggacttttct atctgcctca tgaataatga 780
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 ataattatag gaatatctac cgatattatt actctggggt ccgtatatct atcctttttt 900
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45 <210> 676
 <211> 32
 <212> DNA
 <213> *Diabrotica virgifera*

50 <400> 676
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55 <210> 677
 <211> 33
 <212> DNA
 <213> *Diabrotica virgifera*

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<400> 677

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<210> 678

<211> 729

<212> DNA

<213> *Diabrotica virgifera*

<400> 678

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actttgttgg tgcagaatgt acatgcacaa ctatatgacg tcaatatgcg ttttggacca 180
cctgttttaa tttgaatttt taatcgctct taggggccaa acgaaagaca aacaaaactt 240
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caggtatgta catcggttat gactataaat atctgaaaaa tacataatac atacttgtaa 540
agtaaacacc actcttacca ttttctaata ttatctaagt attgactgga cttttctatc 600
tgcccatga ataatgaggt aaattagaat ttcatttatt ttgcataaaa aatacatgta 660
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<210> 679

<211> 988

<212> DNA

<213> *Diabrotica virgifera*

<400> 679

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acagatgcgc cctggactaa aacaatttta agtactctca ttgttaaaaa gttgattcac 180
cacattttca taacgatttt tagggcggct gtacacggac tgctgaggtc gtttatcact 240
gagcgacata cacggactgc tgcagcgatc gttgtagact tctggagcgg tccattgttg 300
actacctgag ttgtcccttg tgcattgca accgctctcg atctgtcgat agcacgatgg 360

aatttcatta tgctattgac agcttgaagc ggtcttgact gctcgagctg tcgtgtgtat 420
ggcaacgaat atacaattat aattcacgcg gcaaacgctg cttcaaaaag tcgacctcaa 480
ctgcttgaag atgtccgtgt acggccgatc ttgggggtatc ttttttactc ttatcgggaa 540
tatttaagaa ccgaaatccc taatgttttc cctatttgtt ccagaatgat atacgtgtta 600
atttccaact gagacttgac ggccagcacg accgtacgac aagacatttt cgaacagtaa 660
aatcattagt tttagtaaca aatacaaaga cagatgggaa ttcggttctc gatattatgc 720
agagtattta cctgatgatg aacacttatt ggaggataga aacgcataat ttgcagaact 780
gacttaccba tgtaatggac aggtatgatg gaaacgtatg tactttaatg ttttgtagt 840
atttttacga gagaagctaa gtaggtttgt gaagaattag ttatttgttg tactcgatac 900
tttttattaa ctcatatatt aattaaatcc taaaaatata caacgtaaga agctacatga 960
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<210> 680

<211> 25

<212> DNA

<213> *Diabrotica virgifera*

<400> 680

ggaccatttt gagtgggagg atagc 25

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<210> 681
 <211> 33
 <212> DNA
 <213> *Diabrotica virgifera*

5

<400> 681
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<210> 682
 <211> 862
 <212> DNA
 <213> *Diabrotica virgifera*

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<400> 682

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aaaaca	at	ttt	taagt	actct	cattgt	ttaa	aaagtt	gattc	accacat	ttt	cataac	gatt	180
tttaggg	gcg	ctgtac	acgg	actgct	gagg	tcgttt	atca	ctgagc	gaca	tacacg	gact	240	
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cctaatt	gttt	tccctat	ttg	ttccaga	aatg	atatac	gtgt	taatttt	ccaa	ctgagac	ttg	600	
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acaggt	atga	tggaaac	gta	tgtactt	ttaa	tgtttt	gtta	gtattttt	tac	gagaga	aagct	840	
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<210> 683
 <211> 978
 <212> DNA
 <213> *Diabrotica virgifera*

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<220>
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 <223> n = a, c, g or t/u

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<400> 683

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50

55

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	aacaaacaga	cagagtgggtg	gtgacaaaaa	aagaggtggc	atagataggt	gtcttttagg	180
5	aaatatttgg	aaaagaacga	ccatacttat	aataatacaa	ctgtaaatgt	gtaaaaaatc	240
	gtattgattt	tgctacttgt	gtctatttgt	tcatTTTTatt	agatcacaat	atatataaac	300
	tgttgaactc	gaccgtaagc	tgcttttaaa	acaataaaat	gttttgaaat	gtagtaaata	360
	tgtcatcgaa	taagtgcagt	catagctaag	tgtagacagt	attgccaaaa	taatttgtat	420
	acataatggg	tcttctatTT	atacaaaact	ttaatctttt	taatttcttc	tctttgtatt	480
	tgactattaa	caaagtgaag	cgaattttgc	aattattttta	gtatattaac	gtagaaaaag	540
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	ccaaaactac	tctgatcaag	tcatgggtctc	tgcatattat	ttatacctta	gagctacact	660
	atttgaacaa	aaatgttaat	ataaacattt	tttaatatagg	attttgagat	agaaagtgtg	720
	tgtgaaaatt	ctgtgtttat	aatgcaaaac	cccatacacg	gcttaggaat	aagtttatgt	780
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15	cgaaatataa	acagtctacg	ggatgtccta	tctgtntata	gccgaatcaa	atttaataata	900
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<210> 684
 <211> 27
 <212> DNA
 <213> Diabrotica virgifera

<400> 684
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<210> 685
 <211> 34
 <212> DNA
 <213> Diabrotica virgifera

<400> 685
 gaccataatg tatgccataa actgtgatg gatc 34

<210> 686
 <211> 857
 <212> DNA
 <213> Diabrotica virgifera

<400> 686

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	aaatcgtatt	catttttgcta	tttgtgtcaa	atgtgtcatt	ttattggatc	acaatatata	180
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	aaatatgtca	tgaataagt	gacgtcatag	ctaagcgtat	acagtgttgc	caaataattt	300
	gtatacataa	tggttcttct	atttatacta	aacttttaatc	tttttaattt	cttctctttt	360
	cgtattttgag	tattaaccaa	gtgaaacgaa	ttttgcaatt	atttttagtgt	attaacgtag	420
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	aagtgtatgt	gaaatttctgt	gttttataatg	caaaacccat	tatacggtct	aggaataagg	660
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	gttcgacgaa	atataaacag	tctacgggat	gtcatatcgt	ggtatagccg	aatcaaaatt	780
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<210> 687

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<211> 977
 <212> DNA
 <213> *Diabrotica virgifera*

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 <223> n = a, c, g or t/u

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15	tatacagtca	ttggaaaatt	gttgaattgt	aaacacggta	gccgtgtccg	tgtcgggtggc	180
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	ttttcagaaa	gtggagaaaa	atcgatttaa	aggtacaaat	tgttttttga	attcacctga	360
	cttgaatatt	ggaatttttt	aaatgcaact	ttaaagaata	aataaaaaaca	gatattttgt	420
20	gccatatttc	gtcacaggaa	ctatgatata	atcaatatta	gatcaatttt	tgtacttaat	480
	gagtttttcc	atgaacaaaa	ttattggata	ttgatatcct	atcagaggta	aaactcacta	540
	actacacttt	gtacttgatg	agtttttcct	tgaacacaat	tattggatat	tgatataccta	600
	tcagaggtaa	aactctttta	ctacactttg	tacttgatga	gttttttcctt	gaacaccatt	660
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	gaactatcan	aattaacagg	caattatgtc	acagggaacta	tgatataatc	atgatacaat	780
25	caatgtttaga	tcaatttttg	tacttaatga	gtttttccat	gaacacaant	attggatatt	840
	gatatcctat	cagaggtaaa	actcgctaac	tacactttgt	attttgatga	gttttttcctt	900
	gaaacacatt	attgaatatt	gatatcccta	tcagaggnta	aaactcacta	actacacttt	960
	gtactttgat	gagtttt					977

30 <210> 688
 <211> 23
 <212> DNA
 <213> *Diabrotica virgifera*

35 <400> 688
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<210> 689
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 40 <212> DNA
 <213> *Diabrotica virgifera*

<400> 689
 caaagtgtag ttacgagtt ttacctotga tagg 34

45 <210> 690
 <211> 509
 <212> DNA
 <213> *Diabrotica virgifera*

50 <400> 690

55

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```

5      ggagacgggt cacaggcttc atgtgcaaca cttaacacct tcagctccag gccaatatct 60
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      ggtagccgtg tcggtggcac ctgattgata agagaatgaa cacgggagcc gtgtcggcag 180
      acttgaaagt gttttgagga aaagtttggt ttaataatca atatttcgtc ctattagagg 240
      taacactcac taactacact tttcagaaaag gggagaaaaa tcgatttaaa ggtacaaaatt 300
      gttcttttaa ttcacctgac ttgaatattg gaatTTTTTT aatgcaactt aaaagaataa 360
      ataaaaacag atatttgagc catagttcgt cacaggaact atgatacaat caatattaga 420
      taaatTTTTg tacttaatga gtttttccat gaacacagtt attggatatt gatatcctat 480
      cagaggtaaa actcgctaac tacacttttg                                     509

```

10

```

<210> 691
<211> 962
<212> DNA
<213> Diabrotica virgifera

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15

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<220>
<221> modified_base
<222> (836) (933)
<223> n = a, c, g or t/u

```

20

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<400> 691

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25      tgtcttttta gtttacttct cttgggttaa aaacaaagct tagctattta tgactgcaat 60
      tttgatatcg tgtgtattag aaacttttagt ttttaaccac gatatttaaa tattgtggac 120
      tttgaacaat taaaaaaaaa tgtacttggt cactttctgt tggcgaaaaa aattagaaat 180
      ttgacttggt caatataagc gacaccgtat taggaaatta tatttattaa ctacgggtctg 240
      tacatagaaa aaaattaaaa tctaatacgt ttctgtgtcg tcgctttcag aagaagctgg 300
      ttacgggtatg aaaacttttt ttgactactg gaatcgattt ataccactca tggaaactctt 360
      gcggaataat tttattttcta cgcaaggagg ctgtttttat tttgctctgg tatagacaaa 420
      agttttttgt ataacattgg aatgttctta ggaataacag ctgggtctgac cttgccacat 480
      actcaagagt aacgcattta attttaacca cgatattttg tttccatttt aatcttagtc 540
      tctgtttttt aagaacatct gtgcttaaga tcgaaaaagt ctgaccgtaa ttcttcaact 600
      ctgtaggcac cgctcttttc gttgcgtctt gtagaacgga ctagcttgaa aatattaaca 660
      gatcgttcat tgtaaaaaat ggcaacattt tcattaacag actatatggc actgtgcatt 720
      gagtttaccg tttacctcca tgtacgaatg tcctttctcc ataaaattat gctgcaaaaat 780
      cttagtgtgt gcgttacaac aacatacaaa ttaatgcggc aatgaacgaa tataanaatc 840
      tctgataagt cagaatataa actgatctct gtgatgcctt ttgatcatgt gattgcagan 900
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40

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<210> 692
<211> 27
<212> DNA
<213> Diabrotica virgifera

```

45

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<400> 692
tgacttggtc aatataagcg acaccgt      27

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50

```

<210> 693
<211> 35
<212> DNA
<213> Diabrotica virgifera

```

55

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<400> 693
gcatcacaga gatcagttta tattctgact tatca      35

```

```

<210> 694
<211> 697
<212> DNA

```

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<213> Diabrotica virgifera

<400> 694

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5      tgacttggtc aatataagcg acaccgtatt aggaaattat atttattaac tacggtctgt 60
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      tacggtatga aaactttttt tgactactgg aatcgattta taccactcat ggaactcttg 180
      cggaataatt ttatttctac gcaaggagggc tgttttttatt ttgctctggt atagacaaaa 240
      gtttttttgta taacattgga atgttcttag gaataacagc tgggtctgacc ttgccacata 300
10     ctcaagagta acgcatttaa ttttaaccac gatattttgt ttccatttta atcttagtct 360
      ctgtttttta agaacatctg tgcttaagat cgaaaaagtc tgaccgtaat tcttcaactc 420
      tgtaggcacc gctcttttcg ttgctgtcttg tagaacggac tagcttgaaa atattcaaca 480
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      gagtttaccg tttacctcca tgtacgaatg tcctttctcc ataaaattat gctgcaaaat 600
15     cttaatgtgt gtgttacaac aacatacaaa ttaatgcggc aatgaacgaa tataaaaaatc 660
      tctgataagt cagaatataa actgatctct gtgatgc 697

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<210> 695

<211> 765

20 <212> DNA

<213> Diabrotica virgifera

<400> 695

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25     gttcaaaaaca gaacaattac actacattta ttgattctaa caatctaata gatgttataa 60
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      taaaagggtta aaagaaaaat ttaaaacaat ttacatgaag aaaaccaagt aatactgaaa 180
      atataaacga tattaagcac ctgtatatatt aaaaaagtat taaaacgaaa aaacttaata 240
30     gtaattggaa tggcgggaaa aatgttttaa agtattttaa taagcactgt accctcacc 300
      aaaaaaacta tacacatatt caacaattta cataatttat tttgtacagg ataatatcaa 360
      aaaagagaaa acctatcttt agttactatc tttagtagcg ccatattaat attcacagaa 420
      gtgagggata gaggccttat tattcttttt gataaatatc gctatatatt taaacttaca 480
      ctgatgaaca aaataggaaa atttccttaa aaagatttaa tcttctaagt ttctgaaggc 540
      ctgctgaata tcttcatata attgatcaaa atctgccttg attttagctt caccatcttt 600
35     tacgggatcc ttaaatctca tactgctaag ttgatataaa attccactca ttgaatctct 660
      tattacgttc caagtgatct tattttctga ttgtgcgggt gattctacag cgtgtctcgc 720
      catgtcgtac aaaccgatca tgtttctcaa cataccgaca gtttt 765

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<210> 696

40 <211> 594

<212> DNA

<213> Diabrotica virgifera

<400> 696

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45     cttattttcga tttgactatg tgatggattg agaccttagg cagagcctta acgttgattg 60
      ccgagtcaag acctgtaggc atctataaag gcgactatat acaagaatta tatgcaagat 120
      atgatgatgt cagtgatgct ccacctccac catctcttcc tgattggtgt acagaaagt 180
50     acgatggaca agggaatggc cttgacgatt tcgatgattt tactgaagat gcaagaaaac 240
      gagtagcttc aacttcttca aataatgatg atacttcacc aaaagctaaa aagggtcgct 300
      tctaggaagt cgcatttatg gagggagtac ctaacgttac ccactttgta gaggaacaag 360
      cgacccgaga ttgcaaacga atggtgccta ggatgtgtag gtgtacacca aaatggtgtt 420
      ccaggaagtc atgtccgtgt ccaatggata tgacaaacat tactcttcta aaagaccacc 480
      cctacagagt ttcttgcgaa gcagacggcc atgaggcatt atgaagctta tcaacggaga 540
55     acacaatgtt tatctttttg acagagatga tgaagcttat taaggcggaa ggca 594

```

<210> 697

<211> 884

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<212> DNA

<213> *Diabrotica virgifera*

<400> 697

```

5      gcttgagtaa aaactgaaat catataaaag agataatttc tattgtgaac taatTTTTca 60
      aaagtttcta cattaagtac atattcatta ctaaataatg gccgaaaaca aaaatccaga 120
      ggatttggcc accgcaattc tccgtaagaa agatcgtcca aatagacttt tggtagaaga 180
10     agcagttaac gatgataact ccgtgggtgc tttgtcacia gcaaaaatgg atgaactaca 240
      acttttcaga ggagacacag tcctactgaa gggcaagcga aggaaagaaa ctgtttgtat 300
      agtattatct gatgatacat gtagcgatga aaaaattcgt atgaatagaa ataatttaag 360
      agttaggctt tcagatgtag tttctatcca agcttgccct gatgtaaagt atggcaagag 420
      aatacatgta cttcccatag atgatacagt ggaaggactc acaggaaatc tcttcgaagt 480
      atacctgaaa ccctacttcc tggaggccta tgcaccaata cacaagatg acgtattcgt 540
15     tgtacgtgga ggaatgagag ctggtgaatt caaagtcgtc gagaccgatc ccgctccgta 600
      ctgtatcgtg gctccagaca ccgtcattca ttgtgatgga gatccaatca agcgcgaaga 660
      ggaagaggaa gctcttaacg cagttggata cgacgaacat ccggaagggt gtaaaaaac 720
      aggttgctca aatcaaagaa atgggtagag ttaccactg agacatccct agtctttttc 780
      aggggtattg gaagtaaacc caccaaaagg tattttactt taccgggtcc accggggaac 840
20     tggtaaaacc cctccttgcc cccgcaagga acctaaacaa aact

```

<210> 698

<211> 642

<212> DNA

<213> *Diabrotica virgifera*

<400> 698

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30     gccctTTTTt tctgtccatt ttatgtcaca agtagggcta aaatgaagca aattgtaaca 60
      aaccaaacgg taaaaattcc tgaggaatt acagtaacca ctaagtcaag ggtagtaact 120
      gtaaaaggac cccgaggtaa tctgaagaga tcttcaaac atcttaccct ggacattcga 180
      atgatcaacc ccaggttact gaaagtagag aaatgggtcg gtaccaagaa ggaattagct 240
      gctgtcagaa cagtatgctc tcatgttgaa aacatgttaa aggggtgttac aaaaggatac 300
      caatacaaga tgagagcagc atatgctcac tttccatta actgtgtcac cactgaagga 360
35     aacacagtta tcgaaattag aaatttcttg ggagaaaaat acatcagaag agtaaagatg 420
      gccccagggtg ttacagtagt aaactccacc aaacaaaagg atgaacttat cattgaagga 480
      aactcattgg aggatgtttc aaagtcagct gcccttattc aacaatctac aacagttaaa 540
      aataaggata tccgtaaatt cttagatggg ctttatgtat ctgaaaaaac aactgttgta 600
40     caagaagaat aacttgtatt tttgaaataa atttaagttt at

```

<210> 699

<211> 652

<212> DNA

<213> *Diabrotica virgifera*

<400> 699

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```

cacgttgaga ggtgcatttg cacgatgagt tccttaaaac ttcagaagag gctagcagcc 60
tctgttatgc gatgtggtaa aaagaaagta tggttggacc ctaatgaaat caacgaaatt 120
gccaacacta actcaagaca gaacatccgt aagttgataa aggatggtct tattattaag 180
aagcccgtag ctgtacattc ccgtgcccgt gttcgcaaaa aactgaagc ccgcaggaaa 240
ggaaggcact gcggttttgg taaaaggaag ggtactgcta atgcccgtac cccgcaaaag 300
gaattatgga ttcaacgcat gagagttttg cgtcgtctcc ttaaaaaata caggggaagct 360
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aagaacaagc gtgtccttat ggaatacatc cacaagaaga aggcagagaa agcccgtgcc 480
aagatgttgg cagaccaggc caatgccaga aggatgaagg taaaacaggc tagagaaaga 540
cgtgaggaac gtatcgccac aaagaaacaa gaagttttgc agaactacat gagggaggat 600
gaagctgcgg ccactaagaa ataagttaat tgttttataa gatgactata tt 652

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<210> 700

<211> 890

<212> DNA

<213> *Diabrotica virgifera*

<400> 700

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acgacaacaa gtttgatatg ttggtaagga actgtatggc tcacgatgga aaaagagctc 120
ccatacagtt agtcgaccaa agaggttgtg tcacaagacc aaaattgatg tccagattta 180
ctaagattaa aaactttggc gcaagcgctt cagtgttatc atatgccac ttccaggcat 240
ttaaattccc tgactccatg gaagttcact tccagtgcac catccaaatc tgcagatatc 300
aatgtccaga tcagtgttca gattcttcag gacaacatct ccacggcttg cttgatttgg 360
tgcattggtc acctgatact gggttatggtg ctccctccac gctacctatc gaagcatatt 420
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aaaaggaagt gggggtgaat aggattatta ggggtgtatc tacaggagat ttgacattta 540
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aaattaacaa cggaggatta atatgtatga ctactccagg ttttgcagca accttagtag 660
ttttatttagc tatattaata gtatcttgtc ttatgtcagc tttcctttgt gtcaaactaa 720
gaccatttgc tgaaaacaac tcgcagggtg cataggatat gccaatcac agaaaacaaa 780
gtcaaggagc tgcttttact cgtaatatta gagcagactg aaaggggtta gatcgaaaag 840
aaaacggcta catgcttgggt catataaatt aaaaatcttt cgacatatgg 890

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<210> 701

<211> 888

<212> DNA

<213> *Diabrotica virgifera*

<220>

<221> modified_base

<222> (775)

<223> n = a, c, g or t/u

<400> 701

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attgatggat tcagagggtt tgctacggac tacaatataa cagctttaac accatgtgta 120
aaagtattag gccaatataa aggagtatgc aaggatgaaa tggtaggagg acaggatagc 180
aaccaaatga atacggcagc gagggaaaat ggtattagca taataactta cagaagatcc 240
5 ttaatttcac ctgatcctgg agataaagag tttccagcag agggttccat atacgccgta 300
tggggggtag gaaaactaga cgaaatgaaa gaacctgctt ttcgatgatct ctactcaaag 360
actgatataa aaatggagat gacaccgaaa gaacctcaga ataactgtgt ctcttttacg 420
agatcgaaac ctgaacccaa agaaccttgg aagaaagggtc aaatattcga taaaactata 480
aggatattta agtcttatat tgggtccatca gggggccaaaa ggggatacca agccattacc 540
10 ggccactcat ccacagcttt agcatgggtac ataaacgggtt tcctcagccc tgagatatgg 600
ctacgacgag gtctttcata tgcattttaa gtatatggag gaaacaatcc acacagtgtct 660
gaatattatc atccattgat aataacagat gaacccacg gaggttttga tagacttact 720
gacgatgtct agtctaaaat aagagtcttg gctggtgttg aatattctag aaggngaaga 780
cctagaccaa ctacatctgg tgtcctttgt ctatcagaac acaaagaagg aaaagacaga 840
15 agactcgatg atgacttcga aacgttcaaa aatttcacaa atcttgat 888

```

<210> 702

<211> 953

<212> DNA

20 <213> *Diabrotica virgifera*

<220>

<221> modified_base

<222> (840) (878)

25 <223> n = a, c, g or t/u

<400> 702

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ttattgaagt tgttccagaa gataccggta aatatgaatg tgtcgtctatc aacaactccg 120
gagaagctag atgtgaagct gaatgtgtag ttacttcacc atctgctgcc cagaaacccg 180
ccaaaccac aactcccgtt gcggaaaagg ctccagccct tctagaacct ctcaaagatc 240
agactattaa agaaggacaa gctgtcgtgt tcagatgtaa gatttcagct aaaccaactc 300
35 cagttattaa gtggcaaaag gctgataagg tcatcaagcc atctaaatac ttccaaatga 360
ccaaagaagg ggacttctgc acgttaaaga tctcagaagc tttccctgaa gatgaaggag 420
tctacaaatg cgtcgtctgaa aatcctgcag gcgctgttag tactcaagct aagttgaagg 480
ttattgcacc agaaacgcaa gaagttgcac catcactaac cccaatgaaa gacgttactg 540
tacctgaagg tagccctgct caattcaaga ctactatttc tggaaaacct aagcccacca 600
tccaatggtt gagggaggga ttccttattc cagaatcgcc agatttccag atgatccaag 660
40 aagggaaacaa cgttattcta ttgatttcct caacctacga agaagacact ggcttattca 720
cctgcagagc aacttcatca gccgggtcaag ttgaacaatc tgcgaaacta accgtaaaaa 780
gtaagaaatg attgctataa aaatattctt ttctaattct caaattgtta atgtccatcn 840
catgtagtta ttgttangta tgacagcttn cagctggnta tttaacacag tataaataag 900
tgatcagtta gcagaactct tttgagatag tcatgatatt ggactaatgg gtt 953

```

45 <210> 703

<211> 905

<212> DNA

50 <213> *Diabrotica virgifera*

<220>

<221> modified_base

<222> (849)

55 <223> n = a, c, g or t/u

<400> 703

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aagaaaatca agaagactca ggaaggcaag ttttaagatag tcgccaggaa cagggaagga 120
gaagcctcag taacatttac tctgaaagta attacttcag agaaagaagc acctgagggtc 180
ttatcacctc tagaatctat taccgtaagg aaaggagaac cagttacact ttccactact 240
atatttgga acccggaacc tactatcgaa tgggtgaagg atggtaaacc ttttaaccaga 300
ccaaaattca aaaaagacgg aaacacatac actttaacta ttcccaagac atctacagat 360

10 gacactgcta catatacagt tcgagctacc aattctatgg gtacaataga aacaagtgca 420
aacctaactg ttgaagaatt ccagaaaaac caggaaccac cattgttcgt caaacgattt 480
gaagagcaaa ctgtaccaca aaagtctcct ctcacctca aagccaaagt gggtggcaat 540
cctactcctg aagtatactg gcttagaaat aatgagcctt tgggaaccatc cgataggggt 600
aagatcacct tcgatggaga aaacattgaa ctaactatta aagaaaccaa ttctgaactt 660
gactctggag actacaaatg tattgctgtg aatccagcag gcaaagcctc gcatgggtgcc 720
aaggatctta ttgaggtaga tactgtcaaa ttactaaag aactgaaaga agtttacgaa 780
15 acaatagaaa gaaagacat cgaattagaa tgtgaaacat cccactcagt tagaacaaaa 840
tgggtgganc acacacggaa attagtggta tggaccatcg cgttgtagta caagatggag 900
gtacc 905

20 <210> 704
<211> 426
<212> DNA
<213> Diabrotica virgifera

25 <400> 704

30 gtcctgggga ggctattcaa aaactcagag agactgaaga aatgttaata aaaaaacagg 60
atTTTTtaga aaagaagata gaagaattta ccatggtagc aaagaaaaat gcgtcgaaaa 120
ataaaagagt tgcactccaa gccctcaaaa agaagaaacg attggaaaag ccccaactac 180
aaatagatgg aacccttaca actattgaaa tgcagaggga agccctcgaa ggagctagca 240
caaatactgc tgtattagat tctatgaaaa atgctgcaga tgcctttaaag aaagctcata 300
agaatttgaa tgtagatgat gttcacgata tcatggatga catagccgaa caacacgaca 360
tagccaacga aatcacaaac gctattagca atcctgtcgg attcaccgac gatctggatg 420
acgatg 426

35 <210> 705
<211> 473
<212> DNA
<213> Diabrotica virgifera

40 <400> 705

45 gtctaggcac ggacaaaagg gaacgtgcgg tatacaatac cgtcaagagg atatgatttt 60
tagtgctgaa ggtattacgc cagacattat cattaatcct cacgctatcc cctcccgtat 120
gacgattggc cacttgatcg agtgcaccca aggttaaggta tcatccaata aaggagaaat 180
cggtgatgct acacctttca acgatgccgt caacgtacag aaaatctcca ctttgttaca 240
agaatatggc tatcaactca gaggcaacga agtaatgtac aacggccata ctggacgtaa 300
gataaatgct cagattttct taggacctac ctattatcaa agattgaagc acacgggtgga 360
cgataagatt cattcaagag ctagaggacc gttgcagatt ctctgcagac agcctatgga 420
50 gggctcgtgca agagacggcg gtctacgttt cgggtgagatg gaacgagatt gtc 473

55 <210> 706
<211> 677
<212> DNA
<213> Diabrotica virgifera

<400> 706

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5
10
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tagtgctgaa ggtattactc cagacattat catcaatcct cacgctatcc cctcccgtat 120
gacgattggc cacttgatcg agtgcattca aggttaaggta tcatccaata aaggagaaat 180
cggtgatgct acacctttca acgatgccgt caacgtacag aaaatctcca ctttggtaca 240
agaatatggc tatcaactca gaggcaacga agtaatgtac aacggccaca ctggacgtaa 300
gataaatgct cagattttct taggacctac ttactatcaa agattgaagc acatgggtgga 360
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gggccgtgca agagacgggt gtctacgttt cgggtgagatg gaacgagatt gtcaaatttc 480
acacgggtgct gcacaattct taagagagag gctgtttgaa gtttcggatc cttatagaat 540
ccatatttgc aacttctgtg gtttgatagc tctcgccaat ttgcgtaaca acacctttga 600
atgtaagggt tgcaaaaata agacacagat atcgcaagtt agactgcctt atgctgcgaa 660
attactgttt caagagc 677

15
<210> 707
<211> 250
<212> DNA
<213> Diabrotica virgifera

20
25
atggcctgta cgtcaagcaa ggccagtcag tgaaaaatta cctgcccaacc gaaattgacg 60
ggcacactga atctattatg aaacgtaccg cattgggtcgc gtttggtctc cttctacgaa 120
cgtgctggtc gcgtttaatg tttaggtaat attgtgcagc tggtaggtaa agcatctctg 180
gcagaaacgg acaaaatcac gatggtgaag ctaaaatcaa ggcagatttt gatcaattat 240
atgaagatat 250

30
<210> 708
<211> 250
<212> DNA
<213> Diabrotica virgifera

35
40
attgtgcagc tggtaggtaa agcatctctg gcagaaacgg acaaaatcac gaaattgacg 60
ggcacactga atctattatg aaacgtaccg cattgggtcgc atggcctgta cgtcaagcaa 120
ggccagtcag tgaaaaatta cctgcccaacc gatggtgaag ctaaaatcaa ggcagatttt 180
gatcaattat atgaagatat gtttggtctc cttctacgaa cgtgctggtc gcgtttaatg 240
tttaggtaat 250

45
<210> 709
<211> 250
<212> DNA
<213> Diabrotica virgifera

50
gaatacttcc gtgatatggg ttacaacgta tctatgatgg ctgactcgac gaatacttcc 60
gtgatatggg ttacaacgta tctatgatgg ctgactcgac gaatacttcc gtgatatggg 120
ttacaacgta tctatgatgg ctgactcgac gaatacttcc gtgatatggg ttacaacgta 180
tctatgatgg ctgactcgac gaatacttcc gtgatatggg ttacaacgta tctatgatgg 240
ctgactcgac 250

55
<210> 710
<211> 273
<212> DNA
<213> Diabrotica virgifera

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<400> 710

```

5      gaagaaagta cgtaaataatg gttccagggc tccaacaaga cgagctattc ttactggggtc 60
      gagaacattt taaaattttt ggataagtac tacgttccca gcaaaatagc taaaggaaat 120
      ggccaaatta aaacatgctc tcatcacgac tatectacta gtggagaagt atgcgaagtc 180
      gatgtcagag attgggaaga atgcaacagg gatcaattct ttaattatca caagaattct 240
      ccatgtattt ttattaaatt gaacaaaata tat 273

```

<210> 711

<211> 278

<212> DNA

<213> *Diabrotica virgifera*

<400> 711

```

15
20      acatttttcc cgccattcca attactatta agtttttttcg ttttaataact tttttaaata 60
      tacagggtgct taatatcggt tatatttttca gtattacttg gttttcttca tgtaaattgt 120
      tttaaattttt tctttttaccc ttttaatctt gtatattaca ttacccaatt aaagttaatt 180
      gtacagatta agataaacga gtatcttata acatctatta gattgtaga atcaataaat 240
      gtagtgtaat tgttctgttt tgaacaaata aatgcac 278

```

<210> 712

<211> 287

<212> DNA

<213> *Diabrotica virgifera*

<400> 712

```

30      aacggttatt tggaaggcct gtgtcgtggc tttaaatgtg ggatcctgaa acaatccgat 60
      tatttgaatt tgggtccagt tgaaactctt gaagatttaa aactgcactt gcaaggcact 120
      gactatggaa cttttttggc caatgaacct tcacctttgt cagtatccgt catcgattca 180
      agacttcgag aaaaactcgt gattgagttc cagcacatgc gtaaccaagc agtagagcct 240
      ctctcgacat ttatggactt cattacctac agttacatga tcgacaa 287

```

<210> 713

<211> 250

<212> DNA

<213> *Diabrotica virgifera*

<400> 713

```

45      atggcctgta cgtcaagcaa ggccagtcag tgaaaaatta cctgccaaacc gaaattgacg 60
      ggcacactga atctattatg aaacgtaccg cattgggtcgc gtttggcttc cttctacgaa 120
      cgtgctggtc gcgttaaatt tttaggtaat attgtgcagc tggtaggtta agcatctctg 180
      gcagaaacgg acaaaatcac gatggtgaag ctaaaatcaa ggcagatatt gatcaattat 240
      atgaagatat 250

```

<210> 714

<211> 250

<212> DNA

<213> *Diabrotica virgifera*

<400> 714

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attgtgcagc tggtaggtaa agcatctctg gcagaaacgg acaaaatcac gaaattgacg 60
ggcacactga atctattatg aaacgtaccg cattgggtcg atggcctgta cgtcaagcaa 120
ggccagtcag tgaaaaatta cctgccaaac gatggtgaag ctaaaatcaa ggcagatttt 180
gatcaattat atgaagatat gtttggtctt cttctacgaa cgtgctggtc gcgttaaagt 240
5 ttttaggtaat 250

<210> 715

<211> 250

<212> DNA

10 <213> Diabrotica virgifera

<400> 715

gaataacttcc gtgatatggg ttacaacgta tctatgatgg ctgactcgac gaataacttcc 60
15 gtgatatggg ttacaacgta tctatgatgg ctgactcgac gaataacttcc gtgatatggg 120
ttacaacgta tctatgatgg ctgactcgac gaataacttcc gtgatatggg ttacaacgta 180
tctatgatgg ctgactcgac gaataacttcc gtgatatggg ttacaacgta tctatgatgg 240
ctgactcgac 250

20 <210> 716

<211> 372

<212> DNA

<213> Diabrotica virgifera

25 <400> 716

cccggttcta ccatggtagc aaagaaaaat gcgtcgaaaa ataaaagagt tgcactccaa 60
gccctcttta ccatggtagc aaagaaaaat gcgtcgaaaa ataaaagagt tgcactccaa 120
30 gccctcttta ccatggtagc aaagaaaaat gcgtcgaaaa ataaaagagt tgcactccaa 180
gccctcttta ccatggtagc aaagaaaaat gcgtcgaaaa ataaaagagt tgcactccaa 240
gccctcttta ccatggtagc aaagaaaaat gcgtcgaaaa ataaaagagt tgcactccaa 300
gccctcttta ccatggtagc aaagaaaaat gcgtcgaaaa ataaaagagt tgcactccaa 360
gccctctcta ga 372

35 <210> 717

<211> 372

<212> DNA

<213> Diabrotica virgifera

40 <400> 717

cccgggcaaa tagatggaac ctttacaact attgaaatgc agagggaagc cctcgaagga 60
gctagccaaa tagatggaac ctttacaact attgaaatgc agagggaagc cctcgaagga 120
45 gctagccaaa tagatggaac ctttacaact attgaaatgc agagggaagc cctcgaagga 180
gctagccaaa tagatggaac ctttacaact attgaaatgc agagggaagc cctcgaagga 240
gctagccaaa tagatggaac ctttacaact attgaaatgc agagggaagc cctcgaagga 300
gctagccaaa tagatggaac ctttacaact attgaaatgc agagggaagc cctcgaagga 360
gctagctcta ga 372

50 <210> 718

<211> 490

<212> DNA

<213> Diabrotica virgifera

55 <400> 718

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catcacgact atcctactag tggagaagta tgcgaagtcg atgtcagaga ttgggaagaa 60
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 tgctactaaa ccaatcaaac gatgaggaac agacagaaca aaccgcaact gaaacggcaa 180
 ctacagaggt acagaaaaag ggtgtcaagg ggtgagatgg aacgagattg tcaaatttca 240
 cacggtgctg cacaattctt aagagagagg ctgtttgaag tctcttcagc aatagacaat 300
 ttgactccct ttctctcttg gagggaaacg aaggccttag ctcccttacc tcatcgtccg 360
 tttggattca caaaaacaca tgcacttctc tctgaaatca cctttgggag gcggtcgtcc 420
 gatccttttc gatttgttgc tgccattggg gatccatctg gacttctgga ggaagcaagg 480
 caggtgcagc 490

<210> 719

<211> 560

<212> DNA

<213> *Diabrotica virgifera*

<400> 719

ggcgcaagcg cttcagtgtt atcatatgcc cacttccagg catttaaatt ccctgactcc 60
 atggaagtgc tccatcaggg gccaaaaggg gataccaagc cattaccggc cactcatcca 120
 cagcttttagc atggtacata tagtgatccc aaccgtgcac ctgactgtga ccaactcaa 180
 tgtgtaattc cggactgttt ctgctcagcg cccgccacca gttagcgccg aagtacaaaa 240
 gggattggac cttatttttg ctggtatcag agctcaacag gcaccacgtg ctcaacgata 300
 aaagactggc caggaaggca cattcctttt tgccttactt attcaaggca ggggtgcatac 360
 agagtagcca cgtaacaaat agcacatagc gaagtgttgt accagcataa tgtataagct 420
 cctgtactta ccaaaggctc gttggcagat ctagaccagt tggacgaatt gggttattgag 480
 tactgtggtg cagcgccccc tttatggcag atgaatgtct gatggccata ccagacatcg 540
 aaggtattga ttacaccacc 560

<210> 720

<211> 372

<212> DNA

<213> *Diabrotica virgifera*

<400> 720

cccggggcta aaggaaatgg ccaaattaaa acatgctctc atcacgacta tcctactagt 60
 ggagaagcta aaggaaatgg ccaaattaaa acatgctctc atcacgacta tcctactagt 120
 ggagaagcta aaggaaatgg ccaaattaaa acatgctctc atcacgacta tcctactagt 180
 ggagaagcta aaggaaatgg ccaaattaaa acatgctctc atcacgacta tcctactagt 240
 ggagaagcta aaggaaatgg ccaaattaaa acatgctctc atcacgacta tcctactagt 300
 ggagaagcta aaggaaatgg ccaaattaaa acatgctctc atcacgacta tcctactagt 360
 ggagaatcta ga 372

<210> 721

<211> 372

<212> DNA

<213> *Diabrotica virgifera*

<400> 721

cccgggctcc atgtatTTTT attaaattga acaaaatata taactgggag ccaatgtatt 60
 acgatgctcc atgtatTTTT attaaattga acaaaatata taactgggag ccaatgtatt 120
 acgatgctcc atgtatTTTT attaaattga acaaaatata taactgggag ccaatgtatt 180
 acgatgctcc atgtatTTTT attaaattga acaaaatata taactgggag ccaatgtatt 240
 acgatgctcc atgtatTTTT attaaattga acaaaatata taactgggag ccaatgtatt 300
 acgatgctcc atgtatTTTT attaaattga acaaaatata taactgggag ccaatgtatt 360
 acgatgtcta ga 372

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<210> 722
 <211> 1000
 <212> DNA
 <213> *Diabrotica virgifera*

5

<400> 722

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10      caagcccgcc aaaatgcgcg aacatctgga actcttctgg tctcgagtga atatcccca 60
      agttcttagg aatgcaatgc ttcctagacg tcgtcgagct ggctctgaaa ctgagcccca 120
      agttatagta ggtaacgata attattggac gtggcattag gttataggga aagtgtcaat 180
      ctgtctcaaa ttcgcacatt tgttgaaatg gactcgcacg cgcggcccaa cgacggcttc 240
      aacaaacaca ggcgcaagtc gacgaagtcg tggatatcat gaaaacgaat gtagaaaaag 300
      gtatggcagg aaagaaatgc tgaatccgcc attgaagctc ttaaagaata tgaaccagaa 360
15      atggggcaaa ttgtccgaca agacaaatcc ggtattcaga aaatccgggc atagcaaaca 420
      tgccaaacac acacacgcag aaaggaaata tcagtcagac tcagaatcag atagtgatct 480
      ggaatggatt ggacacagag gtgaatcaga ccagaggacg ttcgggggta tattaaaaat 540
      aacgttgtgt gcgcacttgg aaccgaaaca agcagaccat catccgcagc tcagtgcgta 600
      gccgaatgtg gccgtgcaca ctgtgcattt gtaggacagg tgtgcggggt tcaacgtcat 660
      gttatgatcc cttgcatata ttgatggaaa aacacgccaa agaagagagc agagtattaa 720
20      aaggagtatt gccaggta tagaccagca aggaactgta atcaaaatgg gcgatgaaa 780
      gaaggccagc gatagcgaac acattaatct caaagtactt ggtcaggata atgcagtggg 840
      gcagaaggtc agacctctcc tcaacgtcac ccgtatcgag gatgagattg ccaaacttga 900
      agagaaagcc caaaaagccc aacgaacacg gcgtagacga aacatcttgt gtagttattg 960
      tagaaggaca aaccagcaca ccagaacaac aagaactagc          1000

```

25

<210> 723
 <211> 478
 <212> DNA
 <213> *Diabrotica virgifera*

30

<400> 723

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35      cctcaagctg tcattggcat ggatattctg tgccaagcta aatccggtat gggaaaaacg 60
      gctgtttttg caaaggatcc aggatgacgt tccctattga taactgtacc tacacgaccc 120
      aaatttcttc ctccagtgat catacccata cgatttacct gaggaaatgc cggataatct 180
      gaagcaacat ataaggggta tcaacaatac tagagagttg agtcaaacat aattatggca 240
      cattgtcctt ggatgtagta tccatcacgc agaccgccga acaacacgac atagccaacg 300
      aaatcacaaa cgctattagc aatcctgtcg gattcacctg aatgcactcc tacgtcgttt 360
40      ggttcgtatt ggagtactag acgagaacag aatgaagctc gattacgtat tgggtctccg 420
      aagtaatgta caacggccac actggacgta agataaatgc tcagattttc ttaggacc 478

```

45

<210> 724
 <211> 584
 <212> DNA
 <213> *Diabrotica virgifera*

<400> 724

50

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      cacttgacga aaacagcaat agcacaactc caccactat ggtctttccc gccaaaggagg 60
      aaattaacat aaagaacaag gagaagccgg taattacaaa gctgcatatg aaaccggaaa 120

```

55

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	caacattatc	gctgaagaag	gaggttactt	gaaggcaagg	atgaaatggt	aggaggacag	180
	gatagcaacc	aatgaatac	ggcagcgagg	gaaaatggta	ttgttgccac	atggtagact	240
	cctgttctaa	tgttcaaact	ggagatcaat	ttgcaagact	actcagacac	aatttcaaca	300
	gacatttgaa	ttcaaaccga	gctccgttgg	gtccagccac	ataggactaa	gtgtggaggg	360
5	ttcattcatc	aaaattcgct	ttatgtgcac	acatagcaca	taagcatata	tggaacaat	420
	gcctatccat	ccagttgtca	gctaacagaa	gtgcccttat	ggagggtggt	ttgaagaaca	480
	cgctggcgaa	tgtgagttgc	agatgggctc	aagaatacac	cgctattgac	caggatctcg	540
	cttcagaata	attccataga	aaagctacca	gcccatgcat	ttaa		584

10 <210> 725
 <211> 869
 <212> DNA
 <213> *Diabrotica virgifera*

15 <400> 725

	ccgaagtgag	atcggagcca	aaaagcattg	gttgcttgac	ggtccaatgg	aaaacgaacg	60
	agaagtggat	ggcttcagca	atgctcggcc	aggctgattg	ctctttatct	tgacactgga	120
20	atgtacagcg	aagcgctaca	actggaatcg	accttactga	ctactcgtct	acgatatcgc	180
	caaacatctg	acatacgaaa	acgttgaacg	ttggttgccg	gaattgcgcc	attcttttct	240
	caggtagcaa	tgttgctgct	ggtaaagcac	gtgggtattgt	tattggaact	ggtcttaaca	300
	ccgccattgg	taaaatcaga	actgaaatgt	ccaacgaaat	tgccaacact	aactcaagac	360
	agaacatccg	taagttgata	aaggatggtc	ttattattaa	gaagcccgtg	gctgtacatt	420
	cccgtgccga	tacctacaca	gaaagctata	ttagtacct	tggcgtagat	tttaaaatca	480
25	ggacaatcga	tttagatggg	ttacaaaagg	ataccaatac	aagatgagag	cagcatatgc	540
	tcactttccc	attaactgtg	tcaccactga	aggaaacaca	gttatccagt	ttgcaagctc	600
	tctggcagat	ttcagtcaaa	tcggcaccag	aaaatccatg	agttacttta	gcaatgtata	660
	caagatctac	gtcttttagct	acaggcgatt	tccgatgaaa	tagtggcatt	aggttatagg	720
	gaaagtgtca	atctgtctca	aattcgcaca	tttgtggaaa	tggaactcgca	cgaagaaaaa	780
30	gtttatcagg	ccgtgagaga	attaaaagtt	caaggaggta	tcgggttcgtg	tgtatcactt	840
	aacgtgaaga	gccccttggt	ttccgacac				869

35 <210> 726
 <211> 737
 <212> DNA
 <213> *Diabrotica virgifera*

<400> 726

40	gtggcgtttt	tctattttaca	gtatgtgaat	gtgtcaaagt	aactgtgttt	ttcaaaaatt	60
	aacaaaagaa	attcaaaatg	tacaagtggg	caaaaaatat	taaacaaatg	tatatagtgt	120
	atctatttct	aatcgaatca	acaaaatatg	atcttactga	acagaatatg	atgcaagcta	180
	atattaaatg	caactcgtat	gtttttattat	atcctaaacc	aaagacttat	tcatcttgaa	240
	ggtgactgtg	tgccgtcatc	tctttttattg	agacaattag	gacgtttttc	gttctcagcg	300
45	gcttctcgga	aatccctggc	ttacagaaac	ggatgggtgac	tatagtcacg	gaactgtcaa	360
	aattaatttt	gtatcttata	tgaagcctca	aacgtttttg	aaatatttct	tctctttatc	420
	aggaactgga	aagaagtata	tgccctcagt	ttgttatctt	tctctagatg	atgggaggaa	480
	aaatttttta	aatacctggt	tgtcagagtt	ttattactat	taagaagaat	tcttcatctt	540
	aaaggtaac	gggtgtcgtc	atcactttta	ttgacacaat	taggacgttt	tttgatctca	600
50	atggcctttt	gtgtggacaa	tagttataga	actttcaaaa	ccaattttgt	gtcctgtcta	660
	gatcatcaaa	cggttttgag	aagatttctt	cccttcatat	ggagctggaa	agaagtattt	720
	gacacctgtt	agttatc					737

55 <210> 727
 <211> 867
 <212> DNA
 <213> *Diabrotica virgifera*

<220>

<221> modified_base

<222> (771)

<223> n = a, c, g or t/u

5

<400> 727

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acctccttca tgagactttt ttttttattg agttattcat gtcgagtttg acgtttctga 180
tatgaaaaat tttcaggagg gagacgggtc gtaaatatgg ggggtttataa acttttgggc 240
atctatggtg gttcctgttt atctgaacca tctcagatag ttaaggggtg gttacccct 300
actatagggg ttgatgaagt aacactactc acagtatatt catttattta taagttgaag 360
taactacggg aaagagttgg tggctaaata tttatccgct gtgatgttta cccgctggga 420
tctcaaatac ccatgattaa tctttacgca atgaatttag aacgtcgaat gtggaatccc 480
ctgtttatgt tttgggtatat ataaaaagtg aaagtgtttg tattataaat gctgaatcaa 540
cttgattata aataaagaat aatatttgcg actacagctg acctgcatt atcgataact 600
gatacacttg tatagtaata taggtcaatc atgtttatga taaacaacgc gtattcgttt 660
accaaggaca tttaaatatt aaaagaatta gtcttgccct taataagatg gttactaaga 720
gatgctgtga atcccaatac acatccgaca actggagtaa gtatccttga naatttgtcg 780
gaaaatatta ccagtgaatt gtatttttat caaaatatac tgcaaaaaaa cccatcattt 840
atgactctat agtggacgca catatcc 867

```

<210> 728

25

<211> 802

<212> DNA

<213> *Diabrotica virgifera*

<400> 728

30

35

40

45

50

55

```

cgtccgtgat aacaaaatca atcaaagagt tgtttattaa atagtattga tagtgtattt 60
gaaaaataat aattttattta aggcgtacaa ttaataaaaa gttattttatt gtttatatat 120
tatttatgga aaatccaagt atttcaagtc attaaaattc aaataaaagt attattttat 180
aagagtttgt tccgataacc gtaaataggt atgagtttag ttataaagta aagtgcccat 240
ggtgtcataa aatgtagtaa atgctaagtc ttcaagtacg tactacattt ttgaagattt 300
cactgcactt aaaaagcatt tgcctttctc cgcagtattt gctactattt accagcctac 360
atagaagaat gtactacgct tttgaagtat atgcttgttt agtagtattt tgcttcagtt 420
taagtgaagt tgggtgggtgg tgcgtcttcg cgtaggtatt tttttgttac aatatggcag 480
catttatgaa tgtgtgtcat agaaaaattt acaaactaag aagaagattc ttaatttttg 540
gggtcattct tttatcaaat aaaatttaat aattgttaag aagattaaca aataacaata 600
attgttcatt tttatcctcg cgtaactctt tgctcgcttc gatctgagtc actcattttt 660
actcatgtac aattctaata atttggtacg taaaaatgtg aatttacaaa tcacaagcac 720
atggaaaact aattccatca cgattggtgt aatgcagaca cggctggcac tacgctttgt 780
agtagatact tctggtcagt ag 802

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<210> 729

<211> 862

<212> DNA

<213> *Diabrotica virgifera*

<400> 729

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	tctgcagggg	agtttgggtc	acctctcaac	gtccacctca	aaacagatgc	gccctggact	120
	aaaacaattt	taagtactct	cattgtttaa	aagttgattc	accacatttt	cataacgatt	180
5	tttagggcgg	ctgtacacgg	actgctgagg	tcgtttatca	ctgagcgaca	tacacggact	240
	gctcgagcga	tcgttgtaga	cttctggagc	gggccattgt	tgactacctg	agttgtccct	300
	tgctgcattg	caaccgctct	cgatctgtcg	atagcacgat	ggaatttcat	tatgctattg	360
	acagcttgaa	gcggtcttga	ctgctcgagc	tgctcgtgtg	atggcaacga	atatacaatt	420
	ataattcacc	gcgcaaacgc	tgcttcaaaa	agtcgacctc	aactgcttga	agatgtccgt	480
	gtacggccga	tcttggggta	tcttttttac	tcttatcggg	aatattttaag	aaccgaaatc	540
10	cctaattgtt	tccctatttg	ttccagaatg	atatacgtgt	taatttccaa	ctgagacttg	600
	acggccagca	cgaccgtacg	acaagacatt	ttcgaacagt	aaaatcatta	gttttagtaa	660
	caaatacaaa	gacagatggg	aattcggttc	tcgatattat	gcagagtatt	tacctgatga	720
	tgaacactta	ttggaggata	gaaacgcata	atttgcagaa	ctgacttacc	catgtaatgg	780
	acaggtatga	tggaacgta	tgtacttta	tgttttgtta	gtatttttac	gagagaagct	840
15	aagtaagttt	gtgaagaatt	ag				862

<210> 730

<211> 603

<212> DNA

20 <213> *Diabrotica virgifera*

<400> 730

25	gctgctcctg	tggcataacg	gccccgtacc	tggagaat	tacaattttc	ccggcaaaca	60
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	attagctatt	acttacgata	aaggagtatt	gataaccgga	gatctggttg	cttcatacgg	180
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	gcttactaga	gtaatgtacc	aacgcaggag	taaattagac	ccttttttga	ataatctggt	420
	tataggagga	atccaggatg	gagtcccctt	tcttggaaac	gtagataaat	tgggaactgc	480
	atatacagac	aaagttatat	gtacaggtta	tggagcccac	atagccttgc	ctcttctgag	540
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	atg						603

35 <210> 731

<211> 545

<212> DNA

40 <213> *Diabrotica virgifera*

<400> 731

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50	gatgtcaatg	cagcaagaga	catccttacc	aaagcccaga	gccagttatc	atctgcaagt	480
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55 <210> 732

<211> 496

<212> DNA

<213> *Diabrotica virgifera*

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<400> 732

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      tttggctgac ccctcacata acgctattcg caaggacccc aaaattaact ggattgtcaa 360
      ctcagtacac aaacacagag aactccgtgg caaaacttcc tctggcaaatt catctcgtgg 420
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<210> 733

<211> 512

15 <212> DNA

<213> *Diabrotica virgifera*

<400> 733

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      atgttttaga tgtaggtgaa ccgtcatcgt gtacttcttc tacagcttga taagcttcag 180
      ttggtaaacc taaatctttt ggttttagcgt ctatgataac tagaacggaa tttggacaat 240
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25     accaacctac tactcgttcc ctggcattaa cttttttgaa cattccatac atgttttcta 360
      agtaatcatg gtccaagaac cacacagact tatccttgtc atcttcgtca aaaggaactg 420
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30     caacacgctt ttgattgccg attttgccca tg

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512

<210> 734

<211> 669

<212> DNA

35 <213> *Diabrotica virgifera*

<400> 734

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      caatcttgcc tgggtcaaca tgtttgatga ttggattttt ttctggagtt ctacttgctt 480
      ctcttttttc tcgtagtact ccataatctt gagcctctgt tgttggacca gacggccctt 540
      ttcgatgttg aattcttctt cagcctttgc atcaatttcc tcggcctttt cattggcttc 600
      ttgctcaatg aaagccatca tgtgcttgat ctgcttttgt acatctgcgt cgctgagagc 660
50     attttgaga

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669

<210> 735

<211> 802

<212> DNA

55 <213> *Diabrotica virgifera*

<400> 735

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 caagctgctg gtgaaactca acagaacggt gtagaagaag ttgacatatc agttggaaaa 180
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 gtaagtgacc taaataaatc cgtgtctgga aaaactgtat ggataagagc aagggttacat 300
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 caagccattht taaatgtctc agacgtcgtt tcaaaatcta tggttaaatt ttcaagtggg 420
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 gcaagttgta gtcaacagga cgtggaacta gttgtttcac agttatgggt agtgtccttg 540
 tctgctccac agcttccttt gcaaataagag gatgcatcca gacctgaaaa accagaggaa 600
 gaagaagggt taaatatccg ggtaaatcaa gacacaaggc tggacaatag aatttttagac 660
 ttgagaacac caactaacca agcaatttac cgattggaag gaggcgtctg tccgctggtt 720
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<210> 736

<211> 579

<212> DNA

<213> *Diabrotica virgifera*

<400> 736

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 agagctgaac agtatgttaa ggaataccgt ttaaaagaaa gagacgaagt taggctagtt 180
 agacaagcca aaaccagagg aaatttctat gttcctgctg aggctaaatt ggcttttgtt 240
 gttcgtatta aggggtatcaa taaagtatga cctaaagtac gcaaagtact ccaactattc 300
 cggttacttc aaatcaacaa tggagttttc gtttaagttga acaaggctac tattaacatg 360
 cttaggatat gcgaacctta cattacatgg ggatataccta acttaaagtc agtaagagaa 420
 ttaatctaca aaagaggatt tgccaaagtt aatggacagc gtgtagcaat taccagcaat 480
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<210> 737

<211> 640

<212> DNA

<213> *Diabrotica virgifera*

<400> 737

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 caagtttttac aaatttttca ggatggagta aagggtgttc aacaacttct ctcaactttt 180
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 gcatcatagt cacagtggga tcaatttttg gaggtagagg aatatgaatt tgatacttat 300
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<210> 738

<211> 669

<212> DNA

<213> *Diabrotica virgifera*

<400> 738

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tggatcccca atggcagcaa caaatcgaaa aggatcttaa agaagcctca gaaactgcac 600
tgcccgatga tgacgaagat ttataaactc attaaccaat tactaaaact ctgtcatcgt 660
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<210> 739

<211> 302

<212> DNA

<213> *Diabrotica virgifera*

<400> 739

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agaggaagca gtgcagggtt tgaccgacac ataacaattt tctcgcccca aggccgactc 120
tatcaagtag agtatgcttt taaagccatt aaccaagccg gccccacttt ggtagcagtc 180
cgaggagtag atgctgcggc gtgtgtgacc cagagaaaga tcccgataa gctgattgat 240
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<210> 740

<211> 838

<212> DNA

<213> *Diabrotica virgifera*

<400> 740

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tagcaggact aacagcacct ggtactactg attgcacacc agcaccaccc atagtgcacat 180
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ttatgtttga acagaatggt acaggacact tgttttctgg gcagtgtttg gcatgatagc 360
aacatagagc gatgagttgt ttgcaaatag ggcaaccacc atttgttttc ctcttgacac 420
at ttgtgtgact cgtttcatct tctgacagct tggtaaccga caattggcat 480

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ctctgcattg acaagcatgt accaaagaat ggatacaacg ctgtatagat aattttctag 540
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<210> 741

<211> 1301

<212> DNA

<213> *Diabrotica virgifera*

<400> 741

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      ccattctcca atgattttgt cgaaggcctt ttgtttcttc tcagcagcat tggcaatggc 180
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20     gtcttcgagt ttggcagtga gtgatgagat ttcttgtct ttgcgttgga tggtttggtc 1260
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<210> 742

<211> 824

25 <212> DNA

<213> *Diabrotica virgifera*

<400> 742

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      ctgttttgtc catgccataa gctaaagctg cagctgtggg ttcatttatg actctcaaaa 180
      cattaagccc agaaatttgt ccagcatctt tggtagcctg acgttggtgag tcattgaaat 240
35     aggcaggtac tgtgattaca gcattcttta ctttgggtgt taagtaggct tctgcagttt 300
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      tatctttttt aacttcctca tcttcaaata ttctaccaat caaacgttta gtggcataaa 480
      atgtatttgc agaatttgtt acagcctgtc tcttagcggg cataccaact agacgttcat 540
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40     ctttggccttg tttaccttcc ataacagcaa cacatgagtt tgtagtacct aaatcaatac 660
      caataacagc ccccttgatt ccttctgatt tgtgtcgtaa ttgaatgtca tattttgggt 720
      ttagagcgta cagggaagat ctattatttg acaaattggt aaaatttctg tttccagctt 780
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45 <210> 743

<211> 704

<212> DNA

<213> *Diabrotica virgifera*

50 <400> 743

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	atgggttctac	tatgatgcc	tagaatgcct	accacaagat	aaatcagaaa	tcactgaaga	180
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	attgttgaag	aactttgcta	tgatgggtgt	aggaacacaa	ggagaagtta	cagtaactga	360
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	ccaacaacca	aaatctgcc	cagctgcaaa	ggcattataa	aagatgaatc	ctgatatcaa	480
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	ggatagaaga	tgtgtctact	accgcaagcc	tcttctagag	tctggaaccc	taggaactaa	660
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<210> 744

15 <211> 971

<212> DNA

<213> *Diabrotica virgifera*

<400> 744

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	tagaaacgat	aaaaatgctc	ttgcccaggt	cgtgaaaggc	tgcataggca	caaaattcat	480
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<210> 745

40 <211> 1049

<212> DNA

<213> *Diabrotica virgifera*

<400> 745

45

50

55

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 agctgatgta gatgcacgga aacaagaag 1049

20 <210> 746
 <211> 547
 <212> DNA
 <213> *Diabrotica virgifera*

25 <400> 746

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<210> 747
 <211> 508
 40 <212> DNA
 <213> *Diabrotica virgifera*

<400> 747

45 cacaaattct actatattct aaagaagcca tcgttaagac tgctgcgaga ccgcaatcac 60
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 ccgtagtccc actacctcga gcgcctttta ccattaccat accaatcacg atttctacgt 180
 tttctaacct gcaagataat gtctgctact attttgacgc gaattaattt agcagttcaa 240
 aatttgaagc atcatgtact taatactttt ggaagagggt ttccaccaga tgcactttgc 300
 50 ctacgaggaa tagaattaaa caaaagtcct cagaatttgc ccaaattttc tattaaagat 360
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 ttaaggacct gtaatgtttg tggatgatg 508

55 <210> 748
 <211> 788
 <212> DNA
 <213> *Diabrotica virgifera*

<400> 748

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      ttaccaatgt gttgatgggt accacctccg tgaggatgtt caacagggtt catagcaaca 180
      ccacgtacct taggccagca gttacgttta actttgtatt tgtggtaagc acgacctgct 240
      ttttaagattg gtttgtcaat acgaccacct ccagcaacga taccaccat ggccctgttg 300
      tttgatggaa taactttctt ggctccagaa ggtaacttaa ctctggtttt ctttgtgtcg 360
      tgattatggg caattacggt agcatagttt ccagatgcac gagctagccg accacgggtca 420
10     ccagtttttt cttctaagtt gcatacaatg gtaccttcag gcatagttcc tacaggcaat 480
      acattttcaa tttgaagggt agctttcttt ccacagtaca aaaattgtcc agtgtacatt 540
      ccttcggggg caataaaciaa ttccttccta gtttggaact tgtagggatc tctgaaatgt 600
      actactgcca atggagcacc acggccaggg tcatgtatga tatcttttac aacaccctta 660
      atgtaaccat gtctttctga gaaatctaaa taacgtagtt tgggtgctcc tttcctcttt 720
15     tttgtgtggg atttgaatac agatcccgca cctttacgtt gtgcacgaat tacacgaccc 780
      attgtaga                                     788

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<210> 749

<211> 752

20 <212> DNA

<213> *Diabrotica virgifera*

<400> 749

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25     gaggcgtagg caaggaaaaa ctgattacta tgcccgtaaa cgattgattg ttcaagacaa 60

      gaacaaatac aacactccca agtaccgttt gatcgtagct atctccaaca ggaacattac 120
30     ttgtcagatt gcttactccc gtattgaggg agacaagatt gtatgtgctg cttactccca 180
      tgaattgccc agatatggaa tcaaaactgg tcttaccacac tatgctgctg cctatgccac 240
      tggtttactt ttggccagaa ggctcctcaa aaaattggga cttgacaatt tatacagtgg 300
      caccactgat gttactgggg acgaatacaa tgttgaagct gctgaacaag gaccaggagc 360
      attcaggtgt tacttggaca caggttttaa ccgtaccagt actggcgccc gtgtctttgg 420
      agccatgaaa ggagctgtcg atggaggctt aaacattccc cactctacaa aaagattccc 480
35     tggttttgac agcgaatcca aaagcttcaa tgctgaagtc cacaggaatc acatttttgg 540
      catccatgtt gctgattata tgaaatcact ggaggaggaa gaccagaggc cattcaagag 600
      gcaattcagt caatacatta agctgggaat taatgctgac cagattgaaa atatgtacaa 660
      gaatgcccat gctgccattc gtgcaaatcc tgaattagaa aagaaggctg aaaaggctcc 720
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40

<210> 750

<211> 436

<212> DNA

<213> *Diabrotica virgifera*

45

<400> 750

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50     ccacataagg gcaaacttgt tagtattgta gacgtaatcg accagacaag gggttttagtt 60
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      aagttccgca ttaggtatcc attttcagct ccaactcgtg ttgtaagaaa agcatggact 180
      gatgctaaga ttgatgaaaa atggaatgaa tctgtctggg ccaaaaaagt agctgccaa 240
      gaaaagagat cacaactcac agatcttgac cggttcaaac ttcgtagggc tcgttcacga 300
      agaaaccaca tccgtacagc aactttcctt gctttaagga aggccgcac aagaaacgg 360
      ttcctctatg gtaaaaagaa gatggctaaa ggaggtgaca aacctaaacc aagcaagaag 420
55     gcgaagaaag aaaagc                                     436

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<210> 751

<211> 1072

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<212> DNA

<213> *Diabrotica virgifera*

<400> 751

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5      tccagttcaa attccgtgcc aaattctacc ccgaagacgt cgccgaagaa ctcatccaag 60
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      actgcccgcc cgaaacttcc gtccttctgg cttcgtacgc cgtacaagcc aggcattggag 180
10     attatgataa atcaactcac acgccaggat tcctagccaa cgatagggtt ttacctcaaa 240
      gggtaaatgga tcaacataaa atgtcaaaaag atgaatggga gaatagcatc atgacctggt 300
      ggaaggaaca tagaggtagg ttaagggaag atgccatgat ggagtacttg aagatagctc 360
      aagatctaga aatgtacgga gttaactatt tcgaaatacg taacaaaaag cagacagaat 420
      tgtacttagg tgtcgtatgc cttggactta acatttacga aaaagatgac caacttacac 480
15     ctaaaatcgg tttcccgtgg tcggaaatcc gcaacatctc tttcaatgat aggaagttca 540
      tcatcaaacc catcgacaag aaagcaccgc atttcgtttt ctttgctcca cgcgtgcgca 600
      tcaacaagag aattctcgct ctttgtatgt gcaaccacga actgtacatg cgcagacgta 660
      aacctgatac catcgacgtg caacaaatga aagcgcaagc gcgtgaagaa aagatggcaa 720
      aacaacagca gaaagaaaag ctccagtcgt aaatagcggc aagagaaaag gccgaaaaga 780
      aacagcaaga gtatgaagat agaatcaaag ccatgcaaga agagatggaa agaagtcaag 840
20     ctaactatat ggaagctcaa gagatgatta gacgattgga ggaacaattg aaacaattgc 900
      aggctgtcaa agaagagatg gaaaagagac agaacgagtt acagtccatg atggagcgtt 960
      tggaagagag caagaacatg gaagccgccg agaggcaaaa attggaagag gagatcaggg 1020
      ccaaacaaga ggaggttcta cgtatccaac aagaagtcga ggctaaggac ag 1072

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<210> 752

<211> 864

<212> DNA

<213> *Diabrotica virgifera*

<400> 752

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      ctctacttgt accctagaat atggttcgat aattctgcaa aggttctgct ccaacatatt 180

      gtcatacaac gttcctaaat gtgctctaac aataacatca tcttctaatt catgttttaa 240
      ctgtttttaca gcttggttga aatctgctag tgatcttttg tgtgcagcct gtgcaactga 300
40     tttcatagcc tctatatctt gaccagcgta tttaaaggcc aatttaccac taacgatttg 360
      ttggacgtct tccggactgt ttatcatgat ttttgacaaa agcatgtatt taagggtctgt 420
      gagggctttt ggggattcaa cactatcaaa accttcaaaa gcttcataaa aataagaata 480
      agctgttttg aaatccttct catctgcagc gtgtaatact ccggattgta aatctaaagc 540
      tgcttgcatac tttggagggc aatagatagc gttagctgtg gttcgtgctg aagttagtgc 600
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45     ttccaccaac aaatttttgt catccaactt ttttaactct ttcagtaagg tcgattccag 720
      ttgtagecgt tcgctgtaca ttccagtgct aaaataaaga gcaatcagcc tggcttcaag 780
      ggactgacgt agaaaagttc ttctctcttc ctttgcccat tctatacatt ctttgcagag 840
      ttgtacttcg ataccaatac cagc 864

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<210> 753

<211> 383

<212> DNA

<213> *Diabrotica virgifera*

<400> 753

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tcaaaagtag ttgttaagtt tttaaactgta atgatgaagc atgggtacat tggcgaattt 180
gaaattgtag acgatcacag aagtggaaag atagtagtaa atttgacagg aagggttaaac 240
aaatgtggag taatttcccc taggtttgat gtaccaatta cacatattga aaaatggaca 300
aataatcttt taccttcccg tcagtttggg tatgttgtgc ttaccacaag tggaggtatc 360
atggatcacg aagaagctag aag
383

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<210> 754

<211> 923

<212> DNA

<213> *Diabrotica virgifera*

<400> 754

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acgaaatagt ccaaatgtgt cgccatttct ctggaaacca tatctaacat tttgctgccg 180
tcaacttttg gtttgacagc agtcttaaag tcagcttcag attgggtttc catcattgcc 240
tcacgcaaga ctactgccag gttaaagatt ccaccaacgg gtcctaattc actggcttct 300
gtaagaagtc ttctggcacc tttgtcagtt gttgcatcgg ctgtagaaac aagtacgttc 360
acaccttttt ctctccatct tctgatacat agtgattggg atccagtttt aattccaactt 420
ctggaggtca acaccatttt cttggcacct ctagtaacca accagttggc taattcaaga 480
ccaaatccac caagacctcc aaccaaaatg taactctttt caggatccat gtatgttctg 540
ggaatagcgc tgacagtctt aacagctggg cgagtggcag ttttaggttc ttcttctctt 600
atgtggagca aaactttacc aatatgttta cctgaagcca taaatctaaa ggcttggtct 660
acttggtggt cattgtatac agtctttgga agtggcctta cagctccgct cttaattcct 720
tcagttacca atctcattac ttgtctcttc tgaggactgt ctgaatcaaa gagagcgtca 780
agaaggattc cgtggaaagt agtggtcttc aagaagatgc tcattcccaa cgcagaattg 840
ttagaaagat ctacttttcc aatttccaag aagcgaccac caattgccaa acatcttaca 900
gaagcctgga gttggtgagc agc
923

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<210> 755

<211> 1312

<212> DNA

<213> *Diabrotica virgifera*

<400> 755

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ggaggacagg tgaatgttat agcgtttttc aaagtgttag gtgtttatct tcaaaaagtt 120
tataaaataa gcaatcacta tgggtaatgt gtttgcaaat ttattcaaag gcctcttttg 180
caaaaaggaa atgaggatat tgatggtagg actcgatgca gctggtaaaa ccacaatttt 240
atataaactt aaattaggag aaattgtaac aactattcca acaattggat ttaatgtgga 300
gactgtagaa tataagaaca ttagttttac agtatgggat gtaggtggtc aagataaaat 360

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	tgaacttaga	gatgccgtac	ttctcatttt	cgccaacaaa	caagatttgc	ccaatgcaat	540
5	gaacgctgca	gaaatcaccg	acaaactcgg	tctccattca	ctacgcaacc	gcaactggta	600
	cattcaagct	acctgtgcaa	ctagcggaga	tggctctctat	gaaggtctgg	actggttgct	660
	caatcaatta	aagaacgcca	atcgctagaa	cataggaaaa	gagaggagtg	cgcaaaaaag	720
	tgtgcgagtg	cagatggttt	ttttcttgta	ctcttgctgt	gtctactacc	tcgcgcgcgc	780
	gcgaaacgtt	tcgtatacca	tatgttgcaa	tttttgtgtc	cgatggggaa	attcgtcatg	840
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10	aaaatagttt	taggcaatat	atcatatgaa	tctcagcttt	ctttaggttg	agagttgttt	960
	ttgtagtaaa	agaaccttaa	acatccttca	ttggcgattt	attatttttt	aactgcatga	1020
	aatccttagt	tttaattgtt	ttatataaca	cttttagatt	gtactaactt	ttaacattcc	1080
	acaaatttct	cataaaattg	tgatatcttt	tctaatacct	cttatatcaa	tgaacttatt	1140
	tttgcaagcc	aaaatatatt	cttagaaagt	aattttgtat	catctatata	aattttaattt	1200
15	tgggaattca	attaaagact	ttaactggca	aatttttaaa	tgttaaaggt	tctagtcacg	1260
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<210> 756

<211> 442

20 <212> DNA

<213> Diabrotica virgifera

<400> 756

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	gtagcttttc	gttggatttt	actctttgca	agaagtcttg	acgacacttg	gagtggttta	120
	catgttcaat	acggagattg	attcttttgg	ggatgattct	tcctcgaacc	cttttggtta	180
	caattacacc	taatgcatgt	gcagtaacgt	tgaaaacacg	tcctgtctta	ccatgggtaca	240
	ctttgtgggg	catacccttt	tgaactgcac	cattaccctt	gatatctaca	atatctccaa	300
30	ctttgtagac	tctcaaatat	gtggaaagtg	gaattacacc	acgtttttta	aacttgccggg	360
	caaatagatc	cctggttcct	cggcggtaac	cttttagagt	ggtcattttg	taccttccaa	420
	atcctaagaa	acacagtaaa	cc				442

<210> 757

35 <211> 404

<212> DNA

<213> Diabrotica virgifera

<400> 757

40	gtgcgagaac	ttcactatct	attcaacatg	cagtttgtgt	taagaggaac	cgcaactcat	60
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	gaatcgctta	aagcatccga	aatcagtctt	tatgctgctg	gagttccagt	ttctgaggaa	180
	aggttggttag	ccgattttga	gaacacagac	attgaattga	ctggtggctt	gcctgggtggg	240
45	aaagttcacg	gatcttttagc	tcgtgcaggt	aaagtaaagg	gacaaactcc	aaaagtagaa	300
	aagcaagaaa	agaaaaagaa	gaagactggg	agagctaaga	ggcgtattca	atataacaga	360
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<210> 758

50 <211> 747

<212> DNA

<213> Diabrotica virgifera

<400> 758

55

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 agcaggcaaa acaatttgtgt ctcgacaatt tgttgaaatg accaaagcta gaatagaagg 180
 5 tttgttggct gcctttccta aattaattcc tacaggaacc cagcatacat ttgtggaaac 240
 agattcagta cggatgtgtt atcaaccctt agagaaactg tatatgggtc ttattacaac 300
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 cacatttggtg gaaatggact cgcacgaaga aaaagtttat caggccgtga gacagactca 540
 10 agagcgcgag gccagaata tgatgagaga aaaggcaaaa gaacttcaga gacagaagat 600

cgaagcggcc aaaaaaggag ggaagacctc gtttggtagt agcgggtggct ttggcagctc 660
 gacagggttat actcctacgc catctgttgg tgatgtagct aaccagacaa atgatgttaa 720
 15 aacttcttca tacacaccag cccctgc 747

<210> 759

<211> 1285

<212> DNA

<213> *Diabrotica virgifera*

<400> 759

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 tatcttctgt ggccaaacat actaatttac cactatctga ccagtaaact gcttttgggt 180
 gtatctcgat tcttctgact aaatcgagag tttcccaatc atagaaagtc aaaccagaaa 240
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 30 catattcgct ggaatcttga gccacacaaa attcttgtgc gctaccaaac gctttgtttc 420
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 taatataatg agtgtgtcct tcgaaaactt gctgacaagc ccattgctttt tcccaattcc 1200
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<210> 760

<211> 442

<212> DNA

<213> *Diabrotica virgifera*

<400> 760

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      acttgtctgg tagagaaact atctccagag tcaactggagg tatgaaagtc aaagctgaca 180
      gagatgaagc ttctccctat gctgctatgt tagcagccca ggatgtagct gaaaaatgca 240
      aaacattagg aatcactgca ctccacatca aattgagggc tacaggtggg aacaaaacca 300
      aaacccttgg accaggagcc caaagcgcac tcagagcttt ggctcggtca aacatgaaaa 360
      ttggtaggat tgaagatgta actccaattc catctgattc cacacgtagg aagggaggtc 420
      gccgtggtcg tagattgtag ac                                     442

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10      <210> 761
      <211> 959
      <212> DNA
      <213> Diabrotica virgifera

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15      <400> 761

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      ttcctttcca ataccactc tcctgatcaa cgggtggcct taatgcttta tctaatacctt 120
      ctattctgtg gtatccatgg cagaagtttc cacagctggg actgcatccc tgggctcgtc 180
      ccccgcatca tctctcaacg gatctgcagg aaggctcctca attgcagcag ctgcagctcc 240
      tcctcctcta cgttcttcac cctcaataag ggacaagtag ggggaagttt cttcttcttc 300
      gagcatatta aaggctctgac ctttgccagt gtatcctatg gagacatttt ttgttgtgag 360
      gtcaacctct ggaggtagag tatctctaag agccctcaat ccatgtttga taagttcttc 420
      taaagaacta gatggcaatt catccagatg tttttctaag tatgtcctgg cactctggga 480

```

```

25      tcgagctcca atggacatag ctttgcaatc gtagaaatta gcagaagggc acgtttggta 540
      gatattgaaa ccagattcgt cataaccagc tactagaaga cctacgcaa atggtctgcg 600
      gtcgtatctt tgggtacatg tctgcatttt gttacctaaa atactgataa gcctattcaa 660
      tggcatataa gtatccaaag agtacttata attcaagcat tcgtttcgca tatatctact 720
      aaggatccta gcatcagctg taagtcccga gatggtgata ccaatgtgat cgtctatggt 780
      gataattttc ttctggtagg cagacagttc tgaagaagcc ctcttcaaag cgataagtac 840
      agcatgagtt ttacttttca gtcccactgt ggctgaacct aggttaactg cttccatggc 900
      atattctacc tgatgcagac ggccctgggg gctccacact gtcacatcac tatcgtatt 959

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35      <210> 762
      <211> 429
      <212> DNA
      <213> Diabrotica virgifera

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40      <400> 762

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      cacgaatggc ttgctccctt tgggccttcc ttacttcagg cctttgggtt ctcttggcca 120
      tgatatcatt taaagaagca cctacaatag ccctttggaa tttctgtgtc cttctgggtac 180
      gttttttggg ggcttcttcc tcctgacctt tcttatgttt acgtctgtac aagacagtcc 240
      atgttacttt acggggggtc cttttcatca agtgcgccct ttcacatttt gagttgagga 300
      aagtgaaggt ctttccatca actttaacca ttgttttgcc atgtccgggg taaattttgt 360
      acccgctgta agcacaaaag ccgatcttca ttttggaatg aaattactac ttaaattgaca 420
      gatgacaac                                     429

```

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50      <210> 763
      <211> 828
      <212> DNA
      <213> Diabrotica virgifera

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55      <400> 763

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cgtatgtagc tttggcaaag ttacctaaag taccagtggg acctctagcg gatgtgtagc 180
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<210> 764

<211> 664

<212> DNA

<213> *Diabrotica virgifera*

<400> 764

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aaaacttaat ctcaaaccatc taaagcattt tattttggat gaatgtgata aaatgttgga 600
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agtc

664

<210> 765

<211> 434

<212> DNA

<213> *Diabrotica virgifera*

<400> 765

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tggtggttata gtcaataaca aaggtgaaat gaaaggatca gccatcactg gtccagttgc 360
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<210> 766

<211> 1283

<212> DNA

<213> *Diabrotica virgifera*

<400> 766

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15     acaaactttc gtgaaaaatt ccttaatagt cttcgggtatc caagtcaatc tgatagcact 780
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      ctttataaga tcattatcta ctggcatata aattggagat atagcggcat aaagtccgat 1260
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```

25 <210> 767

<211> 685

<212> DNA

<213> *Diabrotica virgifera*

30 <400> 767

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      cttagatttac aaaagatgat actggaaagg ctctaaaaat taattttgat catggtacca 180
      caaccttggg attcatgtat cagggaggag ttgtacttgc agtagattcc agagctactg 240
      gaggccagtt tattggttca caaacaatga agaaaattgt agaaatcaat gattttctgt 300
      taggtactct ggctggaggc gcagcagatt gtgtctattg ggacagagtt ttggccaagc 360
      agtgtagaat gtatgaactc agaaatagag aacggatttc agtagcggct gcttctaaat 420
      taatggcaaa tatggtttac aattataaag gaatgggatt gtcaatgggt atgatgttag 480
40     ctggatggga caaaagggga ccacaattgt attacgtgga ctcagaaggc ctgagaacag 540
      caggaaaagt tttcagtggt ggttccgggt ccatatatgc ttttggtgta ctagactctg 600

```

```

45     ggcacaaatg ggatcttacg gacgaagaag catatgattt gggccgtaga tcgattttatc 660
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```

<210> 768

<211> 859

<212> DNA

50 <213> *Diabrotica virgifera*

<400> 768

55

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	catcagaaac	caagaaaggc	tgaaaccaca	agaagaaaaa	aatgaggagg	agagatcgaa	180
5	ggttgatgat	cttagaggaa	ctcccatgtc	tggttggtaca	ttggaagaaa	tcattgatga	240
	caaccatgca	attgtttcca	catcagtagg	cagtgaacat	tacgtgagca	ttttatcctt	300
	tgttgacaag	gatcaacttg	aaccaggatg	ttcagtactt	ttgaaccata	aggtgcacgc	360
	cgttgtaggt	gttttaggtg	atgatactga	cccaatggta	acagtaatga	agcttgaaaa	420
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	agaatctggt	gaattacctc	ttacctatcc	tgagtattat	gaagaaatgg	gtatcaaacc	540
10	acctaaaggt	gttatccttt	atggccctcc	aggtactgga	aaaactcttc	tggaagaaagc	600
	tggtgctaac	cagacttctg	caacattttt	gagggttggt	gggttcagaac	ttatacaaaa	660
	atatttgggt	gatggacctg	aactagtcgg	agaattattt	agggtagctg	aagagcatgc	720
	tccttccatt	gtatttatag	atgaaatcga	cgctgttggt	acgaagaggt	acgattccaa	780
	ttctggcggt	gaaagagaaa	ttcagagaa	tatgttagag	ttattgaatc	agttggatgg	840
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<210> 769

<211> 586

<212> DNA

20 <213> Diabrotica virgifera

<400> 769

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	taaaatacac	tctagccaaa	atccgtaagg	ccgccagaga	actgcttact	ctagaagaga	180
	aagaacccaa	aaggttggtt	gaaggtaatg	cactcctacg	tcgtttgggt	cgtattggag	240
	tacttagacga	gaacagaatg	aagctcgatt	acgtattggg	tctcaagatt	gaagatttct	300
	tggaagagcg	tctgcaaaca	caagtcttca	aatctggtct	agctaagtca	atccatcatg	360
30	ctagggtatt	gatcagacaa	cgacacattc	gggtccgcaa	acaagttgtg	aacattccct	420
	ccttcatcgt	ccgtttggat	tcacaaaaac	acatcgactt	ctctctgaaa	tcacctttgg	480
	gaggcggtcg	tccaggacgt	gttaagagga	agaacctcac	caagaagagc	ggtggtggag	540
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35 <210> 770

<211> 563

<212> DNA

<213> Diabrotica virgifera

40 <400> 770

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	atgttgaagc	acggccgagc	tgaggtaccc	atggaagtaa	tggtgtcttat	gttaggagaa	180
	ttcgtagatg	actataccgt	tcgtgtaatc	gatgtatttg	ctatgcctca	gactgggtacc	240
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	cagactggta	ggccagaaat	gggtgtgggg	tggtatcatt	cccatccagg	tttcgggatgt	360
	tggttgtctg	gagtggatat	caacacccag	caaagttttg	aggctctctc	ggaaagagct	420
	gtagcagtag	tagttgatcc	aatccagtc	gtgaaaggca	aagtcgttat	tgatgccttt	480
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<210> 771

<211> 1216

<212> DNA

<213> Diabrotica virgifera

<400> 771

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 10 aaatcagctg ctaacttggt tttggacaca gtaagcactt ttacatcata cgaactaatg 600
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 15 tatgtaagag agatgaagat acttgcttat acacaattat tggagtcata taggtctctt 900
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<210> 772

<211> 617

<212> DNA

25 <213> *Diabrotica virgifera*

<400> 772

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 cagtaggaat taaagcatca aatgggtgtg ttattgcaac agagaacaag cacaaatcaa 120
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 ttatttctgg tatgggtcct gactatcgcc ttcttgtag acaagcacgc aagatggctc 240
 agcagtatta cctagtatac catgaaccca ttctacagt acagttgggtg caaagagtag 300
 cgactgtaat gcaagaatac acccaatcag gaggagttag accatttgga gtgtcgctac 360
 35 tgatttgtgg ttgggataac aacagacctt acttggtcca atgcgatcct tctggagctt 420
 actttgcttg gaaagctact gcaatgggaa agaattatgt caatggaaaa acgttcttag 480
 aaaaaaggta cagtgaagag ctagaactcg acgatgctgt gcacactgct atccttacc 540
 tgaaagaaag ttttgaaggc cagatgacag ctgacaacat agaagttggt atttgcgatg 600
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40

<210> 773

<211> 736

<212> DNA

45 <213> *Diabrotica virgifera*

<400> 773

50

55

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	gtctcagcct	gaagcaactt	tccttaaaga	attaacatat	aggagtacca	atacaaaaaga	60
	accaggagta	gtaactgctc	cctcgtctaa	ccttaataca	gcctttcgtc	taattaaaga	120
	agttcaaagg	aaattttaaga	cacgagaagc	tgaagaaaaa	gaaaaagagg	atttggttaa	180
5	acagggcaca	ttagtacttt	cacagaataa	aggaaatcct	aaattaaaag	atctgtatat	240
	taggccaaat	attgtttcaa	aacgtatgac	aggatcatta	gaagctcaca	ctaattggtt	300
	taggtatact	tctgtgaggg	gtgataaagt	agacattctt	tacaacaaca	tcaagaatgc	360
	cttctttcaa	ccgtgtgatg	gagaaatgat	aatttctgtt	catttttcacc	taaaacatgc	420
	tatcatgttc	ggaaaaaaga	aacatgttga	cgttcaattc	tgtacggaag	tcgagaaat	480
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10	gtcggaaaga	gagctcagac	aaaaattgaa	aactgcattc	aaaagttttt	gtgaaaaggt	600
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	gactgaatgg	gcctcc					736

15 <210> 774
 <211> 718
 <212> DNA
 <213> Diabrotica virgifera

20 <400> 774

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25	gtgtcttttag	ccgatttaca	aaatgataat	gacgccgaaa	ggtctttcag	aaagttccgt	180
	ttgatagctg	aagatgttca	aggtagaaat	gttttaacaa	atttccacgg	tatggattta	240
	accactgaca	agctgaggtc	catggtttaag	aaatggcaaa	ccttaattga	agcatctgct	300
	gatgtcaaga	catcagatgg	atatttactt	aggggtgttct	gcataggctt	taccaacaaa	360
	gaccaacttt	ctcaaaggaa	aacatgctat	gcacaacata	cacaagttag	agctatccgt	420
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	tccaaattgt	tggaattgca	tgggtgatgga	ggcaaagggtg	gtgctggtga	ctccactggt	660
	gaagctgggt	ctaaagtcca	caggcctgag	ggatacgaac	caccagtaca	agaatccg	718

35 <210> 775
 <211> 598
 <212> DNA
 <213> Diabrotica virgifera

40 <400> 775

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45	aacactaact	caagacagaa	catccgtaag	ttgataaagg	atggtcttat	tattaagaag	180
	cccgtagctg	tacattccc	tgcccgtgtt	cgcaaaaaca	ctgaagccc	caggaaagga	240
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	aacaagcgtg	tccttatgga	atacatccac	aagaagaagg	cagagaaagc	ccgtgccaa	480
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55 <210> 776
 <211> 683
 <212> DNA
 <213> Diabrotica virgifera

<400> 776

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 ttataaaact tgtacactta cttatatattt actttatcaa taaaagatcc ctctctctcc 480
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 10 atacattgca tttcaaattg tctagttgga aacattgtac ttaactgact ctattagagt 600
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 ccgaaggcaa cagtcccaa aca 683

<210> 777

15 <211> 321

<212> DNA

<213> *Diabrotica virgifera*

<400> 777

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 ccgctaggtt gaaggggatc caaaccaaac acaccaaatt tgtcagagac atcatccgtg 180
 aagtcgtagg acatgctcca tatgaaaaga gagccatgga attgttaaag gtgtcaaagg 240
 25 ataagagggc cctgaaattc ctgaagcgtc gtcttggcac acacatcaga gccaaagagg 300
 agcgtgaaga actatccaac a 321

<210> 778

30 <211> 311

<212> DNA

<213> *Diabrotica virgifera*

<400> 778

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 ttggataaaa gacaagccgt actttgtgtg ctgctgaaa actgtgacga gcctatgtat 180
 aagaaactag tctcagcttt atgctcagaa catcaaattc ctcttattaa ggtagacaat 240
 40 aacaaaaaat taggcgagtg gtcagggtta tgcaaaattg ataacactgg taaagcacga 300
 aaggtcgttg g 311

<210> 779

45 <211> 501

<212> DNA

<213> *Diabrotica virgifera*

<400> 779

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 gtcagctact caacagtttt tggaaagagt attagttgca ttaagagcca cagcaccagt 180
 tccatctttg ctggaagaaa aagcaaagcc aaagccttct ggtgaaggag aggggtgctat 240
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 cactgctact gtaatcgcaa a 501

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<210> 780
 <211> 370
 <212> DNA
 <213> *Diabrotica virgifera*

5
 <400> 780

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	tgaaaaacgt	agaaacatac	cacttaaata	taacagagaa	acctgggtcaa	aggctgtaga	180
	agcaatgaaa	acggtagaga	aaataaaaca	gaaaaggcaa	ggagcctaca	tcatgcaaag	240
	attacgtaaa	ggtagagaaa	tccaacaaga	acgagacatc	aaagaggtag	aaagggtatc	300
	gtctcttatt	agatccccag	ctgtttggact	taaagaaaag	aaacaagaag	aatctatggc	360
	gcaagatcac						370

15
 <210> 781
 <211> 673
 <212> DNA
 <213> *Diabrotica virgifera*

20
 <400> 781

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 <210> 782
 <211> 411
 <212> DNA
 <213> *Diabrotica virgifera*

<400> 782

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55
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 <211> 553
 <212> DNA
 <213> *Diabrotica virgifera*

<400> 783

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<210> 784

<211> 902

<212> DNA

15 <213> *Diabrotica virgifera*

<400> 784

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      ctttacgaag acctttgtgt gtcttacggg gcaatttctt tgtgtgcca cgagaagtaa 480
      cacctttgta tccatgacct ttagtaacac caatgcaatc aatcatttca tcttgagcaa 540
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      taaatgcctt cttcttgctc ttgtaccagt tctttagtaa gcgcctgcgg caatcttcag 840
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35

<210> 785

<211> 1026

<212> DNA

<213> *Diabrotica virgifera*

40

<400> 785

45

50

55

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 gatgtgacag taactaatga cggagctacc attttacgtc ttttagaagt tgaacatcct 180
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 gttgccaaaa cctcgatgag ctcaaaaatt attggagctg atgctgatct tttttcacia 480
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 gttggtt 1026

20 <210> 786
 <211> 469
 <212> DNA
 <213> *Diabrotica virgifera*

25 <400> 786

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35 <210> 787
 <211> 1159
 <212> DNA
 <213> *Diabrotica virgifera*

40 <400> 787

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<210> 788

<211> 1261

<212> DNA

10 <213> *Diabrotica virgifera*

<400> 788

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	agcttcacaa	taagaccaga	tgttggagaa	ccattgggac	gtggtacaaa	aattgttctg	540
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25	gaactaagtg	atgatgaagc	agaagaagaa	aagaaggaag	aagaggaaga	caaagataaa	720
	cctaaaattg	aagatgtagg	agaggatgaa	gatgaagata	aaaaagatga	gaaaaagaaa	780
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30	gagtttagag	ctttattgtt	tgttcctcgt	cgtgtacctt	ttgatttgtt	tgaaaacaag	1020
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<210> 789

<211> 905

<212> DNA

40 <213> *Diabrotica virgifera*

<400> 789

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55	tgaacttcct	gatggacaag	tcatcaccat	tggtaatgaa	agattccgtt	gcccagaagc	780
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<210> 790
 <211> 873
 <212> DNA
 <213> *Diabrotica virgifera*

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 <211> 877
 <212> DNA
 <213> *Diabrotica virgifera*

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 <400> 791

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 <211> 375
 <212> DNA
 <213> *Diabrotica virgifera*

<400> 792

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<210> 793

10 <211> 547

<212> DNA

<213> *Diabrotica virgifera*

<400> 793

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20
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<210> 794

30 <211> 334

<212> DNA

<213> *Diabrotica virgifera*

<400> 794

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<210> 795

45 <211> 630

<212> DNA

<213> *Diabrotica virgifera*

<400> 795

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<210> 796

<211> 1152

<212> DNA

<213> *Diabrotica virgifera*

<400> 796

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gttccacttc gtccaggatt ggtagtattt tttcatcgag aaggaagggg tcgtaacaga 1140
tagacatcat tc                                     1152

```

<210> 797

<211> 988

<212> DNA

<213> *Diabrotica virgifera*

<400> 797

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	ctcttggatt	gatgcgtgag	tttagatctt	cgattctaac	atgtcgacgt	tcagcttgta	60
	gtaaacgtat	gggtaatact	ctgattggcc	gaatccgagg	cctggaatgt	caacgctatc	120
	aacgtaggt	cctgaaaggg	cagcactact	atcgagggtg	ccgtaaagtt	ggttcaagac	180
5	atctcttaaa	cgttttaatt	gtttcttatt	ggggtggatt	aaaatagctt	ggaaattgac	240
	ggggaggcca	tatcttaaaa	cagattcaac	aaataccctc	aacgctttaa	cgtgaatcca	300
	ggcgcagaaa	cactcgctga	agttgacttt	aagccatcta	actaatggac	caaattgctt	360
	ctttttatcg	gtgacgagtt	tggttatctc	gttctttcca	gctgccagtt	cctcttcggt	420
	atatatgaaa	tcacgaacga	tgaacttctt	ttctctagcg	tgttaacttga	attcttcgac	480
	gacctttttg	aatagggata	cagtatatag	accgtgttcg	ttatcctggt	taatcagttg	540
10	tgaagaacga	gggactatca	tgtcggtaat	cttttcggtat	gtcgcatcc	attcgttgaa	600
	ttgggctttt	ggaactataa	ccaacaatgt	ctgcaaata	tcagaatcca	aaataaaatg	660
	ttcctttttc	accaaactctg	ccaagtttct	tgttagtaaa	cttcctgtct	gtttcttctc	720
	caaattctga	agacttcctt	tcaagttatt	gtacgcagac	gatttggtct	tcagatcagc	780
	gtcaatttgg	ccaacttgtt	tgctgattat	atcggcgatg	ttacggagcg	attgcttgat	840
15	gggatatttg	gcgatgtccc	aagtaaactc	ggttaaataa	gtgggcaa	cgctgttatt	900
	ggcctgcagg	ttttctgacc	acttgtctct	ctgttcttca	agtacttctc	caagggtactg	960
	agctaccttt	ctgggtgacct	gctccacg				988

<210> 798

20 <211> 208

<212> DNA

<213> Diabrotica virgifera

<400> 798

	gagtgcctgg	agagctgctg	gattaaacta	cattaactat	tccaacattg	ctgccaaact	60
	tctgaggcag	gcacttaaac	ctgaacttag	aacagaagca	atgagaagaa	atgaaaccca	120
	tattaaagta	accaaattggc	aagatggaaa	gccaaataagg	gagtcacacat	tttaaatacca	180
30	taatttaagt	ccaagtctat	gtagtgtt				208

<210> 799

<211> 1326

<212> DNA

<213> Diabrotica virgifera

35 <400> 799

	ctgtatctgg	tgtcaacggg	ccactagtaa	tcctcgaaga	tgtcaaattt	cctaagttca	60
40	acgaaattgt	ccaactcaga	ttatctgacg	gaagtttaag	atcagggtcaa	gtacttgaag	120
	tcagcgggtc	caaggctgta	gtacaagtat	tcgaagggtac	atcagggtatc	gatgccaac	180
	acactgtctg	tgagttcaca	ggagatattc	tcagaactcc	agtctctgag	gatattgttg	240
	gaagagtatt	caacggctct	ggaaaacctc	ttgacaaagg	tcccccaatt	ctggctgaag	300
	actacctaga	tattcaagga	caacccatca	acccatgggtc	ccgtatctac	ccagaggaaa	360
	tgatccaaac	tggatcact	gccatcgatg	tgatgaactc	gattgcccgt	ggtcagaaga	420
45	ttcccatatt	ctcagctgct	ggtctgccac	ataacgatat	tgtctgcccc	atttgtaggc	480
	aagccgggtc	tgtcaaaatc	ccaggcaaat	cagtttttga	tgaccacgaa	gacaactttg	540
	ccatcgtgtt	cgctgctatg	ggtgttaaca	tggagactgc	tagattcttc	aaacaagatt	600
	tcgaagaaaa	tggttctatg	gaaaacgtat	gtttgttctt	gaacttgggt	aacgatccaa	660
	ccatcgaaag	aatcatcacc	ccacgtcttg	ctctaacagc	cgctgaattc	ttggcttacc	720
50	agtgcgaaaa	acacgtgtta	gtcattttta	ctgacatgtc	ttcatacgtc	gaagctttgc	780
	gtgaggtatc	tgccgccaga	gagggaagtac	ccggctcgtc	tggtttcccc	ggttacatgt	840
	acaccgattt	ggccaccatc	tacgaacgtg	ccggctcgtg	cgaaggccgt	aacgggtcca	900
	tcactcaaat	ccccatcttg	actatgccta	acgacgatat	tactcaccct	attccccgatt	960

55

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tgacagggtta	tattaccgaa	ggacagatct	acgtcgaccg	tcaattgcac	aacaggcaga	1020
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aagggtatgac	caggaaggac	cactctgacg	tttctaacca	attgtatgct	tggtatgcta	1140
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atctttctcta	cctcgagttc	ctaacgaaat	tcgaaaagaa	cttcatcacc	caaggaaact	1260
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ctaagg						1326

<210> 800

<211> 1034

<212> DNA

<213> *Diabrotica virgifera*

<400> 800

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gataaatgag	ttatcagcgt	cgaatctaca	gtcactacct	cgatttcgcc	tttctggtct	180
tccaaacacg	gtttcggtat	catcgtttca	tcgctatttt	ctggtaatac	gtgtaacaaa	240
atatccactt	tgactttagt	ttgggttttg	ctttgtcctt	gtttattttt	gcgccccgga	300
ataatctctt	ggaccttttt	gaagttaacc	acagcgcccc	aatcgtattc	atcttcagtc	360
gatttttatct	ttaaaagtct	accagggttg	agaaacggca	acaaatattg	cgagcttgtg	420
agatatgtcc	taaacttgac	acccaacagg	tctaactctg	ttctaattac	gtgataagac	480
tgtattcgct	cttcatcttt	gatttcaagc	gaattgaaaa	gttctaattt	ttcggtataa	540
tcatacataat	atccgggtat	tgcagcttga	ttctgaaact	ggaagaacga	tcgctccaac	600
atatactcag	gattgatttc	ttcgacctt	agcaagttca	gtaccatatt	gtaagtcaaa	660
tggaaggcgg	agttgatggg	gtccggcaaa	cctttaacta	tgttcctacc	ggctgccgga	720
ggcactttct	cgtccaccat	caatattacg	atacctttat	cgtccaggcc	tcttcttctt	780
gcccttccag	acatttggat	gtattctcca	gaagtaatcc	atctgtactc	actgccatca	840
aatttctca	ttccagtaaa	caacacagtt	cttgcaggca	tatttaaacc	catagcgaac	900
gtttctgtgg	caaatagcgc	ttttatgagc	ccctcgccga	ataaaatctc	gatgggttcc	960
ttcaaaatcg	gcaacaaaacc	accgtgatgg	atgcctattc	ctcttcttaa	caacggcaga	1020
aggttctcga	cttg					1034

<210> 801

<211> 721

<212> DNA

<213> *Diabrotica virgifera*

<400> 801

ggagaaacca	tcccctatac	aggaagcctc	tatccctata	gcactgtctg	gaaaagatgt	60
acttgctaga	gcaaaaaatg	gaacaggtaa	gactgggtgt	tacagtattc	ctgtgttaga	120
gcaaatacgac	cctaaaaaag	actgtattca	agcactaatt	atagtaccaa	cgagagaatt	180
agcattacaa	acttcacaaa	tatgcataga	actagccaaa	tacctagagg	tacgtgttat	240
ggtgacaaca	ggtggaacaa	acttacgaga	tgacattatg	cgtatatacc	aaaaagtgca	300
agttatcata	gcaactccag	ggcgtatact	tgacttaatg	gaaaaaggag	tagcagttat	360
ggaccaatgt	aaaattcttg	tattagatga	agctgacaaa	ttactgtctc	aagattttta	420
gggaatgctt	gacactgtga	ttaaaaatth	accacaagag	aggcaaattt	tactattttc	480
tgcaactttc	cctttgacag	ttgaacaatt	tatgagaaag	catttacgag	atccgtacga	540
gataaatctc	atggaagaac	ttacattaaa	aggtgttaca	cagtattatg	catttgtcca	600
ggaaagacag	aaagtgcact	gtttaaatac	tctattttcc	aagttacaaa	ttaatcaaa	660
tattattttt	tgcaattcta	cacaacgagt	agaattgctg	gcgaagaaat	aacagaactg	720
g						721

<210> 802

<211> 361

<212> DNA

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<213> *Diabrotica virgifera*

<400> 802

```

5      gcttttagggc agtgtgtaga aactcctcgt ctttacgata tttcagtaca aggccttttg 60
      cagtcacatt agtaaataga tgcagtgata ttttacaaaa tagctcacaa agtaaacctg 120
      gttctttgat cgatatacag acaagattct attcaccaga ggtaataaaa cctaaacctt 180

10     ctgaagaaga aatcaaaca aggggtgctga aagtgtgttc ttcatatgat aaagtaactg 240
      cagaaaagct gactttgaac tcccacttca tcaatgatct tggattagat tccctagacc 300
      atgtcgaagt catcatggcg atggaagatg aattcggtct tgaaatccca gatgctgatg 360
      c                                                    361

```

15 <210> 803
 <211> 183
 <212> DNA
 <213> *Diabrotica virgifera*

20 <400> 803

```

      ggtcttttcta gcacaattta caattccatt tttaaaagaa cctcaacaat ggcttttagct 60
      gttgttggttt ctgcattttt cttcgagaga actttcgatt tagcaacaga cacctttttt 120
      gaaagatata atgaagggaa attatggaaa cacatcaagg acaaatatga gcaggaataa 180
25     gtg                                                    183

```

<210> 804
 <211> 372
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: C4_Dv49_CG8055 concatemer; putative binding, carrier activity: CG8055 ortholog

35 <400> 804

```

      cccgggttta ccatggtagc aaagaaaaat gcgtcgaaaa ataaaagagt tgcactccaa 60
      gccctcttta ccatggtagc aaagaaaaat gcgtcgaaaa ataaaagagt tgcactccaa 120
40     gccctcttta ccatggtagc aaagaaaaat gcgtcgaaaa ataaaagagt tgcactccaa 180
      gccctcttta ccatggtagc aaagaaaaat gcgtcgaaaa ataaaagagt tgcactccaa 240
      gccctcttta ccatggtagc aaagaaaaat gcgtcgaaaa ataaaagagt tgcactccaa 300
      gccctcttta ccatggtagc aaagaaaaat gcgtcgaaaa ataaaagagt tgcactccaa 360
      gccctctcta ga                                                    372

```

45 <210> 805
 <211> 372
 <212> DNA
 <213> Artificial Sequence

50 <220>
 <223> Description of Artificial Sequence: Synthetic Primer

<400> 805

55

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```

      cccgggcaaa tagatggaac ccttacaact attgaaatgc agaggggaagc cctcgaagga 60
      gctagccaaa tagatggaac ccttacaact attgaaatgc agaggggaagc cctcgaagga 120
      gctagccaaa tagatggaac ccttacaact attgaaatgc agaggggaagc cctcgaagga 180
      gctagccaaa tagatggaac ccttacaact attgaaatgc agaggggaagc cctcgaagga 240
5      gctagccaaa tagatggaac ccttacaact attgaaatgc agaggggaagc cctcgaagga 300
      gctagccaaa tagatggaac ccttacaact attgaaatgc agaggggaagc cctcgaagga 360
      gctagctcta ga 372

```

<210> 806

10 <211> 490

<212> DNA

<213> Artificial Sequence

<220>

15 <223> Description of Artificial Sequence: C6 concatemer of highly effective WCR targets, ~50% GC criterion, consisting of segments in order 5'-3' from Dv26, Dv49, Dv23, Dv20, Dv13, Dv22, Dv18

<400> 806

```

20      catcacgact atcctactag tggagaagta tgcgaagtgc atgtcagaga ttgggaagaa 60
      tgcaacaggg ctccaagtgc caggtccaac tcaactgccg gctgtgtctg ctgatgcagt 120
      tgctactaaa ccaatcaaac gatgaggaac agacagaaca aaccgcaact gaaacggcaa 180
      ctacagaggt acagaaaaag ggtgtcaagg ggtgagatgg aacgagattg tcaaatttca 240
      cacggtgctg cacaattctt aagagagagg ctgtttgaag tctcttcagc aatagacaaat 300
25      ttgactccct ttcctcttgg gagggaaacg aaggccttag ctcccttacc tcatcgtccg 360
      tttggattca caaaaacaca tcgacttctc tctgaaatca cctttggggag gcggtcgtcc 420
      gatccttttc gatttgttgc tgccattggg gatccatctg gacttctgga ggaagcaagg 480
      caggtgcagc 490

```

30 <210> 807

<211> 560

<212> DNA

<213> Artificial Sequence

<220>

35 <223> Description of Artificial Sequence: Synthetic Primer

<400> 807

```

40      ggcgcaagcg cttcagtgtt atcatatgcc cacttccagg catttaaatt ccctgactcc 60
      atggaagtgc tccatcaggg gccaaaaggg gataccaagc cattaccggc cactcatcca 120
      cagcttttagc atggtacata tagtgatccc aaccgtgcac ctgactgtga cccaactcaa 180
      tgtgtaatc cggactgttt ctgctcagcg cccgccacca gttagcgccg aagtacaaaa 240
      gggattggac cttatttttg ctggtatcag agctcaacag gcaccacgtg ctcaacgata 300
45      aaagactggc caggaaggca cattcctttt tgccttactt attcaaggca ggggtgcatac 360
      agagtagcca cgtaacaaat agcacatagc gaagtgttgt accagcataa tgtataagct 420
      cctgtactta ccaaaggctc gttggcagat ctagaccagt tggacgaatt gggtattgag 480
      tactgtggtg cagcgcccc tttatggcag atgaatgtct gatggccata ccagacatcg 540
      aaggtattga ttacaccacc 560

```

50 <210> 808

<211> 372

<212> DNA

<213> Artificial Sequence

<220>

55 <223> Description of Artificial Sequence: C8 concatemer; putative sodium/potassium-exchanging ATPase: CG9261 ortholog

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<400> 808

```

5      cccgggggcta aaggaaatgg ccaaattaaa acatgctctc atcacgacta tcctactagt 60
      ggagaagcta aaggaaatgg ccaaattaaa acatgctctc atcacgacta tcctactagt 120
      ggagaagcta aaggaaatgg ccaaattaaa acatgctctc atcacgacta tcctactagt 180
      ggagaagcta aaggaaatgg ccaaattaaa acatgctctc atcacgacta tcctactagt 240
      ggagaagcta aaggaaatgg ccaaattaaa acatgctctc atcacgacta tcctactagt 300
      ggagaagcta aaggaaatgg ccaaattaaa acatgctctc atcacgacta tcctactagt 360
      ggagaatcta ga                                     372

```

<210> 809

<211> 372

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: C9 concatemer; putative sodium/potassium-exchanging ATPase: CG9261 ortholog

<400> 809

```

25      cccggggctcc atgtatTTTT attaaattga acaaaatata taactgggag ccaatgtatt 60
      acgatgctcc atgtatTTTT attaaattga acaaaatata taactgggag ccaatgtatt 120
      acgatgctcc atgtatTTTT attaaattga acaaaatata taactgggag ccaatgtatt 180
      acgatgctcc atgtatTTTT attaaattga acaaaatata taactgggag ccaatgtatt 240
      acgatgctcc atgtatTTTT attaaattga acaaaatata taactgggag ccaatgtatt 300
      acgatgctcc atgtatTTTT attaaattga acaaaatata taactgggag ccaatgtatt 360
      acgatgtcta ga                                     372

```

<210> 810

<211> 1000

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: C10 concatemer of genes with putative same/different mode of action, ~50% GC criterion

<400> 810

```

40      caagcccgcc aaaatgcgcg aacatctgga actcttctgg tctcgagtga atatcccca 60
      agttcttagg aatgcaatgc ttcctagacg tcgtcgagct ggctctgaaa ctgagcccca 120
      agttatagta ggtaacgata attattggac gtggcattag gttataggga aagtgtcaat 180
      ctgtctcaaa ttcgcacatt tgtggaaatg gactcgcacg cgcggcccaa cgacggcttc 240
45      aacaaacaca ggcgcaagtc gacgaagtcg tggatatcat gaaaacgaat gtagaaaaag 300
      gtatggcagg aaagaaatgc tgaatccgcc attgaagctc ttaaagaata tgaaccagaa 360
      atgggcaaaag ttgtccgaca agacaaatcc ggtattcaga aaatccgggc atagcaaaca 420
      tgccaaacac acacacgcag aaaggaaata tcagtcagac tcagaatcag atagtgatct 480
      ggaatggatt ggacacagag gtgaatcaga ccagaggacg ttcgggggta tattaaaaat 540
50      aacgttgtgt gcgcacttgg aaccgaaaca agcagaccat catccgcagc tcagtgcgta 600
      gccgaatgtg gccgtgcaca ctgtgcattt gtaggacagg tgtgcgggtt tcaacgtcat 660
      gttatgatcc cttgcatata ttgatggaaa aacacgcaa agaagagagc agagtattaa 720
      aagggtattt gccaggtaca tagaccagca aggaactgta atcaaatgg gcgatgaaa 780
      gaaggccagc gatagcgaac acattaatct caaagtactt ggtcaggata atgcagtgg 840
55      gcagaaggtc agacctctcc tcaacgtcac ccgtatcgag gatgagattg ccaaaacttga 900
      agagaaagcc caaaaagccc aacgaacacg gcgtagacga aacatcttgt gtagttattg 960
      tagaaggaca aaccagcaca ccagaacaac aagaactagc                                     1000

```

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<210> 811
 <211> 478
 <212> DNA
 <213> Artificial Sequence

5

<220>
 <223> Description of Artificial Sequence: C12 concatemer of highly effective WCR targets, ~50% GC criterion, consisting of segments in order 5'-3' from Dv23-Dv13-Dv26-Dv18-Dv49-Dv22-Dv20.

10

<400> 811

15

```
cctcaagctg tcattggcat ggatattctg tgccaagcta aatccggtat gggaaaaacg 60
gctgtttttt caaaggatcc aggatgacgt tccctattga taactgtacc tacacgaccc 120
aaattttctt ctccagtgat catacccata cgatttacct gaggaaatgc cggataaatct 180
gaagcaacat ataaggggta tcaacaatac tagagagttg agtcaaacat aattatggca 240
cattgtcctt ggatgtagta tccatcacgc agaccgccga acaacacgac atagccaacg 300
aaatcacaaa cgctattagc aatcctgtcg gattcacctg aatgcactcc tacgtcgttt 360
ggttcgtatt ggagtactag acgagaacag aatgaagctc gattacgtat tgggtctccg 420
aagtaatgta caacggccac actggacgta agataaatgc tcagattttt ttagggacc 478
```

20

<210> 812
 <211> 869
 <212> DNA
 <213> Artificial Sequence

25

<220>
 <223> Description of Artificial Sequence: C14 concatemer of gene targets active in several different organisms, ~50% GC criterion

30

<400> 812

35

```
ccgaagtgag atcggagcca aaaagcattg gttgcttgac ggtccaatgg aaaacgaacg 60
agaagtggat ggcttcagca atgctcggcc aggctgattg ctctttatct tgacactgga 120
atgtacagcg aagcgctaca actggaatcg accttactga ctactcgtct acgatatcgc 180
caaacatctg acatacgaaa acgttgaacg ttgggtgcgc gaattgcgcc attcctttct 240
caggtaccaa tgttgctgct ggtaaagcac gtggtattgt tattggaact ggtcttaaca 300
ccgccattgg taaaatcaga actgaaatgt ccaacgaaat tgccaacact aactcaagac 360
agaacatccg taagttgata aaggatggtc ttattattaa gaagcccgtg gctgtacatt 420
cccgtgccga tacctacaca gaaagctata ttagtaccat tggcgtagat tttaaaatca 480
ggacaatcga tttagatggg ttacaaaagg ataccaatac aagatgagag cagcatatgc 540
tcactttccc attactgtg tcaccactga aggaaacaca gttatccagt ttgcaagctc 600
tctggcagat ttcagtcaaa tcggcaccag aaaatccatg agttacttta gcaatgtata 660
caagatctac gtcttttagct acaggcgatt tccgatgaaa tagtggcatt aggttatagg 720
gaaagtgtca atctgtctca aattcgcaca tttgtggaaa tggactcgca cgaagaaaaa 780
gtttatcagg ccgtgagaga attaaaagtt caaggaggta tcggttcgtg tgtatcactt 840
aacgtgaaga gccccttggt ttccgacac 869
```

45

<210> 813
 <211> 2694
 <212> DNA
 <213> Artificial Sequence

50

<220>
 <223> Description of Artificial Sequence: xx

55

<400> 813

	ggtcgaccca	cgcgctccggc	ttgagtaaaa	actgaaatca	tataaaaagag	ataattttcta	60
	ttgtgaacta	atTTTTTcaaa	agtttctaca	ttaagtacat	attcattact	aaataatggc	120
	cgaaaacaaa	aatccagagg	atTTggccac	cgcaattctc	cgtaagaaag	atcgtccaaa	180
5	tagacttttg	gtagaagaag	cagttaacga	tgataactcc	gtgggtgctt	tgtcacaagc	240
	aaaaatggat	gaactacaac	ttttcagagg	agacacagtc	ctactgaagg	gcaagcgaag	300
	gaaagaaact	gtttgtatag	tattatctga	tgatacatgt	agcgatgaaa	aaattcgtat	360
	gaatagaaat	aattttaagag	ttaggctttc	agatgtagtt	tctatccaag	cttgccctga	420
	tgtaaagtat	ggcaagagaa	tacatgtact	tcccatagat	gatacagtgg	aaggactcac	480
	aggaaatctc	ttcgaagtat	acctgaaacc	ctacttcctg	gaggcctatc	gaccaataca	540
10	caaagatgac	gtattcgttg	tacgtggagg	aatgagagct	gttgaattca	aagtcgtcga	600
	gaccgatccc	gctccgtact	gtatcgtggc	tccagacacc	gtcattcatt	gtgatggaga	660
	tccaatcaag	cgcgaaagag	aagaggaagc	tcttaacgca	gttggtatcg	acgacatcgg	720
	aggttgtaga	aaacagcttg	ctcaaatcaa	agaaatggta	gagttaccac	tgagacatcc	780
	tagtcttttc	aaggctattg	gagttaaacc	accaagaggt	atTTTacttt	acgggtccacc	840
15	gggtactggg	aaaacactca	ttgcacgtgc	agtagctaac	gaaactggag	cgttcttctt	900
	cttgattaac	ggtcctgaga	ttatgagcaa	attggccggg	gaatccgaaa	gcaatcttcg	960
	taaagctttc	gaggaagccg	acaagaattc	cccagctatt	atTTTcattg	atgaattgga	1020
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<210> 814

<211> 622

<212> DNA

50 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: xx

55 <400> 814

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aagagatcct tcaaacatct taccctggac attcgaatga tcaaccccag gttactgaaa 180
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gctcactttc ccattaactg tgtcaccact gaaggaaaca cagttatcga aattagaaat 360
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tccaccaaac aaaaggatga acttatcatt gaaggaaact cattggagga tgtttcaaag 480
tcagctgccc ttattcaaca atctacaaca gttaaaaata aggatatccg taaattctta 540
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aaataaattt aagtttatat tt 622

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<210> 815

<211> 670

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: xx

<400> 815

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<210> 816

<211> 871

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: xx

<400> 816

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	tgctgaagag	agagacaaga	ggttagcagc	caaaacacat	taaatgtaat	ggttgattac	840
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<210> 817

<211> 2410

<212> DNA

20 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: xx

25 <400> 817

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	gacgctactg	atagtattta	catccccaag	ggtattaacg	taccttcttt	atcgagaaca	420
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	ttggaaactg	aatttgatgg	tgatcgtacc	aaatatacta	tggtgcaagt	atggcctgta	660
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<210> 818

<211> 988

<212> DNA

<213> Artificial Sequence

<220>

<221> modified_base

<222> (884)..(965)

<223> n = a, c, g or t/u

<220>

<223> Description of Artificial Sequence: pMON98501 Dv49 dsRNA Expression Cassette

<400> 818

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agtcatagtt caaccanacg tttcataaat agaattacag ggggtgtcaga attctacngt 960
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<210> 819

<211> 3001

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: pMON98502 Dv49 dsRNA Expression Cassette

<400> 819

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<210> 820

<211> 2719

<212> DNA

55 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: pMON98503 Dv49 dsRNA Expression Cassette

<400> 820

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      tgatcatcgtg aacatcatct acattcaaat tcttatgagc tttcttaagg gcatctgcag 1620
30     cgtttttcat agaactaat acagcagtat ttgtgctagc tccttcgagg gcttccctct 1680
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      tctctctgag tttttgaata gcctccccag gacaagtaact gcgatcgcgt taacgcttta 1920
35     tcacgatacc ttctaccaca tatcactaac aacatcaaca ctcatcactc tcgacgacat 1980
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45     agacatctct gtattgtgtt tctttcccca gtgttttctg tacttggtga atcggctaata 2640
      cgccaacaga ttcggcgatg aataaatgag aaataaattg ttctgatttt gagtgcacaaa 2700
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<210> 821

<211> 2367

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: pMON98504 Dv49 Concatemer dsRNA Expression Cassette

<400> 821

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	catcattg	ataaaaggaaa	ggccatcggt	gaagatgcct	ctgccgacag	tgggtccaaa	180
5	gatggacccc	cacccacgag	gagcatcggt	gaaaaagaag	acgttccaac	cacgtcttca	240
	aagcaagtgg	attgatgtga	tgggtccgatt	gagacttttc	aacaaaggggt	aatatccgga	300
	aacctcctcg	gattccattg	cccagctatc	tgtcacttta	ttgtgaagat	agtggaaaag	360
	gaaggtggct	cctacaaatg	ccatcattgc	gataaaggaa	aggccatcgt	tgaagatgcc	420
	tctgccgaca	gtggtcccaa	agatggaccc	ccaccacga	ggagcatcgt	ggaaaaagaa	480
	gacgttccaa	ccacgtcttc	aaagcaagtg	gattgatgtg	atatctccac	tgacgtaagg	540
10	gatgacgcac	aatcccacta	tccttcgcaa	gacccttcct	ctatataagg	aagttcattt	600
	catttgagga	ggacacgctg	agggcccacc	gtcttcggta	cgcgctcact	ccgccctctg	660
	cctttgttac	tgccacgttt	ctctgaatgc	tctcttgtgt	ggtgattgct	gagagtgggt	720
	tagtggatc	tagaattaca	ctctgaaatc	gtgttctgcc	tgtgctgatt	acttgcctgc	780
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	tagggcactt	ggattcagaa	gtttgctgtt	aatttaggca	caggcttcat	actacatggg	960
	tcaatagtat	agggattcat	attataggcg	atactataat	aatttggttcg	tctgcagagc	1020
	ttattatttg	ccaaaattag	atattcctat	tctgtttttg	tttgtgtgct	gttaaattgt	1080
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	tgtgaccata	agtcaagatc	agatgcactt	gttttaata	ttgttgtctg	aagaaataag	1200
	tactgacagt	atttttgatgc	attgatctgc	ttgtttgttg	taacaaaatt	taaaaaataa	1260
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35	ctacgaacgt	gctggtcg	ttaaatgitt	aggtaatat	gtgcagctgg	taggtaaaagc	2040
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	caattatatg	aagatattag	atcgccagcg	gtactcgctg	aggcctaggc	tgcatgcgtt	2160
	tggacgtatg	ctcattcagg	ttggagccaa	tttggttgat	gtgtgtgcga	gttcttgcga	2220
	gtctgatgag	acatctctgt	attgtgtttc	tttccccagt	gttttctgta	cttgtgtaat	2280
	cggctaatac	ccaacagatt	cggcgatgaa	taaatgagaa	ataaattgtt	ctgattttga	2340
40	gtgcaaaaaa	aaaggaatta	agcttac				2367

<210> 822

<211> 45

<212> DNA

45 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic Primer

50 <400> 822

ccaagccctc aaaaagaaga aacgattgga aaagacccaa ctaca 45

<210> 823

<211> 50

55 <212> DNA

<213> Artificial Sequence

<220>

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<223> Description of Artificial Sequence: Synthetic Primer

<400> 823

acgacatagc caacgaaatc acaaacgcta ttagcaatcc tgcggattc 50

<210> 824

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic Primer

<400> 824

tgtgtctgct gatgcagttg ctactaaacc aatcaaacca gcagct 46

<210> 825

<211> 113

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic Primer

<400> 825

acaccctaca caaccttata tattaacaag tagtgatgat atgcttatca agctttggaa 60
ttgggaaaaa gcatgggctt gtcagcaagt tttcgaagga cacactcatt ata 113

<210> 826

<211> 153

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic Primer

<400> 826

tgtagtatg gatgccagtg gaggcaaaat tatttggggc agacactctg aacttcaaca 60
ggcaaatctc aaggcgtag ctgaagggtgc ggaaataaga gatggagaac gccttccagt 120
ttctgtaaaa gatatgggtg cttgcgagat ata 153

<210> 827

<211> 183

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic Primer

<400> 827

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gttgcttctt gctacgagct cgggtgatga aaatttagtc cgtactctag gagaaacgac 60
acaagctgaa agcaaacata acttagcatt tttgtcacac ttgttagtag gtgattttaa 120
caaatgtcta gacattctta ttaataccgg tagattgcca gaagctgcat ttttcgccag 180
atc 183

5

<210> 828
<211> 95
<212> DNA
<213> Artificial Sequence

10

<220>
<223> Description of Artificial Sequence: Synthetic Primer

<400> 828

15

ccaagccctc aaaaagaaga aacgattgga aaagacccaa ctacaacgac atagccaacg 60
aatcacaaa cgctatttagc aatcctgtcg gattc 95

20

<210> 829
<211> 96
<212> DNA
<213> Artificial Sequence

25

<220>
<223> Description of Artificial Sequence: Synthetic Primer

<400> 829

30

acgacatagc caacgaaatc acaaacgcta ttagcaatcc tgtcggattc tgtgtctgct 60
gatgcagttg ctactaaacc aatcaaacca gcagct 96

35

<210> 830
<211> 266
<212> DNA
<213> Artificial Sequence

40

<220>
<223> Description of Artificial Sequence: Synthetic Primer

<400> 830

45

acaccctaca caaccttata tattaacaag tagtgatgat atgcttatca agctttggaa 60
ttgggaaaaa gcatgggctt gtcagcaagt tttcgaagga cacactcatt atatgttagt 120
atggatgcca gtggaggcaa aattattttg gccagacact ctgaacttca acaggcaa 180
ctcaaggcgt tagctgaagg tgcggaaata agagatggag aacgccttcc agtttctgta 240
aaagatatgg gtgcttgcca gatata 266

50

<210> 831
<211> 336
<212> DNA
<213> Artificial Sequence

55

<220>
<223> Description of Artificial Sequence: Synthetic Primer

<400> 831

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ggcaaatctc aaggcgtag ctgaagggtgc ggaaataaga gatggagaac gccttccagt 120
ttctgtaaaa gatatgggtg cttgcgagat atagttgctt cttgctacga gctccggtga 180
tgaaaattta gtccgtactc taggagaaac gacacaagct gaaagcaaac ataacttagc 240
atTTTTgtca cacttgtag taggtgattt aaacaaatgt ctagacattc ttattaatac 300
cggtagattg ccagaagctg catttttcgc cagatc 336

<210> 832

<211> 141

10 <212> DNA

<213> Artificial Sequence

<220>

15 <223> Description of Artificial Sequence: Synthetic Primer

<400> 832

20 **ccaagccctc aaaaagaaga aacgattgga aaagacccaa ctacaacgac atagccaacg 60**
aatcacaaa cgctattagc aatcctgtcg gattctgtgt ctgctgatgc agttgctact 120
aaaccaatca aaccagcagc t 141

<210> 833

<211> 449

25 <212> DNA

<213> Artificial Sequence

<220>

30 <223> Description of Artificial Sequence: Synthetic Primer

<400> 833

35 **acaccctaca caaccttata tattaacaag tagtgatgat atgcttatca agctttggaa 60**
ttgggaaaaa gcatgggctt gtcagcaagt ttctgaagga cacactcatt atatgttagt 120
atggatgcca gtggaggcaa aattatttgg gccagacact ctgaacttca acaggcaaat 180
ctcaaggcgt tagctgaagg tgcggaaata agagatggag aacgccttcc agtttctgta 240
aaagatatgg gtgcttgca gatatagttg cttcttgcta cgagctccg tcatgaaaat 300
ttagtccgta ctctaggaga aacgacacaa gctgaaagca aacataactt agcatttttg 360
tcacacttgt tagtaggtga tttaaacaaa tgtctagaca ttcttattaa taccggtaga 420
ttgccagaag ctgcattttt cgccagatc 449

<210> 834

<211> 590

45 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic Primer

50 <400> 834

55

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ccaagccctc aaaaagaaga aacgattgga aaagacccaa ctacaacgac atagccaacg 60
aatcacaaa cgctattagc aatcctgtcg gattctgtgt ctgctgatgc agttgctact 120
aaaccaatca aaccagcagc tacaccctac acaaccttat atattaacaa gtagtgatga 180
tatgcttata aagcttttga attgggaaaa agcatgggct tgtcagcaag ttttcgaagg 240
5 acacactcat tatatgttag tatggatgcc agtggaggca aaattatttg ggccagacac 300
tctgaacttc aacaggcaaa tctcaaggcg ttagctgaag gtgcgggaaat aagagatgga 360
gaacgccttc cagtttctgt aaaagatatg ggtgcttgcg agatatagtt gcttcttgct 420
acgagctccg gtgatgaaaa tttagtccgt actctaggag aaacgacaca agctgaaagc 480
aaacataact tagcattttt gtcacacttg ttagtaggtg atttaaacia atgtctagac 540
10 attcttatta ataccggtag attgccagaa gctgcatttt tcgccagatc 590

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<210> 835

<211> 657

<212> DNA

15 <213> *Diabrotica virgifera*

<400> 835

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gtaaattcaa attacaaacc atattagtca cccgtaaaat gtataaactc accattatta 60
caaaactttt tctttgactt ctcaaaaaca aacaatgtgg cgcttacaat gtttttcagc 120
ggaccatttc aattatttta aacttatcac ttggatccga tgcacttcat caatagctaa 180
aaaaattttg ctctttgtat ctcatcttct agtataagtt cacattttct ttcattttct 240
agaaccgcga aaactttaat aagtacctct tgattcattc caaaaaagat tgcactctgaa 300
acatcctctc cttgtgtgag ttcaataaat gtaaccactg tattttgcat acccctttca 360
25 caaatagaat catatacaat gctagcccat tctcttggg tatgccaata gatttccac 420
cggtttttgt ttttatctac aggagatgca tggccacttt tttgcaattc gcttagtata 480
gagattataa cgttttgttc taattttctg tttattgatg aattattaaa taaagggtgac 540
tggttttgtg ctcttacatc taggggtgta gttttgggtt gttcgcaaaa gttttaaatt 600
aatgacttcc atgcatctac ttgctttgct cttgtttcag gatgtggctg caacgtg 657

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30

<210> 836

<211> 1251

<212> DNA

35 <213> *Diabrotica virgifera*

<400> 836

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catatctctc caaactatgg cgcgttcgga ttcatttttc agacggacaa accggccttt 60
tggegcacatc tttgcattaa agctctgagc atgaactgtt tcctggacaa ggttcgcact 120
tgtctcaaaa acacctctaa atcgatgaat ccacatctca atgcctctcc catgtaataa 180
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gctgtcgttg ttaccgcac atctacatct atagattctt gattacttat tcgttctatg 300
gccttattta gttcttggtc tttgtcttgt agcattgtaa tatttttgtc tagatcattc 360
45 ttttcttttt ctaatcggct caatataccg tccaacttca attttccttg cttcaactcc 420

```

45

50

55

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	tcctgtgtcc	tcttgagcgt	ctctagttca	gcttgattct	gctggaattg	ttccttcatt	480
	cttctaagca	gcttctcttc	caaagctgtc	atcagagatt	ccctgatatg	ttcttctttt	540
	atagtacctg	ttccggcctg	aggtccaggg	gggaaattaa	atggatactg	cgggttgcgaa	600
5	gaagggtagg	gtggatatcc	ttggaaagaa	ttgttgctgg	ttggaggata	tgaggggtag	660
	ccgccgaaac	ctcctgatgc	tggtgggtag	ggggtaggat	acggaggcat	gtaaccacca	720
	gatggttgag	gcatgaatga	at ttgacgga	tacgattcat	tgtctttggc	cctagcaaac	780
	actggagggtt	gttcgccaaa	tgtaaccaatc	ataacttgga	ttaatcctag	caaatctgat	840
	tcattcggca	cccaatcgtg	caaatatggc	agataaactt	ttccattttg	atctacaaac	900
	atggaaactt	ttatggacat	gtcgggaagtc	ggtttaacat	agcaaattggg	agcattctct	960
10	ggatgtgtgt	caattaacca	tatacaaatt	ggaatattat	aaatattgcc	tttghtaacgc	1020
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	acactctgtt	ctggatgtaa	acctctgtat	tgtgtggtga	tggtgattat	ttctctataa	1140
	gctacatcag	gattgtgata	agcaggttagc	caagtcctaa	gtctctccgt	atctaccatt	1200
	ttctacgaat	taattttctt	ccagctaaaa	ctatcgagat	ctagagttct	c	1251

<210> 837

<211> 669

<212> DNA

<213> *Diabrotica virgifera*

<400> 837

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25	aagagagaag	tacgataatt	tagcagattt	gtatgctgta	ataaacactt	tgcaacaatt	120
	agagaaggca	tatattcgag	attgtgtagt	ggcaaaggaa	tatacaggag	cttgtagtaa	180
	attattagtt	cagtataaag	ctgcgtttctg	acaagtcaag	agtgatgaat	ttcctacacc	240
	agacgccttt	gttaagaagt	acaggcttga	ctgtcctgca	gctttagaac	gtatcaaggga	300
	agataggcca	atcactatca	aagacgacaa	aggcaacact	agtcgatgca	ttgtgatata	360
30	cgtatcgcta	ttcatcacta	taatggacaa	actgcggttg	gacattcggt	cgatggataa	420
	cttacatcct	gacgtgaggg	acttagtaga	tactatgaac	agacttagca	ttctgccatc	480
	ggatttctgat	ggaaaggtaa	aagtggctga	atgggttaaat	actttaaatg	aaatgcaggc	540
	ctctgatgaa	ttatccgaag	ctcaagttag	gcaactgttg	tttgatcttg	aaagtgcgta	600
	tgcgtccttt	aataaagtcc	ttcataattc	tgccataaatg	tacgagatag	ttgttatgat	660
	tgttacacg						669

<210> 838

<211> 793

<212> DNA

<213> *Diabrotica virgifera*

<400> 838

	gatggtaggg	tgacgagcag	tgtgactcat	ttttaatttt	atattgtcaa	atatttaggt	60
45	gttttgctgg	ttattattat	tatattattt	aaaaatggag	tggttatttg	gaaaaaaagt	120
	aacccccgaa	gaaatgcttc	gtaaaaacca	acgagcatta	aataaagcca	tgagagattt	180
	agatagagaa	aagcaaaaga	tggaaacagca	ggagaaaaaa	gtaataaacg	atattaaaaa	240
	attagccaag	gaagggtcaa	tggacgctgt	caaaataatg	gctaaagatc	tggtcagaac	300
	tagaagggtat	gtgaagaaat	tcatgtttgat	gaaggctaac	attcaagcag	tatcattgaa	360
	aattcagact	cttagatccc	aaaatacaat	ggcacaagct	atgaaagggtg	tcactaaagc	420
50	tatgcaaagt	atgaataggc	agctaaattt	accacagata	caaaggatat	tacaagaatt	480
	tgaaaagcag	tctgaaatta	tggatatgaa	ggaagaagtt	atgaatgatg	ccattgatga	540
	tgcgatggaa	ggagatgatg	atgaggagga	aactgacgca	gttgtcaatc	aagttttaga	600
	tgaattgggt	cttcaattga	atgatactct	ttctggactg	cctcaaaccg	ctggatctct	660
	tcctgcctct	gggcaaaaac	atcctgcagc	tgcagctgct	gttgaggag	gaggtaatgg	720
55	tggcactggg	actggaggca	gtggtggaaa	cagtggcggc	ggagggtggc	tttctgatgc	780
	cgatgcggat	ttg					793

<210> 839

<211> 767
 <212> DNA
 <213> *Diabrotica virgifera*

5 <400> 839

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10 ggcacggaag gcatctcttg ctcaatcata ccagccaatt cttcttctac agctgcttca 120
 tcttcatctg tcaattgacc actaagaagt tcgttaatct cattctgttt gtcaaccctt 180
 tctcttggtt catccaatat acgttcaata tcttcaattt tgagggaatc attaatgtgt 240
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 tctatatcac tagccatttt atcgagatta tcaagttgta catctagctt ggacaacagc 360
 15 tgttcttgat acctcttctt ctttaagtaa agttttgctc tgtctctttg gccattgtta 420
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 tgtctcaatt tatctctttg ctggttgagc tgtaacactg ctttatcgtg ttctgttact 540
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 aaatttctct tgatttgtgt tattcaaaaa attgatacca tccttatatt atagttttcc 660
 20 tattatcaca cgttttatgc tgttttctta tatcttttag gactaatttt taatcaggggt 720
 tgccagatga aatttcagaa tatccctaga cgggagcttc aatttcc 767

<210> 840
 <211> 588
 25 <212> DNA
 <213> *Diabrotica virgifera*

<400> 840

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 taagttctct gatcatttcc tccaacttat tagcattttc accttcttgt tgttctgcct 180
 ttggagattc cccaacagcc atattaaaca taacaacttt aggtgtcata gttgacatct 240
 tgtttgagaa acaatatgta tatataccag atgtgtgggc tgcaaagtgt tattttccgg 300
 35 cagtttccct ttcacctgg tataagttct ggccgtttgg atctataata cgcacatcta 360
 tgtcaaggaa tcctccttct gctatttcaa aagtgagacc catttttgtg ccagcttcca 420
 ctttgtcaaa gaaacattct tctgcatgtg catctactgt gataaaatag gccaaacttt 480
 gatttatgcc caaacaacc agtgaaataa ggaagccgaa aagatacatg tttactttaa 540
 attaaaatta gaaaacttgc gccacgtaac ctctcacact tgacgttc 588

40 <210> 841
 <211> 1098
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 <213> *Diabrotica virgifera*

45 <400> 841

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 <212> DNA
 <213> *Diabrotica virgifera*

25

<400> 842

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 35 ctgggatatc attaaacttt ggctcttcca aaaaaccatc tggaccattg ttttctacca 480
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 <212> DNA
 <213> *Diabrotica virgifera*

45

<400> 843

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20 <213> Diabrotica virgifera

<400> 844

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	tacaatactg	ttatgaaatt	tgtatTTTTTg	gccacatcgt	atgcaactat	ttattttaatc	180
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	atcttaccat	cgtttgggtt	ggctatgctt	atcaatcacg	agttttcatt	tatggagggtc	300
	ttgtggactt	tcagtattta	tttggaatca	gtggctatat	tgccgcaatt	gttcattggtc	360
30	agtaaaacag	gagaagcaga	aagtattact	tgcgactact	tattcgcaatt	gggatcttat	420
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	attactaaag	tactcaaggg	aaagaaacta	caattgcccg	cttaaaccoc	tcttatataa	600
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<210> 845

<211> 725

<212> DNA

40 <213> Diabrotica virgifera

<400> 845

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	ttcgccaaca	tccacatcaa	acaagaaata	caaatacctc	aagtgtcctc	ccttacctca	180
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	tcgtcgatgg	tcatggggcc	ggataacaaa	ctctggggcc	aagcgaactc	caccaccaca	360
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	ccttcgagta	aagtgtcgcc	gctcattagg	gatttcggtg	ccgccgttga	cgatcgcgaa	480
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	aggaattcga	tattcttttaa	agatctcaag	gtggacgatc	aaatgaaact	tctgcagcat	660
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<210> 846
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 <213> *Diabrotica virgifera*

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gagcttttat atacggagta actagtggga gaaaaggaaa aggatctatt ttcgtttggg 240
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tctttacctt gagtatatct agtgctacac aaggagggtta caaaccttgg tatttggaag 360
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<210> 847
 <211> 140
 <212> DNA
 <213> *Diabrotica virgifera*

25
 <400> 847

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tgctactaaa ccaatcaaac 140
  
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35
 <210> 848
 <211> 210
 <212> DNA
 <213> *Diabrotica virgifera*

40
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tgcaacaggg ctccaagtgc caggtccaac tcaactgccg gctgtgtctg ctgatgcagt 120
tgctactaaa ccaatcaaac gatgaggaac agacagaaca aaccgcaact gaaacggcaa 180
ctacagaggt acagaaaaag ggtgtcaagg 210
  
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 <210> 849
 <211> 280
 <212> DNA
 <213> *Diabrotica virgifera*

<400> 849

55

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 tgctactaaa ccaatcaaac gatgaggaac agacagaaca aaccgcaact gaaacggcaa 180
 ctacagaggt acagaaaaag ggtgtcaagg ggtgagatgg aacgagattg tcaaatttca 240
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<210> 850

<211> 350

<212> DNA

10 <213> Diabrotica virgifera

<400> 850

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<210> 851

<211> 420

<212> DNA

<213> Diabrotica virgifera

25

<400> 851

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<212> DNA

<213> Diabrotica virgifera

40

<400> 852

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<210> 853

<211> 210

50 <212> DNA

<213> Diabrotica virgifera

<400> 853

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 acagaaaaag ggtgtcaagg ggtgagatgg aacgagattg tcaaatttca cacggtgctg 180
 cacaattctt aagagagagg ctgtttgaag 210

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<210> 854
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<212> DNA
<213> *Diabrotica virgifera*

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	acagaaaaag	ggtgtcaagg	ggtgagatgg	aacgagattg	tcaaatttca	cacggtgctg	180
	cacaattctt	aagagagagg	ctgtttgaag	tctcttcagc	aatagacaat	ttgactccct	240
	ttcctcttgg	gagggaaacg	aaggccttag	ctcccttacc			280

<210> 855
<211> 350
<212> DNA
<213> *Diabrotica virgifera*

15
<400> 855

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	acagaaaaag	ggtgtcaagg	ggtgagatgg	aacgagattg	tcaaatttca	cacggtgctg	180
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25	ttcctcttgg	gagggaaacg	aaggccttag	ctcccttacc	tcacgtcccg	tttggattca	300
	caaaaacaca	tcgacttctc	tctgaaatca	cctttgggag	gcgggtcgtcc		350

<210> 856
<211> 420
<212> DNA
<213> *Diabrotica virgifera*

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<400> 856

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	acagaaaaag	ggtgtcaagg	ggtgagatgg	aacgagattg	tcaaatttca	cacggtgctg	180
	cacaattctt	aagagagagg	ctgtttgaag	tctcttcagc	aatagacaat	ttgactccct	240
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40	caaaaacaca	tcgacttctc	tctgaaatca	cctttgggag	gcgggtcgtcc	gacccctttc	360
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<210> 857
<211> 140
<212> DNA
<213> *Diabrotica virgifera*

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<400> 857

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<210> 858
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<213> *Diabrotica virgifera*

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<400> 858

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      aagagagagg ctgtttgaag tctcttcagc aatagacaat ttgactccct ttcctcttgg 180
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<210> 859

<211> 280

10 <212> DNA

<213> *Diabrotica virgifera*

<400> 859

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      aagagagagg ctgtttgaag tctcttcagc aatagacaat ttgactccct ttcctcttgg 180
      gagggaaacg aaggccttag ctcccttacc tcatcgctcg tttggattca caaaaacaca 240
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20

<210> 860

<211> 350

<212> DNA

<213> *Diabrotica virgifera*

25

<400> 860

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      aagagagagg ctgtttgaag tctcttcagc aatagacaat ttgactccct ttcctcttgg 180
      gagggaaacg aaggccttag ctcccttacc tcatcgctcg tttggattca caaaaacaca 240
      tcgacttctc tctgaaatca cctttggggag gcggtcgctc gatccttttc gatttgttgc 300
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```

35

<210> 861

<211> 140

<212> DNA

<213> *Diabrotica virgifera*

40

<400> 861

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      aaggccttag ctcccttacc
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```

45

<210> 862

<211> 210

<212> DNA

<213> *Diabrotica virgifera*

50

<400> 862

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      ctgtttgaag tctcttcagc aatagacaat ttgactccct ttcctcttgg gagggaaacg 120
      aaggccttag ctcccttacc tcatcgctcg tttggattca caaaaacaca tcgacttctc 180
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55

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<210> 863
 <211> 280
 <212> DNA
 <213> *Diabrotica virgifera*

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 aaggccttag ctcccttacc tcatcggtccg tttggattca caaaaacaca tcgacttctc 180
 tctgaaatca cctttgggag gcggtcggtcc gatccttttc gatttggtgc tgccattggg 240
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<210> 864
 <211> 140
 <212> DNA
 <213> *Diabrotica virgifera*

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 25
 cctttgggag gcggtcggtcc 140

<210> 865
 <211> 210
 <212> DNA
 <213> *Diabrotica virgifera*

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 <400> 865
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 cctttgggag gcggtcggtcc gatccttttc gatttggtgc tgccattggg gatccatctg 180
 gacttctgga ggaagcaagg caggtgcagc 210

<210> 866
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 <213> *Diabrotica virgifera*

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 <400> 866
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 ggaagcaagg caggtgcagc 140

<210> 867
 <211> 70
 <212> DNA
 <213> *Diabrotica virgifera*

55
 <400> 867

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tgcaacaggg 70

5 <210> 868
<211> 70
<212> DNA
<213> Diabrotica virgifera

10 <400> 868

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ccaatcaaac 70

15 <210> 869
<211> 70
<212> DNA
<213> Diabrotica virgifera

20 <400> 869

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ggtgtcaagg 70

25 <210> 870
<211> 70
<212> DNA
<213> Diabrotica virgifera

30 <400> 870

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ctgtttgaag 70

35 <210> 871
<211> 70
<212> DNA
<213> Diabrotica virgifera

<400> 871

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ctcccttacc 70

45 <210> 872
<211> 70
<212> DNA
<213> Diabrotica virgifera

<400> 872

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gcggtcgtcc 70

<210> 873

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<211> 70
<212> DNA
<213> *Diabrotica virgifera*

5 <400> 873

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cagggtgcagc 70
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10

<210> 874
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<213> Diabrotica balteata

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EP 2 431 473 B1

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<211> 2714

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<213> *Diabrotica virgifera virgifera*

<400> 879

55

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<210> 880

<211> 669

<212> DNA

50 <213> *Epilachna varivestis*

<400> 880

55

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5
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<210> 881

15 <211> 1033

<212> DNA

<213> Leptinotarsa decemlineata

<400> 881

20
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30
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<210> 882

40 <211> 601

<212> DNA

<213> Diabrotica balteata

<400> 882

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50
55
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ataaaagagt tgcactccaa gctctcaaaa agaagaaacg attggaaaag acccaactac 180
aaatagatgg aacccttaca actattgaaa tgcagaggga agccctcgaa ggagctagca 240
caaatactgc tgtattagat tctatgaaaa atgctgcaga tgcccttaag aaagctcata 300
agaacttgaa tgtggatgat gttcacgaca tcatggatga catagccgaa caacacgaca 360
tagccaacga aatcacaac gctattagca accctgttgg attcaccgac gatctggacg 420

acgatgaatt agagaaagaa ttagaagagc tcgaacaaga aggattggaa gaagacctgc 480
ttcaagtgcc aggtcccact caactgcgg ctgtgcctac tgatgcagtt gctaataaac 540
caatcaaacc agcagctaga aaagttgaag atgatgacga tatgaaagaa ttggaagcct 600
g 601

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<210> 883
<211> 601
<212> DNA
<213> *Diabrotica barberi*

5
<400> 883

```

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atTTTTtaga aaagaagata gaagaattta ccatggtagc aaagaaaaat gcgtcgaaaa 120
ataaaagagt tgcactccaa gccctcaaaa agaagaaacg attggaaaag actcaactac 180
aaatagatgg aacccttaca actattgaaa tgcagaggga agccctcgaa ggagctagca 240
caaatactgc tgtattagat tctatgaaaa atgctgcaga tgcctttaag aaagctcata 300
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15 acgatgaatt agaaaaagaa ttagaagagc tcgaacaaga aggattggaa gaagacctgc 480
tccaagtgcc aggtccaact caactgccgg ctgtgcctgc tgatgcagtt actactaaac 540
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g 601

```

20
<210> 884
<211> 601
<212> DNA
<213> *Diabrotica undecimpunctata howardii*

25
<400> 884

```

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atTTTTtaga aaagaagata gaagaattta ccttagtagc aaagaaaaat gcgtcgaaaa 120
ataaaagagt tgcactccaa gccctcaaaa agaagaaacg attggaaaag acccaactac 180
aaatagatgg aacccttaca actattgaaa tgcagaggga agccctcgaa ggagctagca 240
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35 ttcaagtgcc aggtccaact caactgccgg ctgtgcctac tgatgcagtt gctaataaac 540
caattaaacc agcagctaga aaagttgaag atgatgacga tatgaaagaa ttggaagcct 600
g 601

```

40
<210> 885
<211> 601
<212> DNA
<213> *Diabrotica virgifera zeae*

45
<400> 885

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ataaaagagt tgcactccaa gccctcaaaa agaagaaacg attggaaaag acccaactac 180
aaatagatgg aacccttaca actattgaaa tgcagaggga agccctcgaa ggagctagca 240
caaatactgc tgtattagat tctatgaaaa atgctgcaga tgcctttaag aaagctcata 300
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tccaagtgcc aggtccaact caactgccgg ctgtgcctgc tgatgcagtt gctactaaac 540
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g 601

```

<210> 886

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<211> 601
 <212> DNA
 <213> *Diabrotica virgifera virgifera*

5 <400> 886

```

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      attttttaga aaagaagata gaagaattta ccatggtagc aaagaaaaat gcgtcgaaaa 120
10  ataaaagagt tgcactccaa gccctcaaaa agaagaaacg attggaaaag acccaactac 180
      aatagatgg aacccttaca actattgaaa tgcagaggga agccctcgaa ggagctagca 240
      caaatactgc tgtattagat tctatgaaaa atgctgcaga tgcccttaag aaagctcata 300
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      tagccaacga aatcacaaac gctattagca atcctgtcgg attcaccgac gatctggatg 420
      acgatgaatt agaaaaagaa ttagaagagc tcgaacaaga aggattggaa gaagacctgc 480
15  tccaagtgcc aggtccaact caactgccgg ctgtgcctgc tgatgcagtt gctactaaac 540
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      g
  
```

20 <210> 887
 <211> 145
 <212> DNA
 <213> Artificial Sequence

25 <220>
 <223> Description of Artificial Sequence: C12 concatemer of highly effective WCR targets, ~50% GC criterion, consisting of segments in order 5'-3' from Dv23-Dv13

<400> 887

```

30  cctcaagctg tcattggcat ggatattctg tgccaagcta aatccggtat gggaaaaaacg 60
      gctgtttttg caaaggatcc aggatgacgt tccctattga taactgtacc tacacgaccc 120
      aaatttcttc ctccagtgat catcac
  
```

35 <210> 888
 <211> 222
 <212> DNA
 <213> Artificial Sequence

40 <220>
 <223> Description of Artificial Sequence: C12 concatemer of highly effective WCR targets, ~50% GC criterion, consisting of segments in order 5'-3' from 23-Dv13-Dv26

45 <400> 888

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      cctcaagctg tcattggcat ggatattctg tgccaagcta aatccggtat gggaaaaaacg 60
      gctgtttttg caaaggatcc aggatgacgt tccctattga taactgtacc tacacgaccc 120
      aaatttcttc ctccagtgat cataccata cgatttacct gaggaatgc cggataatct 180
      gaagcaacat ataaggggta tcaacaatac tagagagttg ag
  
```

50 <210> 889
 <211> 275
 <212> DNA
 <213> Artificial Sequence

55 <220>
 <223> Description of Artificial Sequence: C12 concatemer of highly effective WCR targets, ~50% GC criterion, consisting of segments in order 5'-3' from Dv23-Dv13-Dv26-Dv18

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<400> 889

cctcaagctg tcattggcat ggatattctg tgccaagcta aatccggtat gggaaaaacg 60

5
gctgtttttg caaaggatcc aggatgacgt tccctattga taactgtacc tacacgaccc 120
aaattttcttc ctccagtgat catacccata cgatttacct gaggaaatgc cggataatct 180
gaagcaacat ataaggggta tcaacaatac tagagagttg agtcaaacat aattatggca 240
cattgtcctt ggatgtagta tccatcacgc agacc 275

<210> 890

<211> 338

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: C12 concatemer of highly effective WCR targets, ~50% GC criterion, consisting of segments in order 5'-3' from Dv23-Dv13-Dv26-Dv18-Dv49

<400> 890

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gctgtttttg caaaggatcc aggatgacgt tccctattga taactgtacc tacacgaccc 120
aaattttcttc ctccagtgat catacccata cgatttacct gaggaaatgc cggataatct 180
gaagcaacat ataaggggta tcaacaatac tagagagttg agtcaaacat aattatggca 240
cattgtcctt ggatgtagta tccatcacgc agaccgccga acaacacgac atagccaacg 300
aatcacaaa cgctattagc aatcctgtcg gattcacc 338

<210> 891

<211> 418

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: C12 concatemer of highly effective WCR targets, ~50% GC criterion, consisting of segments in order 5'-3' from Dv23-Dv13-Dv26-Dv18-Dv49-Dv22

<400> 891

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gctgtttttg caaaggatcc aggatgacgt tccctattga taactgtacc tacacgaccc 120
aaattttcttc ctccagtgat catacccata cgatttacct gaggaaatgc cggataatct 180
gaagcaacat ataaggggta tcaacaatac tagagagttg agtcaaacat aattatggca 240
cattgtcctt ggatgtagta tccatcacgc agaccgccga acaacacgac atagccaacg 300
aatcacaaa cgctattagc aatcctgtcg gattcaccgt aatgcactcc tacgtcgttt 360
ggttcgtatt ggagtactag acgagaacag aatgaagctc gattacgtat tgggtctc 418

<210> 892

<211> 152

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: C12 concatemer of highly effective WCR targets, ~50% GC criterion, consisting of segments in order 5'-3' from Dv13-Dv26

<400> 892

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```

    caaaggatcc aggatgacgt tccctattga taactgtacc tacacgaccc aaattttcttc 60
    ctccagtgat cataccata cgatttacct gaggaatgc cggataatct gaagcaacat 120
    ataaggggta tcaacaatac tagagagttg ag                                     152

```

5

<210> 893
 <211> 205
 <212> DNA
 <213> Artificial Sequence

10

<220>
 <223> Description of Artificial Sequence: C12 concatemer of highly effective WCR targets, ~50% GC criterion, consisting of segments in order 5'-3' from Dv13-Dv26-Dv18

15

<400> 893

```

    caaaggatcc aggatgacgt tccctattga taactgtacc tacacgaccc aaattttcttc 60
    ctccagtgat cataccata cgatttacct gaggaatgc cggataatct gaagcaacat 120
    ataaggggta tcaacaatac tagagagttg agtcaaacaat aattatggca cattgtcctt 180
    ggatgtagta tccatcacgc agaccgccga acaacacgac atagccaacg aaatcacaaa 205

```

20

<210> 894
 <211> 268
 <212> DNA
 <213> Artificial Sequence

25

<220>
 <223> Description of Artificial Sequence: C12 concatemer of highly effective WCR targets, ~50% GC criterion, consisting of segments in order 5'-3' from Dv13-Dv26-Dv18-Dv49

30

<400> 894

```

    caaaggatcc aggatgacgt tccctattga taactgtacc tacacgaccc aaattttcttc 60
    ctccagtgat cataccata cgatttacct gaggaatgc cggataatct gaagcaacat 120
    ataaggggta tcaacaatac tagagagttg agtcaaacaat aattatggca cattgtcctt 180
    ggatgtagta tccatcacgc agaccgccga acaacacgac atagccaacg aaatcacaaa 240
    cgctattagc aatcctgtcg gattcacc                                     268

```

35

<210> 895
 <211> 348
 <212> DNA
 <213> Artificial Sequence

40

<220>
 <223> Description of Artificial Sequence: C12 concatemer of highly effective WCR targets, ~50% GC criterion, consisting of segments in order 5'-3' from Dv13-Dv26-Dv18-Dv49-Dv22

45

<400> 895

50

```

    caaaggatcc aggatgacgt tccctattga taactgtacc tacacgaccc aaattttcttc 60
    ctccagtgat cataccata cgatttacct gaggaatgc cggataatct gaagcaacat 120
    ataaggggta tcaacaatac tagagagttg agtcaaacaat aattatggca cattgtcctt 180
    ggatgtagta tccatcacgc agaccgccga acaacacgac atagccaacg aaatcacaaa 240
    cgctattagc aatcctgtcg gattcaccgt aatgcaactcc tacgtcgttt ggttcgtatt 300
    ggagtactag acgagaacag aatgaagctc gattacgtat tgggtctc                                     348

```

55

<210> 896

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<211> 408
 <212> DNA
 <213> Artificial Sequence

5 <220>
 <223> Description of Artificial Sequence: C12 concatemer of highly effective WCR targets, ~50% GC criterion, consisting of segments in order 5'-3' from Dv13-Dv26-Dv18-Dv49-Dv22-Dv20

10 <400> 896

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 caaaggatcc aggatgacgt tccctattga taactgtacc tacacgaccc aaatttcttc 60
 ctccagtgat cataccata cgatttacct gaggaatgc cggataatct gaagcaacat 120
 ataaggggta tcaacaatac tagagagttg agtcaaacaat aattatggca cattgtcctt 180
 ggatgtagta tccatcacgc agaccgccga acaacacgac atagccaacg aaatcacaaa 240
 cgctatttagc aatcctgtcg gattcacctt aatgcactcc tacgtcgttt ggttcgtatt 300
 ggagtactag acgagaacag aatgaagctc gattacgtat tgggtctccg aagtaatgta 360
 caacggccac actggacgta agataaatgc tcagattttc ttaggacc 408

20 <210> 897
 <211> 130
 <212> DNA
 <213> Artificial Sequence

25 <220>
 <223> Description of Artificial Sequence: C12 concatemer of highly effective WCR targets, ~50% GC criterion, consisting of segments in order 5'-3' from Dv26-Dv18

30 <400> 897

ccatacgatt tacctgagga aatgccggat aatctgaagc aacatataag gggatatcaac 60
 aatactagag agttgagtca aacataatta tggcacattg tccttggatg tagtatccat 120
 cacgcagacc 130

35 <210> 898
 <211> 193
 <212> DNA
 <213> Artificial Sequence

40 <220>
 <223> Description of Artificial Sequence: C12 concatemer of highly effective WCR targets, ~50% GC criterion, consisting of segments in order 5'-3' from Dv26-Dv18-Dv49

45 <400> 898

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 aatactagag agttgagtca aacataatta tggcacattg tccttggatg tagtatccat 120
 cacgcagacc gccgaacaac acgacatagc caacgaaatc acaaacgcta ttagcaatcc 180
 tgtcggattc acc 193

50 <210> 899
 <211> 273
 <212> DNA
 <213> Artificial Sequence

55 <220>
 <223> Description of Artificial Sequence: C12 concatemer of highly effective WCR targets, ~50% GC criterion, consisting of segments in order 5'-3' from Dv26-Dv18-Dv49-Dv22

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<400> 899

```

5      ccatacgatt tacctgagga aatgccggat aatctgaagc aacatataag gggatatcaac 60
      aatactagag agttgagtca aacataatta tggcacattg tccttggatg tagtatccat 120
      cacgcagacc gccgaacaac acgacatagc caacgaaatc acaaacgcta ttagcaatcc 180
      tgtcggattc accgtaatgc actcctacgt cgtttgggtc gtattggagt actagacgag 240
      aacagaatga agctcgatta cgtattgggt ctc                                     273

```

<210> 900

10 <211> 333

<212> DNA

<213> Artificial Sequence

<220>

15 <223> Description of Artificial Sequence: C12 concatemer of highly effective WCR targets, ~50% GC criterion, consisting of segments in order 5'-3' from Dv26-Dv18-Dv49-Dv22-Dv20

<400> 900

```

20      ccatacgatt tacctgagga aatgccggat aatctgaagc aacatataag gggatatcaac 60
      aatactagag agttgagtca aacataatta tggcacattg tccttggatg tagtatccat 120
      cacgcagacc gccgaacaac acgacatagc caacgaaatc acaaacgcta ttagcaatcc 180
      tgtcggattc accgtaatgc actcctacgt cgtttgggtc gtattggagt actagacgag 240
      aacagaatga agctcgatta cgtattgggt ctccgaagta atgtacaacg gccacactgg 300
25      acgtaagata aatgctcaga ttttcttagg acc                                     333

```

<210> 901

<211> 116

<212> DNA

30 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: C12 concatemer of highly effective WCR targets, ~50% GC criterion, consisting of segments in order 5'-3' from Dv18-Dv49

35

<400> 901

```

40      tcaaacataa ttatggcaca ttgtccttgg atgtagtata catcacgcag accgccgaac 60
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```

<210> 902

<211> 196

<212> DNA

45 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: C12 concatemer of highly effective WCR targets, ~50% GC criterion, consisting of segments in order 5'-3' from Dv18-Dv49-Dv22

50

<400> 902

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55      tcaaacataa ttatggcaca ttgtccttgg atgtagtata catcacgcag accgccgaac 60
      aacacgacat agccaacgaa atcacaaacg ctattagcaa tcctgtcgga ttcaccgtaa 120
      tgcactccta cgtcgtttgg ttcgtattgg agtactagac gagaacagaa tgaagctcga 180
      ttacgtattg ggtctc                                     196

```

<210> 903

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<211> 256
 <212> DNA
 <213> Artificial Sequence

5 <220>
 <223> Description of Artificial Sequence: C12 concatemer of highly effective WCR targets, ~50% GC criterion, consisting of segments in order 5'-3' from Dv18-Dv49-Dv22-Dv20

10 <400> 903

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tcaaacataa ttatggcaca ttgtccttgg atgtagtata catcacgcag accgccgaac 60
aacacgacat agccaacgaa atcacaaacg ctattagcaa tcctgtcgga ttcaccgtaa 120
tgcactccta cgtcgttttg ttctgtattgg agtactagac gagaacagaa tgaagctcga 180
ttacgtattg ggtctccgaa gtaatgtaca acggccacac tggacgtaag ataaatgctc 240
agattttctt aggacc 256
```

15 <210> 904
 <211> 143
 <212> DNA
 20 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: C12 concatemer of highly effective WCR targets, ~50% GC criterion, consisting of segments in order 5'-3' from Dv49-Dv22

25 <400> 904

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gccgaacaac acgacatagc caacgaaatc acaaacgcta ttagcaatcc tgctcgattc 60
accgtaatgc actcctacgt cgtttgggtc gtattggagt actagacgag aacagaatga 120
agctcgatta cgtattgggt ctc 143
```

30 <210> 905
 <211> 203
 <212> DNA
 35 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: C12 concatemer of highly effective WCR targets, ~50% GC criterion, consisting of segments in order 5'-3' from Dv49-Dv22-Dv20

40 <400> 905

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accgtaatgc actcctacgt cgtttgggtc gtattggagt actagacgag aacagaatga 120
agctcgatta cgtattgggt ctccgaagta atgtacaacg gccacactgg acgtaagata 180
aatgctcaga ttttcttagg acc 203
```

45 <210> 906
 <211> 140
 <212> DNA
 50 <213> Artificial Sequence

55 <220>
 <223> Description of Artificial Sequence: C12 concatemer of highly effective WCR targets, ~50% GC criterion, consisting of segments in order 5'-3' from Dv22-Dv20

Claims

(a) a polynucleotide comprising the nucleic acid sequence of SEQ ID NO:704;
(b) a polynucleotide that hybridizes to the nucleic acid sequence of SEQ ID NO:704 under wash conditions of 5X SSC, 50% formamide and 42°C for 10 minutes;
(c) a polynucleotide having at least 70% sequence identity to the nucleic acid sequence of SEQ ID NO:704;
(d) a fragment of at least 21 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:704; and
(e) a complement of the sequence of (a), (b), (c) or (d), wherein said polynucleotide is operably linked to a heterologous promoter; and

growth of the pest.

9. A commodity product produced from a plant according to claim 7, wherein said commodity product comprises a detectable amount of a ribonucleotide expressed from the polynucleotide of claim 1.

10. A method for controlling coleopteran pest infestation comprising providing in the diet of a coleopteran pest an agent comprising a first polynucleotide sequence that functions upon ingestion by the pest to inhibit a biological function within said pest, wherein said polynucleotide sequence exhibits from about 95 to about 100% nucleotide sequence identity along at least from about 19 to about 25 contiguous nucleotides to a coding sequence derived from said pest and is hybridized to a second polynucleotide sequence that is complementary to said first polynucleotide sequence, and wherein said coding sequence derived from said pest is SEQ ID NO:70 or the complement thereof.

11. The method of claim 10, wherein said coleopteran pest is a *Diabrotica* spp., which preferably is selected from *Diabrotica virgifera*, *Diabrotica virgifera virgifera*, *Diabrotica virgifera zea*, *Diabrotica balteata*, *Diabrotica barberi*, *Diabrotica viridula*, *Diabrotica speciosa*, and *Diabrotica undecimpunctata*.

12. A method for controlling a coleopteran pest infestation comprising providing in the diet of a coleopteran pest a plant cell expressing a polynucleotide sequence according to claim 1, wherein the polynucleotide is expressed to produce a double stranded ribonucleic acid that functions upon ingestion by the pest to inhibit the expression of a target sequence within said pest and results in decreased feeding on said diet relative to a diet lacking the plant cell.

13. The method of claim 12, wherein

(i) the pest exhibits reduced growth following ingestion of the cell; or

(ii) the plant cell further comprises a polynucleotide sequence encoding a pesticidal agent selected from a patatin, a *Bacillus thuringiensis* insecticidal protein, a *Xenorhabdus* insecticidal protein, a *Photorhabdus* insecticidal protein, a *Bacillus laterosporus* insecticidal protein, and a *Bacillus sphaericus* insecticidal protein, preferably said *Bacillus thuringiensis* insecticidal protein is selected from a Cry1, a Cry3, a TIC851, a CryET70, a Cry22, a TIC901, a TIC201, a TIC407, a TIC417, a binary insecticidal protein CryET33 and CryET34, a binary insecticidal protein CryET80 and CryET76, a binary insecticidal protein TIC100 and TIC101, a combination of the insecticidal proteins ET29 or ET37 with insecticidal proteins TIC810 or TIC812, and a binary insecticidal protein PS149B1; or

(iii) the target sequence encodes a protein, the predicted function of which is selected from muscle formation, juvenile hormone formation, juvenile hormone regulation, ion regulation and transport, digestive enzyme synthesis, maintenance of cell membrane potential, amino acid biosynthesis, amino acid degradation, sperm formation, pheromone synthesis, pheromone sensing, antennae formation, wing formation, leg formation, development and differentiation, egg formation, larval maturation, digestive enzyme formation, haemolymph synthesis, haemolymph maintenance, neurotransmission, cell division, energy metabolism, respiration, and apoptosis; or

(iv) said coleopteran pest is a *Diabrotica* spp., which preferably is selected from *Diabrotica virgifera*, *Diabrotica virgifera virgifera*, *Diabrotica virgifera zea*, *Diabrotica balteata*, *Diabrotica barberi*, *Diabrotica viridula*, *Diabrotica speciosa*, and *Diabrotica undecimpunctata*; or

(v) the polynucleotide functions upon ingestion by the pest to suppress a gene that performs a function essential for insect survival, said function being selected from feeding by the pest, pest cell apoptosis, cell differentiation and development, capacity or desire for sexual reproduction, muscle formation, muscle twitching, muscle contraction, juvenile hormone formation, juvenile hormone regulation, ion regulation and transport, maintenance of cell membrane potential, amino acid biosynthesis, amino acid degradation, sperm formation, pheromone synthesis, pheromone sensing, antennae formation, wing formation, leg formation, egg formation, larval maturation, digestive enzyme formation, haemolymph synthesis, haemolymph maintenance, neurotransmission, larval stage transition, pupation, emergence from pupation, cell division, energy metabolism, respiration, and formation of cytoskeletal structure.

14. A method for improving the yield of a crop produced from a crop plant subjected to insect pest infestation, said method comprising the steps of,

a) introducing a polynucleotide according to claim 1 into said crop plant,

b) cultivating the crop plant to allow the expression of said polynucleotide, wherein expression of the polynucleotide inhibits feeding by insects pests and loss of yield due to pest infestation.

15. The method of claim 14, wherein

(i) expression of the polynucleotide produces an RNA molecule that suppresses at least a first target gene in an insect pest that has ingested a portion of said crop plant, wherein the target gene performs at least one essential function selected from feeding by the pest, viability of the pest, pest cell apoptosis, differentiation and development of the pest or any pest cell, sexual reproduction by the pest, muscle formation, muscle twitching, muscle contraction, juvenile hormone formation and/or reduction, juvenile hormone regulation, ion regulation and transport, maintenance of cell membrane potential, amino acid biosynthesis, amino acid degradation, sperm formation, pheromone synthesis, pheromone sensing, antennae formation, wing formation, leg formation, egg formation, larval maturation, digestive enzyme formation, haemolymph synthesis, haemolymph maintenance, neurotransmission, larval stage transition, pupation, emergence from pupation, cell division, energy metabolism, respiration, cytoskeletal structure synthesis and maintenance, nucleotide metabolism, nitrogen metabolism, water use, water retention, and sensory perception; or

(ii) the insect pest is a corn rootworm pest selected from *Diabrotica undecimpunctata howardi* (Southern Corn Rootworm (SCR)), *Diabrotica virgifera virgifera* (Western Corn Rootworm (WCR)), *Diabrotica barberi* (Northern Corn Rootworm (NCR)), *Diabrotica virgifera zea* (Mexican Corn Rootworm (MCR)), *Diabrotica balteata* (Brazilian Corn Rootworm (BZR)), *Diabrotica viridula* (Brazilian Corn Rootworm (BZR)), and *Diabrotica speciosa* (Brazilian Corn Rootworm (BZR)).

16. A method for improving the drought tolerance of a crop produced from a crop plant subjected to insect pest infestation, said method comprising the steps of

- a) introducing a polynucleotide according to claim 1 into said crop plant,
- b) cultivating the crop plant to allow the expression of said polynucleotide, wherein expression of the polynucleotide inhibits feeding by insects pests and loss of drought tolerance due to pest infestation.

17. A method of producing a commodity product, food or feed comprising obtaining a plant according to claim 7 or a part thereof, and preparing a commodity product, food or feed from the plant or part thereof.

18. The method of claim 17, wherein the food or feed is defined as oil, meal, protein, starch, flour or silage.

Patentansprüche

1. Polynucleotid, ausgewählt aus:

- (a) einem Polynucleotid, das eine Nucleinsäuresequenz der SEQ ID Nr. 704 umfasst;
- (b) einem Polynucleotid, das unter den Waschbedingungen 5x SSC, 50% Formamid und 42 °C während 10 Minuten mit einer Nucleinsäuresequenz der SEQ ID Nr. 704 hybridisiert;
- (c) einem Polynucleotid mit wenigstens 70% Sequenzidentität mit der Nucleinsäuresequenz der SEQ ID Nr. 704;
- (d) einem Fragment aus wenigstens 21 aufeinanderfolgenden Nucleotiden der Nucleinsäuresequenz der SEQ ID Nr. 704; und
- (e) einem Komplement der Sequenz von (a), (b), (c) oder (d);

wobei das Polynucleotid funktionell mit einem heterologen Promotor verknüpft ist; und wobei das Wachstum eines Coleoptera-Pflanzenschädling dadurch gehemmt wird, dass der Schädling eine doppelsträngige Ribonucleotidsequenz, die wenigstens einen Strang umfasst, der zu dem Polynucleotid oder dem Fragment komplementär ist, aufnimmt.

2. Polynucleotid gemäß Anspruch 1, das als Bestandteil eines Pflanzentransformationsvektors definiert ist.

3. Doppelsträngige Ribonucleotidsequenz, die durch Expression eines Polynucleotids gemäß Anspruch 1 hergestellt ist, wobei das Wachstum eines Coleoptera-Pflanzenschädling dadurch gehemmt wird, dass der Schädling die Ribonucleotidsequenz aufnimmt.

4. Doppelsträngige Ribonucleotidsequenz gemäß Anspruch 3,

- (i) definiert als erzeugt durch Herstellen einer rekombinanten Polynucleotidsequenz, die eine erste, zweite und

5 dritte Polynucleotidsequenz umfasst, wobei die erste Polynucleotidsequenz das isolierte Polynucleotid von Anspruch 1 umfasst, wobei die dritte Polynucleotidsequenz durch die zweite Polynucleotidsequenz mit der ersten Polynucleotidsequenz verknüpft ist und wobei die dritte Polynucleotidsequenz im Wesentlichen das reverse Komplement der ersten Polynucleotidsequenz ist, so dass die erste und die dritte Polynucleotidsequenz miteinander hybridisieren, wenn sie unter Bildung des doppelsträngigen Ribonucleotidmoleküls, das durch die verknüpfte zweite Ribonucleotidsequenz stabilisiert ist, zu einer Ribonucleinsäure transkribiert werden; oder
 (ii) wobei die Expression einer Nucleotidsequenz, die zu der Polynucleotidsequenz im Wesentlichen komplementär ist, dadurch gehemmt wird, dass der Schädling die Polynucleotidsequenz aufnimmt.

10 5. Zelle, die mit dem Polynucleotid gemäß Anspruch 1 transformiert ist.

6. Zelle gemäß Anspruch 5, definiert als

- 15 (i) eine prokaryontische Zelle; oder
 (ii) eine eukaryontische Zelle; oder
 (iii) eine Pflanzen- oder Bakterienzelle.

7. Pflanze, transformiert mit dem Polynucleotid gemäß Anspruch 1 oder 2, oder ein Samen davon, der das Polynucleotid umfasst.

20 8. Pflanze gemäß Anspruch 7, wobei das Polynucleotid in einer Zelle der Pflanze als doppelsträngige Ribonucleotidsequenz exprimiert wird und die Aufnahme einer das Schadinsekt hemmenden Menge der doppelsträngigen Ribonucleotidsequenz durch die Nahrung die weitere Aufnahme der Nahrung durch den Schädling hemmt, wobei vorzugsweise

25 (i) das Schadinsekt aus *Diabrotica virgifera*, *Diabrotica virgifera virgifera*, *Diabrotica virgifera zea*, *Diabrotica balteata*, *Diabrotica barberi*, *Diabrotica viridula*, *Diabrotica speciosa* und *Diabrotica undecimpunctata* ausgewählt ist; oder

30 (ii) die Aufnahme einer das Schadinsekt hemmenden Menge der doppelsträngigen Ribonucleotidsequenz das Wachstum des Schädlings hemmt.

9. Grunderzeugnis, hergestellt aus einer Pflanze gemäß Anspruch 7, wobei das Grunderzeugnis eine nachweisbare Menge eines Ribonucleotids umfasst, das ausgehend von dem Polynucleotid gemäß Anspruch 1 exprimiert wird.

35 10. Verfahren zur Bekämpfung des Befalls mit einem Coleoptera-Schädling, umfassend das Einbringen eines Mittels, das eine erste Polynucleotidsequenz umfasst, die nach Aufnahme durch den Schädling eine Hemmung einer biologischen Funktion innerhalb des Schädlings bewirkt, in die Nahrung eines Coleoptera-Schädlings, wobei die Polynucleotidsequenz etwa 95 bis etwa 100% Nucleotidsequenzidentität entlang wenigstens etwa 19 bis etwa 25 aufeinanderfolgenden Nucleotiden mit einer von dem Schädling stammenden codierenden Sequenz aufweist und mit einer zweiten Polynucleotidsequenz, die zu der ersten Polynucleotidsequenz komplementär ist, hybridisiert und wobei es sich bei der von dem Schädling stammenden codierenden Sequenz um SEQ ID Nr. 704 oder deren Komplement handelt.

45 11. Verfahren gemäß Anspruch 10, wobei es sich bei dem Coleoptera-Schädling um eine *Diabrotica*-Spezies handelt, die vorzugsweise aus *Diabrotica virgifera*, *Diabrotica virgifera virgifera*, *Diabrotica virgifera zea*, *Diabrotica balteata*, *Diabrotica barberi*, *Diabrotica viridula*, *Diabrotica speciosa* und *Diabrotica undecimpunctata* ausgewählt ist.

50 12. Verfahren zur Bekämpfung des Befalls mit einem Coleoptera-Schädling, umfassend das Einbringen einer Pflanzenzelle, die eine Polynucleotidsequenz gemäß Anspruch 1 exprimiert, in die Nahrung eines Coleoptera-Schädlings, wobei das Polynucleotid unter Bildung einer doppelsträngigen Ribonucleinsäure exprimiert wird, die nach Aufnahme durch den Schädling eine Hemmung der Expression einer Zielsequenz innerhalb des Schädlings bewirkt und zu einem reduzierten Fressen der Nahrung im Vergleich zu einer Nahrung, die die Pflanzenzelle nicht enthält, führt.

55 13. Verfahren gemäß Anspruch 12, wobei

- (i) der Schädling nach Aufnahme der Zelle ein reduziertes Wachstum zeigt; oder
 (ii) die Pflanzenzelle weiterhin eine Polynucleotidsequenz umfasst, die ein Pestizid codiert, das aus einem Patatin, einem insektiziden *Bacillus-thuringiensis*-Protein, einem insektiziden *Xenorhabdus*-Protein, einem in-

sektiziden *Photorhabdus*-Protein, einem insektiziden *Bacillus-laterosporus*-Protein und einem insektiziden *Bacillus-sphaericus*-Protein ausgewählt ist, wobei das insektizide *Bacillus-thuringiensis*-Protein vorzugsweise aus einem Cry1, Cry3, TIC851, CryET70, Cry22, TIC901, TIC201, TIC407, TIC417, einem binären insektiziden Protein CryET33 und CryET34, einem binären insektiziden Protein CryET80 und CryET76, einem binären insektiziden Protein TIC100 und TIC101, einer Kombination der insektiziden Proteine ET29 oder ET37 mit den insektiziden Proteinen TIC810 oder TIC812 und einem binären insektiziden Protein PS 149B1 ausgewählt ist; oder

(iii) die Zielsequenz ein Protein codiert, dessen vorhergesagte Funktion aus Muskelbildung, Bildung von Juvenilhormon, Regulation von Juvenilhormon, Ionenregulation und -transport, Synthese von Verdauungsenzym, Aufrechterhaltung des Zellmembranpotentials, Aminosäure-Biosynthese, Aminosäureabbau, Spermbildung, Pheromonsynthese, Pheromonwahrnehmung, Antennenbildung, Flügelbildung, Beinbildung, Entwicklung und Differenzierung, Eibildung, Larvenreifeung, Bildung von Verdauungsenzym, Synthese der Hämolymphe, Aufrechterhaltung der Hämolymphe, Nervenleitung, Zellteilung, Energiestoffwechsel, Atmung und Apoptose ausgewählt ist; oder

(iv) es sich bei dem Coleoptera-Schädling um eine *Diabrotica*-Spezies handelt, die vorzugsweise aus *Diabrotica virgifera*, *Diabrotica virgifera virgifera*, *Diabrotica virgifera zea*, *Diabrotica balteata*, *Diabrotica barberi*, *Diabrotica viridula*, *Diabrotica speciosa* und *Diabrotica undecimpunctata* ausgewählt ist; oder

(v) das Polynucleotid nach Aufnahme durch den Schädling eine Unterdrückung eines Gens bewirkt, das eine für das Überleben des Insekts essentielle Funktion ausübt, wobei die Funktion aus der Ernährung des Schädlings, Apoptose von Zellen des Schädlings, Zelldifferenzierung und -entwicklung, Fähigkeit zu oder Verlangen nach geschlechtlicher Vermehrung, Muskelbildung, Muskelzuckung, Muskelkontraktion, Bildung von Juvenilhormon, Regulation von Juvenilhormon, Ionenregulation und -transport, Aufrechterhaltung des Zellmembranpotentials, Aminosäure-Biosynthese, Aminosäureabbau, Spermbildung, Pheromonsynthese, Pheromonwahrnehmung, Antennenbildung, Flügelbildung, Beinbildung, Eibildung, Larvenreifeung, Bildung von Verdauungsenzym, Synthese der Hämolymphe, Aufrechterhaltung der Hämolymphe, Nervenleitung, Übergang in ein Larvenstadium, Verpuppung, Schlüpfen aus der Puppe, Zellteilung, Energiestoffwechsel, Atmung und Bildung der Cytoskelettstruktur ausgewählt ist.

14. Verfahren zur Verbesserung des Ertrags einer Feldfrucht, die von einer Kulturpflanze erzeugt wird, welche einem Befall durch Schadinsekten unterliegt, wobei das Verfahren die Schritte umfasst:

- a) Einführen eines Polynucleotids gemäß Anspruch 1 in die Kulturpflanze;
- b) Kultivieren der Kulturpflanze, um die Expression des Polynucleotids zu ermöglichen, wobei die Expression des Polynucleotids den Befall durch Schadinsekten und den Ertragsverlust aufgrund des Schädlingsbefalls hemmt.

15. Verfahren gemäß Anspruch 14, wobei

(i) bei der Expression des Polynucleotids ein RNA-Molekül entsteht, das wenigstens ein erstes Zielgen in einem Schadinsekt, das einen Teil der Kulturpflanze aufgenommen hat, unterdrückt, wobei das Zielgen wenigstens eine essentielle Funktion ausübt, die aus der Ernährung des Schädlings, Lebensfähigkeit des Schädlings, Apoptose von Zellen des Schädlings, Differenzierung und Entwicklung des Schädlings oder irgendeiner Zelle des Schädlings, der geschlechtlichen Vermehrung des Schädlings, Muskelbildung, Muskelzuckung, Muskelkontraktion, Bildung und/oder Reduktion von Juvenilhormon, Regulation von Juvenilhormon, Ionenregulation und -transport, Aufrechterhaltung des Zellmembranpotentials, Aminosäure-Biosynthese, Aminosäureabbau, Spermbildung, Pheromonsynthese, Pheromonwahrnehmung, Antennenbildung, Flügelbildung, Beinbildung, Eibildung, Larvenreifeung, Bildung von Verdauungsenzym, Synthese der Hämolymphe, Aufrechterhaltung der Hämolymphe, Nervenleitung, Übergang in ein Larvenstadium, Verpuppung, Schlüpfen aus der Puppe, Zellteilung, Energiestoffwechsel, Atmung, Synthese und Aufrechterhaltung der Cytoskelettstruktur, Nucleotidstoffwechsel, Stickstoffmetabolismus, Wasserverwertung, Wasserretention und sensorischer Wahrnehmung ausgewählt ist; oder

(ii) das Schadinsekt ein Maiswurzelbohrer-Schädling ist, der aus *Diabrotica undecimpunctata howardi* (Südlicher Maiswurzelbohrer (SCR)), *Diabrotica virgifera virgifera* (Westlicher Maiswurzelbohrer (WCR)), *Diabrotica barberi* (Nördlicher Maiswurzelbohrer (NCR)), *Diabrotica virgifera zea* (Mexikanischer Maiswurzelbohrer (MCR)), *Diabrotica balteata* (Gestreifter Gurkenblattkäfer (BZR)), *Diabrotica viridula* (Gestreifter Gurkenblattkäfer (BZR)) und *Diabrotica speciosa* (Gestreifter Gurkenblattkäfer (BZR)) ausgewählt ist.

16. Verfahren zur Verbesserung der Trockenheitstoleranz einer Feldfrucht, die von einer Kulturpflanze erzeugt wird,

welche einem Befall durch Schadinsekten unterliegt, wobei das Verfahren die Schritte umfasst:

- a) Einführen eines Polynucleotids gemäß Anspruch 1 in die Kulturpflanze;
- b) Kultivieren der Kulturpflanze, um die Expression des Polynucleotids zu ermöglichen, wobei die Expression des Polynucleotids den Befall durch Schadinsekten und den Verlust der Trockenheitstoleranz aufgrund des Schädlingsbefalls hemmt.

17. Verfahren zur Herstellung eines Grunderzeugnisses, Nahrungs- oder Futtermittels, umfassend das Gewinnen einer Pflanze gemäß Anspruch 7 oder eines Teils davon und das Herstellen eines Grunderzeugnisses, Nahrungs- oder Futtermittels aus der Pflanze oder ihrem Teil.

18. Verfahren gemäß Anspruch 17, wobei das Nahrungs- oder Futtermittel als Öl, Schrot, Protein, Stärke, Mehl oder Silage definiert ist.

Revendications

1. Polynucléotide choisi parmi :

- (a) un polynucléotide comprenant la séquence d'acide nucléique de SEQ ID NO: 704 ;
- (b) un polynucléotide qui s'hybride à la séquence d'acide nucléique de SEQ ID NO: 704 dans des conditions de lavage de SSC 5X, 50 % de formamide et 42 °C pendant 10 minutes ;
- (c) un polynucléotide ayant au moins 70 % d'identité de séquence avec la séquence d'acide nucléique de SEQ ID NO: 704 ;
- (d) un fragment d'au moins 21 nucléotides contigus de la séquence d'acide nucléique de SEQ ID NO: 704 ; et
- (e) un complément de la séquence de (a), (b), (c) ou (d),

dans lequel ledit polynucléotide est lié de manière fonctionnelle à un promoteur hétérologue, et dans lequel l'ingestion par un phytovore coléoptère d'une séquence ribonucléotidique double brin comprenant au moins un brin qui est complémentaire dudit polynucléotide ou dudit fragment inhibe la croissance dudit organisme nuisible.

2. Polynucléotide selon la revendication 1, qui est défini comme étant constitué sur un vecteur de transformation végétale.

3. Séquence ribonucléotidique double brin produite à partir de l'expression d'un polynucléotide selon la revendication 1, dans laquelle l'ingestion de ladite séquence ribonucléotidique par un phytovore coléoptère inhibe la croissance dudit organisme nuisible.

4. Séquence ribonucléotidique double brin selon la revendication 3,

- (i) définie comme étant produite par la préparation d'une séquence polynucléotidique recombinée comprenant une première, une deuxième et une troisième séquence polynucléotidique, dans laquelle la première séquence polynucléotidique comprend le polynucléotide isolé selon la revendication 1, dans laquelle la troisième séquence polynucléotidique est liée à la première séquence polynucléotidique par la deuxième séquence polynucléotidique, et dans laquelle la troisième séquence polynucléotidique est sensiblement le complément inverse de la première séquence polynucléotidique de sorte que les première et troisième séquences polynucléotidiques s'hybrident lorsqu'elles sont transcrites en un acide ribonucléique pour former la molécule ribonucléotidique double brin stabilisée par la deuxième séquence ribonucléotidique liée ; ou
- (ii) dans laquelle l'ingestion de la séquence polynucléotidique par l'organisme nuisible inhibe l'expression d'une séquence nucléotidique sensiblement complémentaire de ladite séquence polynucléotidique.

5. Cellule transformée avec le polynucléotide selon la revendication 1.

6. Cellule selon la revendication 5, définie comme étant

- (i) une cellule procaryote ; ou
- (ii) une cellule eucaryote ; ou

(iii) une cellule végétale ou bactérienne.

7. Plante transformée avec le polynucléotide selon la revendication 1 ou 2, ou une graine de celle-ci comprenant le polynucléotide.

8. Plante selon la revendication 7, dans laquelle ledit polynucléotide est exprimé dans une cellule de la plante comme une séquence ribonucléotidique double brin et l'ingestion d'une quantité inhibitrice pour un insecte nuisible de ladite séquence ribonucléotidique double brin dans une alimentation empêche l'organisme nuisible de se nourrir davantage sur ladite alimentation, de préférence

(i) l'insecte nuisible est choisi parmi *Diabrotica virgifera*, *Diabrotica virgifera virgifera*, *Diabrotica virgifera zea*, *Diabrotica balteata*, *Diabrotica barberi*, *Diabrotica viridula*, *Diabrotica speciosa* et *Diabrotica undecimpunctata* ; ou

(ii) l'ingestion de la quantité inhibitrice pour un insecte nuisible de la séquence ribonucléotidique double brin entrave la croissance de l'organisme nuisible.

9. Produit de base produit à partir d'une plante selon la revendication 7, dans lequel ledit produit de base comprend une quantité détectable d'un ribonucléotide exprimé à partir du polynucléotide selon la revendication 1.

10. Procédé pour lutter contre une infestation par un organisme nuisible coléoptère, comprenant la fourniture dans l'alimentation d'un organisme nuisible coléoptère d'un agent comprenant une première séquence polynucléotidique qui fonctionne lors de l'ingestion par l'organisme nuisible pour inhiber une fonction biologique chez ledit organisme nuisible, dans lequel ladite séquence polynucléotidique présente d'environ 95 à environ 100 % d'identité de séquence nucléotidique le long au moins d'environ 19 à environ 25 nucléotides contigus avec une séquence codante dérivée dudit organisme nuisible et est hybridée à une deuxième séquence polynucléotidique qui est complémentaire de ladite première séquence polynucléotidique, et dans lequel ladite séquence codante dérivée dudit organisme nuisible est SEQ ID NO: 704 ou le complément de celle-ci.

11. Procédé selon la revendication 10, dans lequel ledit organisme nuisible coléoptère est un *Diabrotica spp.*, qui est de préférence choisi parmi *Diabrotica virgifera*, *Diabrotica virgifera virgifera*, *Diabrotica virgifera zea*, *Diabrotica balteata*, *Diabrotica barberi*, *Diabrotica viridula*, *Diabrotica speciosa* et *Diabrotica undecimpunctata*.

12. Procédé pour lutter contre une infestation par un organisme nuisible coléoptère, comprenant la fourniture dans l'alimentation d'un organisme nuisible coléoptère d'une cellule végétale exprimant une séquence polynucléotidique selon la revendication 1, dans lequel le polynucléotide est exprimé pour produire un acide ribonucléique double brin qui fonctionne lors de l'ingestion par l'organisme nuisible pour inhiber l'expression d'une séquence cible chez ledit organisme nuisible et entraîne une diminution du nourrissage sur ladite alimentation par rapport à une alimentation dépourvue de la cellule végétale.

13. Procédé selon la revendication 12, dans lequel

(i) l'organisme nuisible présente une croissance réduite suite à l'ingestion de la cellule ; ou

(ii) la cellule végétale comprend en outre une séquence polynucléotidique codant pour un agent pesticide choisi parmi une patatine, une protéine insecticide de *Bacillus thuringiensis*, une protéine insecticide de *Xenorhabdus*, une protéine insecticide de *Photorhabdus*, une protéine insecticide de *Bacillus laterosporous* et une protéine insecticide de *Bacillus sphaericus*, de préférence ladite protéine insecticide de *Bacillus thuringiensis* est choisie parmi une Cry1, une Cry3, une TIC851, une CryET70, une Cry22, une TIC901, une TIC201, une TIC407, une TIC417, une protéine insecticide binaire CryET33 et CryET34, une protéine insecticide binaire CryET80 et CryET76, une protéine insecticide binaire TIC100 et TIC101, une combinaison de protéines insecticides ET29 ou ET37 avec des protéines insecticides TIC810 ou TIC812 et une protéine insecticide binaire PS149B1 ; ou

(iii) la séquence cible code pour une protéine, dont la fonction prédite est choisie parmi la formation des muscles, la formation de l'hormone juvénile, la régulation de l'hormone juvénile, la régulation et le transport des ions, la synthèse des enzymes digestives, le maintien du potentiel de membrane cellulaire, la biosynthèse des acides aminés, la dégradation des acides aminés, la formation du sperme, la synthèse de phéromones, la détection de phéromones, la formation des antennes, la formation des ailes, la formation des pattes, le développement et la différenciation, la formation des oeufs, la maturation des larves, la formation des enzymes digestives, la synthèse de l'hémolymphe, le maintien de l'hémolymphe, la neurotransmission, la division cellulaire, le métabolisme énergétique, la respiration et l'apoptose ; ou

(iv) ledit organisme nuisible coléoptère est un *Diabrotica spp.*, qui est de préférence choisi parmi *Diabrotica virgifera*, *Diabrotica virgifera virgifera*, *Diabrotica virgifera zea*, *Diabrotica balteata*, *Diabrotica barberi*, *Diabrotica viridula*, *Diabrotica speciosa* et *Diabrotica undecimpunctata* ; ou

(v) le polynucléotide fonctionne lors de l'ingestion par l'organisme nuisible pour supprimer un gène qui remplit une fonction essentielle pour la survie de l'insecte, ladite fonction étant choisie parmi le nourrissage par l'organisme nuisible, l'apoptose des cellules de l'organisme nuisible, la différenciation et le développement cellulaire, la capacité ou le désir de reproduction sexuée, la formation des muscles, les spasmes musculaires, la contraction musculaire, la formation de l'hormone juvénile, la régulation de l'hormone juvénile, la régulation et le transport des ions, le maintien du potentiel de membrane cellulaire, la biosynthèse des acides aminés, la dégradation des acides aminés, la formation du sperme, la synthèse de phéromones, la détection de phéromones, la formation des antennes, la formation des ailes, la formation des pattes, la formation des oeufs, la maturation des larves, la formation des enzymes digestives, la synthèse de l'hémolymph, le maintien de l'hémolymph, la neurotransmission, la transition au stade larvaire, la nymphose, l'émergence de la nymphose, la division cellulaire, le métabolisme énergétique, la respiration et la formation de la structure du cytosquelette.

14. Procédé pour améliorer le rendement d'une culture produite à partir d'une plante cultivée soumise à une infestation par un insecte nuisible, ledit procédé comprenant les étapes de,

- a) introduction d'un polynucléotide selon la revendication 1 dans ladite plante de culture,
- b) culture de la plante de culture pour permettre l'expression dudit polynucléotide, dans laquelle l'expression du polynucléotide inhibe le nourrissage par les insectes nuisibles et la perte de rendement due à l'infestation par les organismes nuisibles.

15. Procédé selon la revendication 14, dans lequel

(i) l'expression du polynucléotide produit une molécule d'ARN qui supprime au moins un premier gène cible chez un insecte nuisible qui a ingéré une partie de ladite plante de culture, dans lequel le gène cible remplit au moins une fonction essentielle choisie parmi le nourrissage par l'organisme nuisible, la viabilité de l'organisme nuisible, l'apoptose des cellules de l'organisme nuisible, la différenciation et le développement de l'organisme nuisible ou d'une cellule de l'organisme nuisible, la reproduction sexuée par le organisme nuisible, la formation des muscles, les spasmes musculaires, la contraction musculaire, la formation et/ou la réduction de l'hormone juvénile, la régulation de l'hormone juvénile, la régulation et le transport des ions, le maintien du potentiel de membrane cellulaire, la biosynthèse des acides aminés, la dégradation des acides aminés, la formation du sperme, la synthèse de phéromones, la détection de phéromones, la formation des antennes, la formation des ailes, la formation des pattes, la formation des oeufs, la maturation des larves, la formation des enzymes digestives, la synthèse de l'hémolymph, le maintien de l'hémolymph, la neurotransmission, la transition au stade larvaire, la nymphose, l'émergence de la nymphose, la division cellulaire, le métabolisme énergétique, la respiration, la synthèse et le maintien de la structure du cytosquelette, le métabolisme des nucléotides, le métabolisme de l'azote, l'utilisation de l'eau, la rétention d'eau et la perception sensorielle ; ou

(ii) l'insecte nuisible est un organisme nuisible de type chrysomèle des racines du maïs choisi parmi *Diabrotica undecimpunctata howardi* (chrysomèle maculée du concombre (SCR)), *Diabrotica virgifera virgifera* (chrysomèle occidentale des racines du maïs (WCR)), *Diabrotica Barberi* (chrysomèle septentrionale des racines du maïs (NCR)), *Diabrotica virgifera zea* (chrysomèle des racines du maïs mexicaine (MCR)), *Diabrotica balteata* (chrysomèle des racines du maïs brésilienne)), *Diabrotica viridula* (chrysomèle des racines du maïs brésilienne (BZR)), et *Diabrotica speciosa* (chrysomèle des racines du maïs brésilienne (BZR)).

16. Procédé pour améliorer la tolérance à la sécheresse d'une culture produite à partir d'une plante de culture soumise à une infestation par un insecte nuisible, ledit procédé comprenant les étapes de

- a) introduction d'un polynucléotide selon la revendication 1 dans ladite plante de culture,
- b) culture de la plante de culture pour permettre l'expression dudit polynucléotide, dans laquelle l'expression du polynucléotide inhibe le nourrissage par les insectes nuisibles et la perte de tolérance à la sécheresse en raison de l'infestation par les organismes nuisibles.

17. Procédé de production d'un produit de base, d'un aliment ou d'un aliment pour animaux comprenant l'obtention d'une plante selon la revendication 7 ou d'une partie de celle-ci, et la préparation d'un produit de base, d'un aliment ou d'un aliment pour animaux à partir de la plante ou de la partie de celle-ci.

- 18.** Procédé selon la revendication 17, dans lequel l'aliment ou l'aliment pour animaux est défini comme étant une huile, un tourteau, une protéine, un amidon, une farine ou un ensilage.

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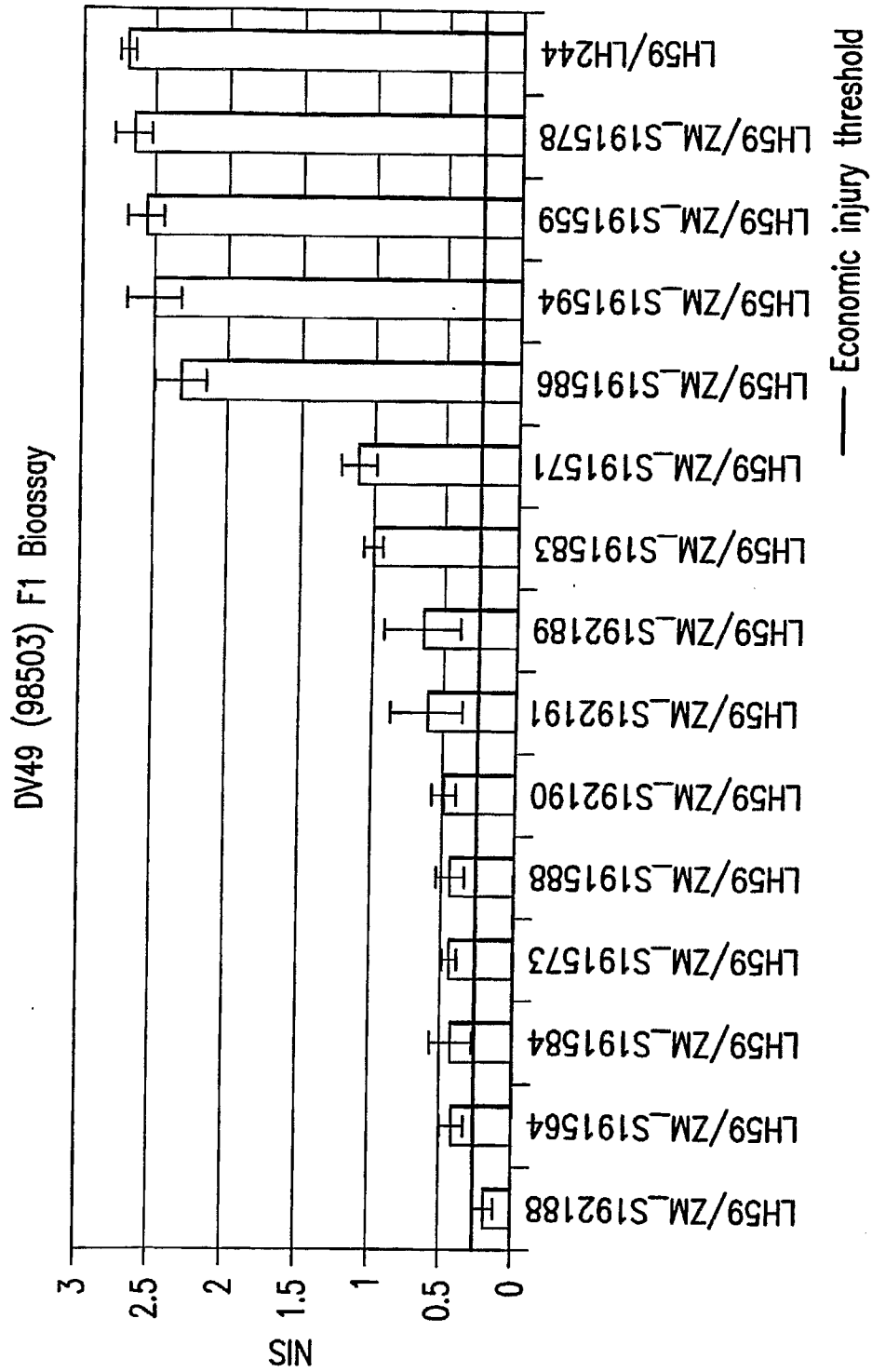


FIG.1

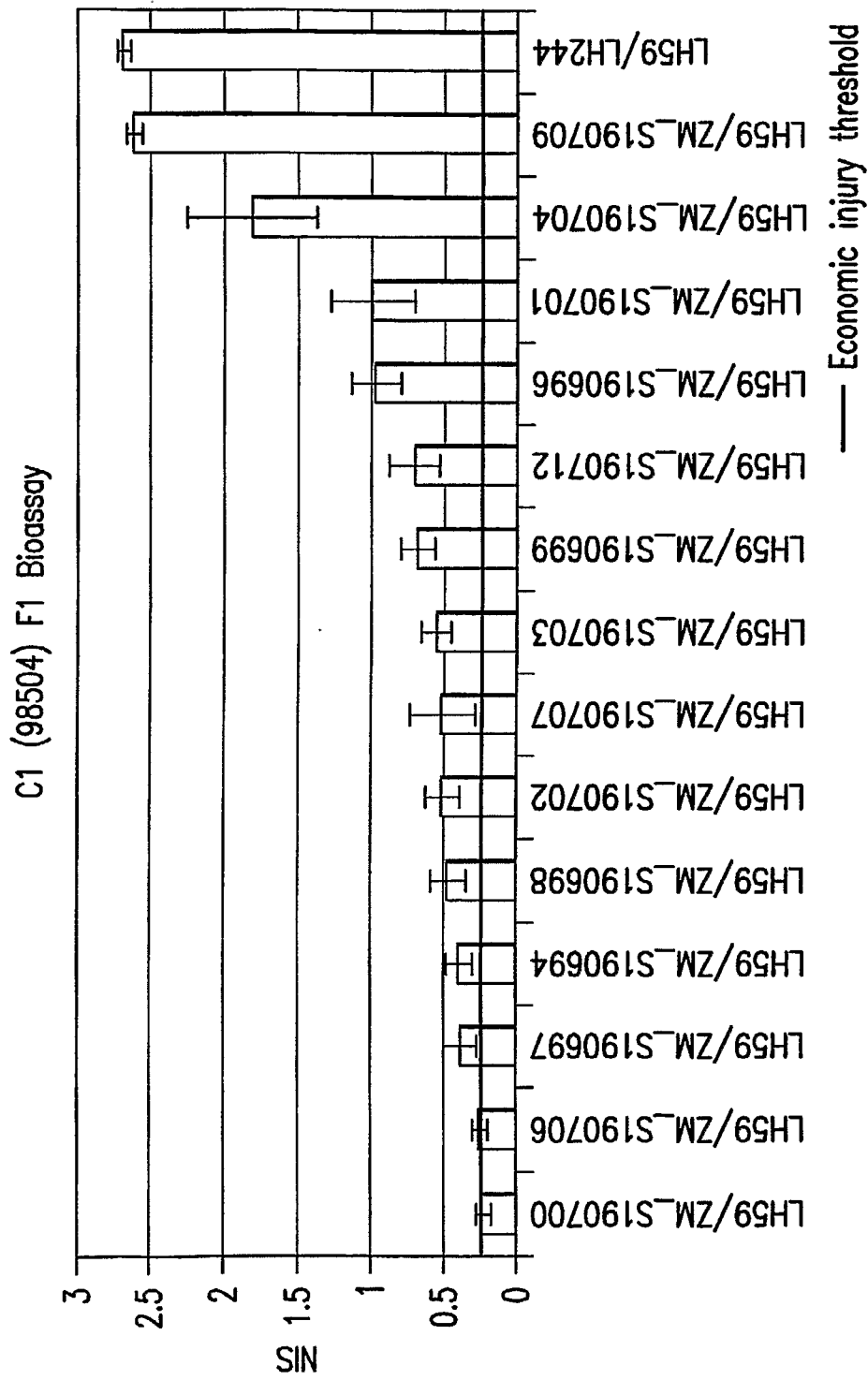


FIG.2

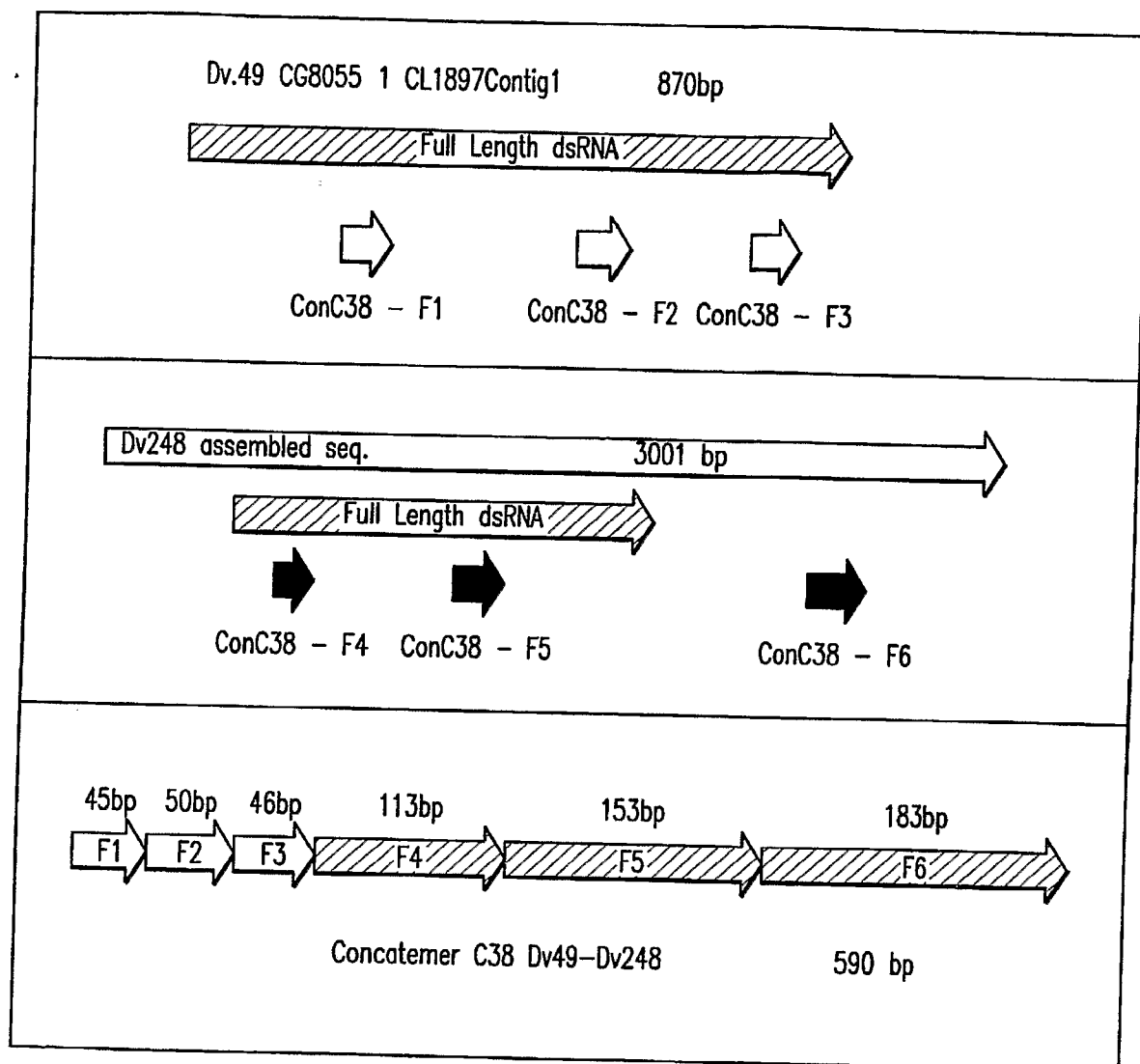


FIG.3

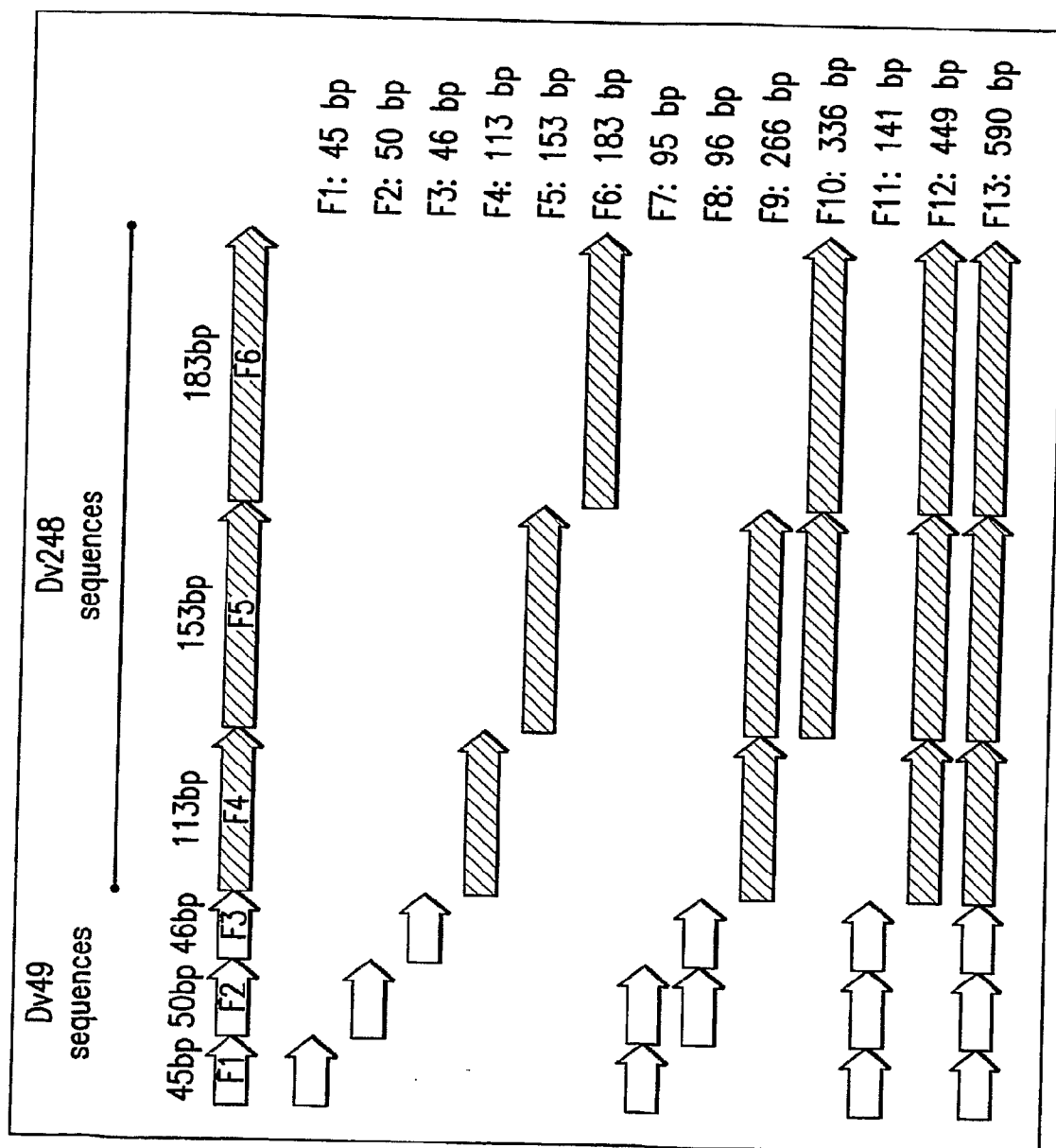


FIG.4

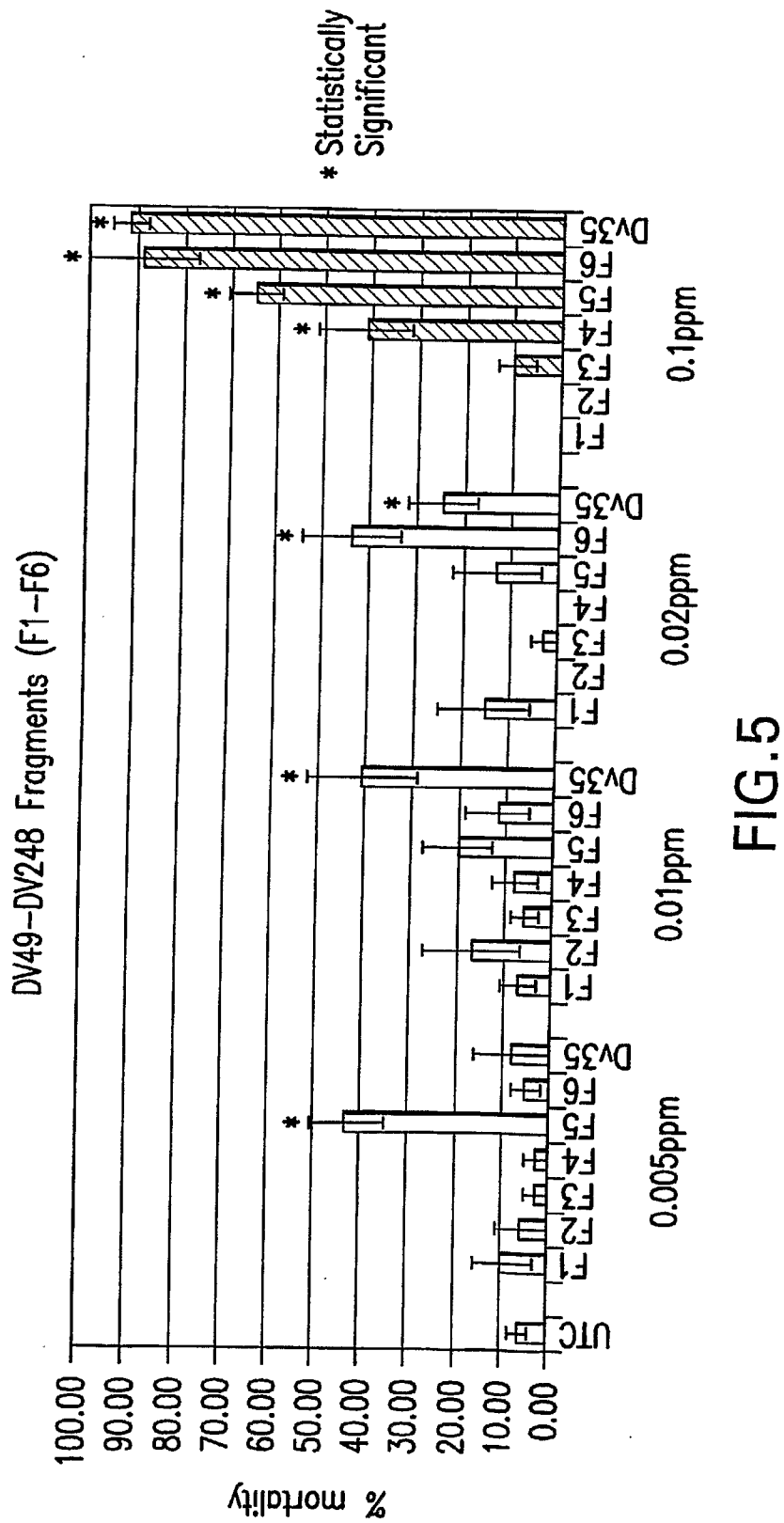
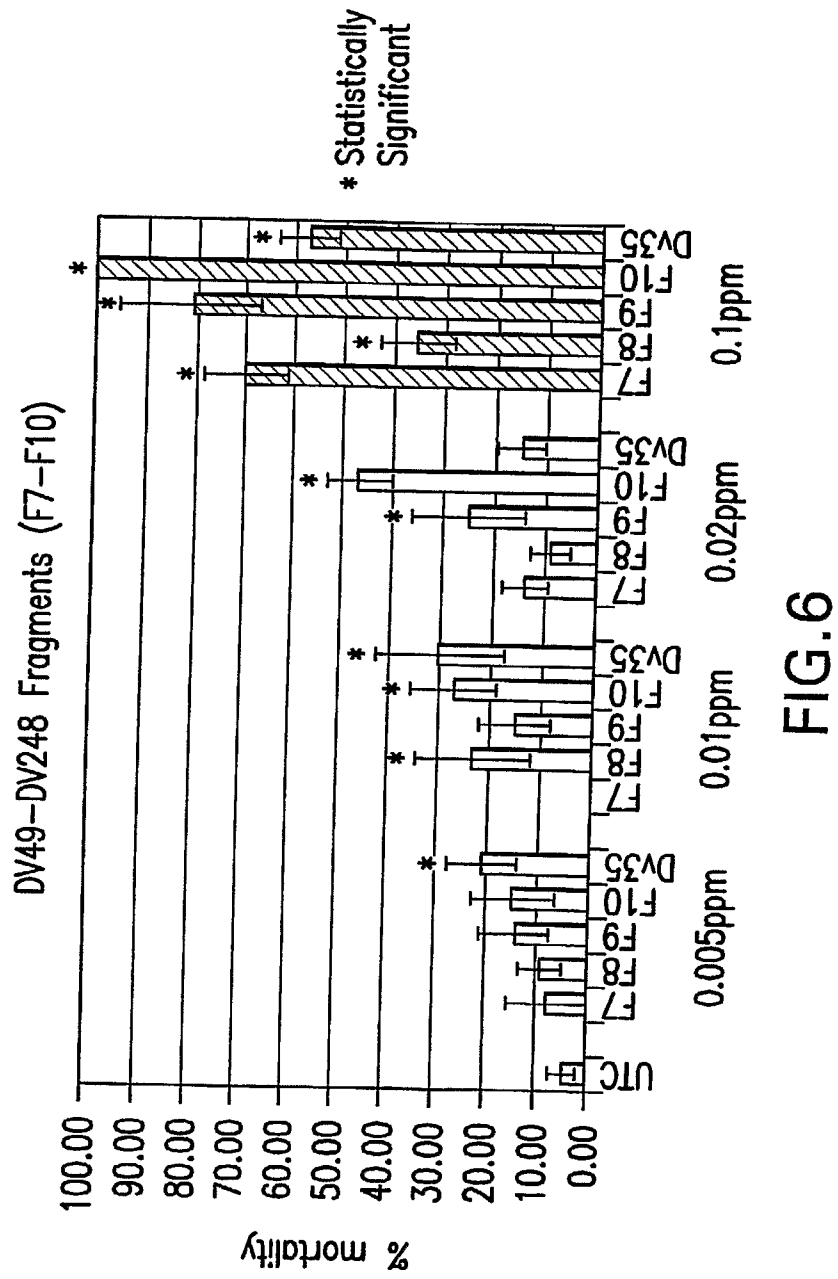


FIG.5



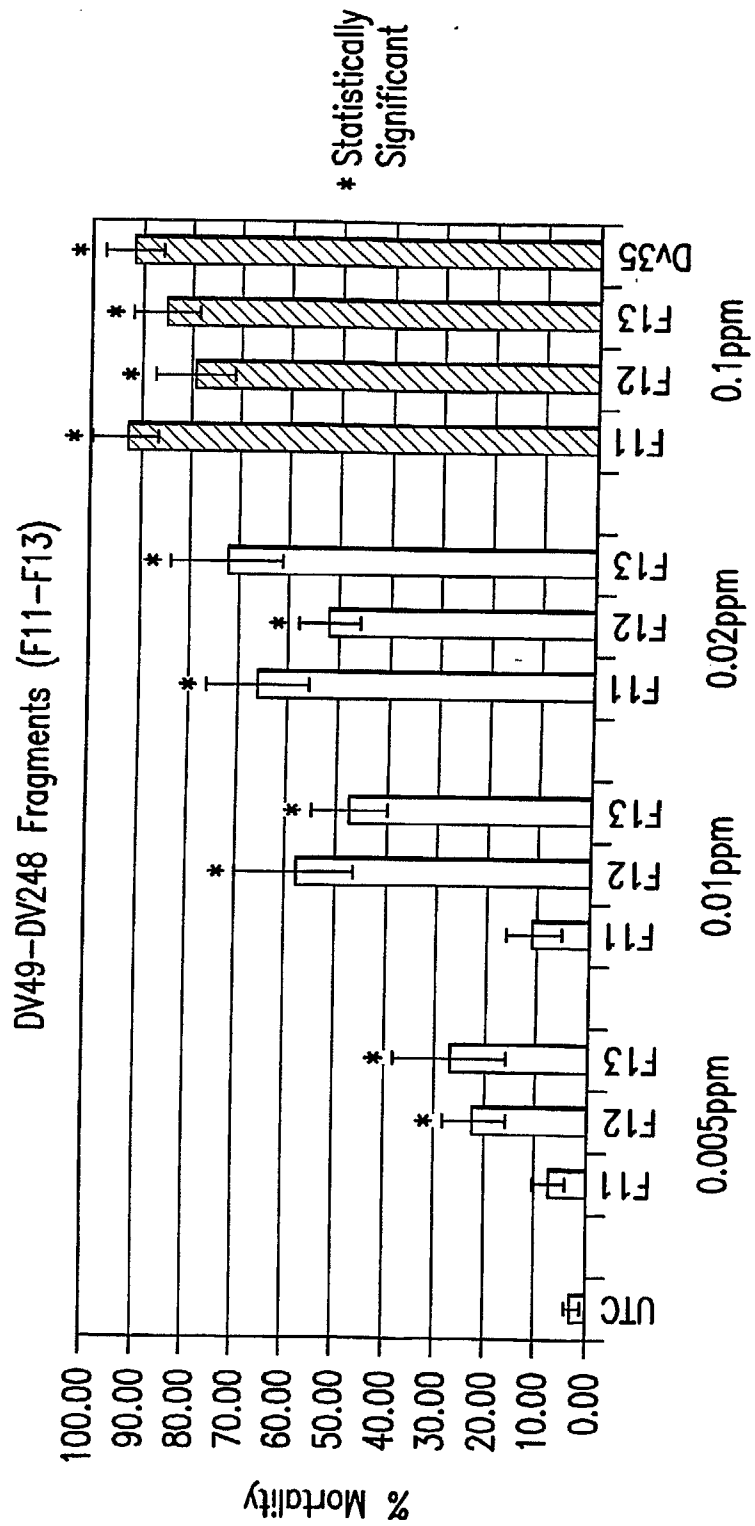


FIG.7

REFERENCES CITED IN THE DESCRIPTION

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Eljárások rovarfertőzések genetikai szabályozására növényekben, valamint ezek készítményei

SZABADALMI IGÉNYPONTOK



1. Polinukleotid, amelyet a következő csoportból választhatunk ki:

(a) egy polinukleotid, amely a 704. számú szekvenciával rendelkező nukleinsav szekvenciát tartalmazza;

(b) egy polinukleotid, amely az 5XSSC, 50% formamid, és 42 °C 10 percig mosási körülmények között hibridizálódik a 704. számú szekvenciával rendelkező nukleinsav szekvenciához;

(c) polinukleotid, amely legalább 70%-os szekvencia azonosságot mutat a 704. számú szekvenciával rendelkező nukleinsav szekvenciával;

(d) a 704. számú szekvenciával rendelkező nukleinsav szekvenciának egy legalább 21 egybefüggő nukleotidból álló fragmense; és

(e) az (a), (b), (c) vagy (d) pont szerinti szekvencia komplementere, ahol a szóban forgó polinukleotid működés szempontjából egy heterológ promoterhez kapcsolódik; és

ahol ha egy fedelesszárnyú növényi kártevő a szóban forgó polinukleotiddal vagy a szóban forgó fragmenssel komplementer szálát tartalmazó kétszálú ribonukleotid legalább egyik szálát szekvenciát lenyeli, az gátolja a szóban forgó kártevő növekedését.

2. Az 1. igénypont szerinti polinukleotid, amely a definíció szerint egy növényi transzformációs vektorban található.

3. Az 1. igénypont szerinti polinukleotid expresszálasával keletkező kétszálú ribonukleotid szekvencia, ahol a szóban forgó ribonukleotid szekvenciának egy fedelesszárnyú növényi kártevő által történő lenyelése gátolja a szóban forgó kártevőt.

4. A 3. igénypont szerinti kétszálú ribonukleotid szekvencia,

(i) amelyet a definíció szerint úgy állítunk elő, hogy készítünk egy rekombináns polinukleotid szekvenciát, amely tartalmaz egy első, egy második és egy harmadik polinukleotid szekvenciát, ahol az első polinukleotid szekvencia tartalmazza az 1. igénypont szerinti izolált polinukleotidot, és ahol a harmadik polinukleotid szekvencia a második polinukleotid szekvencián keresztül kapcsolódik az első polinukleotid szekvenciához, és ahol a harmadik polinukleotid szekvencia lényegében az első polinukleotid szekvencia reverz komplementere, oly módon, hogy az első és a harmadik polinukleotid szekvencia hib-

ridizálódik, amikor átíródik egy ribonukleinsavvá, egy kétszálú ribonukleotid molekulát képezve, amelyet a kapcsolódó második ribonukleotid szekvencia stabilizál; vagy

(ii) ahol a polinukleotid szekvenciának a kártevő által történő lenyelése gátolja egy olyan nukleotid szekvencia expresszióját, amely lényegében komplementer a szóban forgó polinukleotid szekvenciával.

5. Az 1. igénypont szerinti polinukleotiddal transzformált sejt.

6. Az 5. igénypont szerinti sejt, amely a definíció szerint

(i) egy prokarióta sejt; vagy

(ii) egy eukarióta sejt; vagy

(iii) egy növényi vagy bakteriális sejt.

7. Az 1. vagy 2. igénypont szerinti polinukleotiddal transzformált növény, vagy annak magja, amely tartalmazza a polinukleotidot.

8. A 7. igénypont szerinti növény, amelyben a szóban forgó polinukleotid a növény egy sejtjében kétszálú ribonukleotid szekvenciaként expresszálódik, és a szóban forgó kétszálú ribonukleotid szekvenciának egy rovarkártevőt gátló mennyiségben történő lenyelése egy tápban gátolja a szóban forgó kártevőt, hogy tovább táplálkozzon a szóban forgó táppal, előnyösen

(i) a rovarkártevőt a következő csoportból választhatjuk ki: *Diabrotica virgifera*, *Diabrotica virgifera virgifera*, *Diabrotica virgifera zea*, *Diabrotica balteata*, *Diabrotica barberi*, *Diabrotica viridula*, *Diabrotica speciosa*, és *Diabrotica undecimpunctata*; vagy

(ii) a kétszálú ribonukleotid szekvencia rovarkártevőt gátló mennyiségének lenyelése gátolja a kártevő növekedését.

9. A 7. igénypont szerinti növényből előállított árucikk, ahol a szóban forgó árucikk kimutatható mennyiségben tartalmaz egy, az 1. igénypont szerinti polinukleotidról expresszált ribonukleotidot.

10. Eljárás fedelesszárný kártevő fertőzés gátlására, azzal jellemezve, hogy a fedelesszárný rovarkártevő táplálékában biztosítunk egy szert, amely tartalmaz egy első polinukleotid szekvenciát, amely a rovarkártevő által való lenyelés után úgy működik, hogy a szóban forgó kártevőben gátol egy biológiai funkciót, ahol a szóban forgó polinukleotid szekvencia körülbelül 95-100% nukleotid szekvencia azonosságot mutat legalább körülbelül 19-25 egybefüggő nukleotid mentén egy, a szóban forgó kártevőből származó kódoló szekvenciával, és hibridizálódik egy második polinukleotid szekvenciához, amely komplementer a szóban forgó első polinukleotid szekvenciával, és ahol a szóban forgó kártevőből származó kódoló szekvencia a 70. számú szekvencia, vagy annak komplementere.

11. A 10. igénypont szerinti eljárás, azzal jellemezve, hogy a szóban forgó fedelesszárnyú kártevő egy *Diabrotica* spp., amelyet előnyösen a következő csoportból választhatunk ki: *Diabrotica virgifera*, *Diabrotica virgifera virgifera*, *Diabrotica virgifera zea*, *Diabrotica balteata*, *Diabrotica barberi*, *Diabrotica viridula*, *Diabrotica speciosa*, és *Diabrotica undecimpunctata*.

12. Eljárás fedelesszárnyú kártevő fertőzés gátlására, azzal jellemezve, hogy a fedelesszárnyú rovarkártevő táplálékában biztosítunk egy növénysejtet, amely egy, az 1. igénypont szerinti polinukleotid szekvenciát expresszál, ahol a polinukleotidot úgy expresszáltatjuk, hogy egy kétszálú ribonukleinsavat termeljen, amely a kártevő által történő lenyelés után úgy működik, hogy a szóban forgó kártevőben gátolja egy megcélzott szekvencia expresszióját, ennek eredményeképpen kevésbé táplálkozik a szóban forgó táplálékból, mint egy olyan táplálékból, amelyből hiányzik a növénysejt.

13. A 12. igénypont szerinti eljárás, azzal jellemezve, hogy

(i) a sejt lenyelése után a kártevő csökkent növekedést mutat; vagy

(ii) a növénysejt tartalmaz még egy polinukleotid szekvenciát, amely egy rovarirtó szert kódol, amelyet a következő csoportból választhatunk ki: egy patatin, egy *Bacillus thuringiensis* rovarirtó fehérje, egy *Xenorhabdus* rovarirtó fehérje, egy *Photorhabdus* rovarirtó fehérje, egy *Bacillus laterosporus* rovarirtó fehérje, és egy *Bacillus sphaericus* rovarirtó fehérje, a szóban forgó *Bacillus thuringiensis* rovarirtó fehérjét előnyösen a következő csoportból választhatjuk ki: egy Cry1, egy Cry3, egy TIC851, egy CryET70, egy Cry22, egy TIC901, egy TIC201, egy TIC407, egy TIC417, egy bináris rovarirtó fehérje CryET33 és CryET34, egy bináris rovarirtó fehérje CryET80 és CryET76, egy bináris rovarirtó fehérje TIC100 és TIC101, az ET29 vagy ET37 rovarirtó fehérje kombinációja a TIC810 vagy TIC812 rovarirtó fehérjével, és egy bináris rovarirtó fehérje PS149B1; vagy

(iii) a megcélzott szekvencia egy fehérjét kódol, amelynek a várható funkcióját a következők közül választhatjuk ki: izomképződés, juvenilis hormon képződés, juvenilis hormon szabályozás, ionszabályozás és -transzport, emésztő enzim szintézis, a sejtmembrán potenciál fenntartása, aminosav bioszintézis, aminosav lebomlás, spermaképződés, feromon szintézis, feromon érzékelés, tapogatók képződése, szárnyképződés, lábképződés, fejlődés és differenciálódás, peteképződés, lárvaérés, emésztő enzim képződés, hemolimfa szintézis, hemolimfa fenntartás, neurotranszmisszió, sejtosztódás, energia metabolizmus, légzés és apoptózis; vagy

(iv) a szóban forgó fedelesszárnyú kártevő egy *Diabrotica* spp., amelyet előnyösen a következő csoportból választhatunk ki: *Diabrotica virgifera*, *Diabrotica virgifera virgifera*, *Diabrotica virgifera zea*, *Diabrotica balteata*, *Diabrotica barberi*, *Diabrotica viridula*, *Diabrotica speciosa*, és *Diabrotica undecimpunctata*; vagy

(v) a kártevő által történő lenyelés után a polinukleotid úgy működik, hogy egy, a rovar túléléséhez lényeges gént szuppresszál, a szóban forgó funkciót a következők közül választhatjuk ki: a kártevő táplálkozása, a kártevő sejt apoptózisa, a sejt differenciálódása és fejlődése, a szexuális reprodukcióra való képesség vagy vágy, izomképződés, izomrángás, izom összehúzódás, juvenilis hormon képződés, juvenilis hormon szabályozás, ionszabályozás és –transzport, a sejtmembrán potenciál fenntartása, aminosav bioszintézis, aminosav lebomlás, spermaképződés, feromon szintézis, feromon érzékelés, tapogatók képződése, szárnyképződés, lábképződés, peteképződés, lárva érés, emésztő enzim képződés, hemolimfa szintézis, hemolimfa fenntartás, neurotranszmisszió, lárva állapotba történő átmenet, bebábozódás, a bábállapotból való kiemelkedés, sejtosztódás, energia metabolizmus, légzés és a citoskeletális szerkezet kialakulása.

14. Eljárás egy rovarkártevő fertőzésnek kitett haszonnövényből előállított termés hozamának a javítására, azzal jellemezve, hogy a szóban forgó eljárás a következő lépéseket tartalmazza:

- a) egy 1. igénypont szerinti polinukleotidot bejuttatunk a szóban forgó haszonnövénybe,
- b) a haszonnövényt tenyésztjük, hogy lehetővé tegyük a szóban forgó polinukleotid expresszióját, ahol a szóban forgó polinukleotid expressziója gátolja a növény rovarkártevők által történő fogyasztását, és a kártevő fertőzés miatti hozamcsökkenést.

15. A 14. igénypont szerinti eljárás, azzal jellemezve, hogy

(i) a polinukleotid expressziója egy RNS molekulát termel, amely elnyom legalább egy első megcélzott gént a rovarkártevőben, amely lenyelte a szóban forgó haszonnövény egy részét, ahol a megcélzott génnek legalább egy lényeges funkciója van, amely a következők közül választható ki: a kártevő táplálkozása, a kártevő életképessége, a kártevő sejt apoptózisa, a kártevő vagy bármelyik kártevő sejt differenciálódása és fejlődése, a kártevő szexuális reprodukciója, izomképződés, izomrángás, izom összehúzódás, juvenilis hormon képződés és/vagy csökkentés, juvenilis hormon szabályozás, ionszabályozás és –transzport, a sejtmembrán potenciál fenntartása, aminosav bioszintézis, aminosav lebomlás, spermaképződés, feromon szintézis, feromon érzékelés, tapogatók képződése, szárnyképződés, lábképződés, peteképződés, lárva érés, emésztő enzim képződés, hemolimfa szintézis, hemolimfa fenntartás, neurotranszmisszió, lárva állapotba történő átmenet, bebábozódás, a bábállapotból való kiemelkedés, sejtosztódás, energia metabolizmus, légzés, a citoskeletális szerkezet szintézise és fenntartása, nukleotid metabolizmus, nitrogén metabolizmus, vízfelhasználás, vízvisszatartás, és érzékszervi észlelés; vagy

(ii) a rovarkártevő egy gabona gyökérféreg kártevő, amelyet a következők közül választhatunk ki: *Diabrotica undecimpunctata howardi* (Déli kukorica gyökérféreg (SCR)), *Diabrotica virgifera virgifera* (Amerikai kukoricabogár (WCR)), *Diabrotica barberi* (Északi kukorica gyökérféreg (NCR)), *Diabrotica virgifera zea* (Mexikói kukorica gyökérféreg (MCR)), *Diabrotica balteata*

(Brazil kukorica gyökérféreg (BZR)), *Diabrotica viridula* (Brazil kukorica gyökérféreg (BZR)), és *Diabrotica speciosa* (Brazil kukorica gyökérféreg (BZR)).

16. Eljárás egy rovarkártevő fertőzésnek kitett haszonnövényből előállított termék szárazság-toleranciájának a javítására, azzal jellemezve, hogy a szóban forgó eljárás a következő lépéseket tartalmazza:

a) a szóban forgó haszonnövénybe bejuttatunk egy 1. igénypont szerinti polinukleotidot,

b) a haszonnövényt tenyésztjük, hogy lehetővé tegyük a szóban forgó polinukleotid expresszióját, ahol a polinukleotid expressziója gátolja, hogy a rovarkártevők a haszonnövényből táplálkozzanak, valamint a szárazságtűrés elvesztését a kártevő fertőzés miatt.

17. Eljárás egy árucikk, élelmiszer vagy táp előállítására, azzal jellemezve, hogy előállítunk egy 7. igénypont szerinti növényt, vagy annak egy részét, és a növényből, vagy annak egy részéből előállítjuk az árucikket, élelmiszert vagy tápot.

18. A 17. igénypont szerinti eljárás, azzal jellemezve, hogy az élelmiszer vagy a táp lehet olaj, liszt, fehérje, keményítő, liszt vagy szilázs.

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