Composition and Methods for Pest Control Management

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COMPOSITIONS AND METHODS FOR PEST CONTROL MANAGEMENT

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C12N 2710/00071 (2013.01)

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None

References Cited
U.S. PATENT DOCUMENTS

FOREIGN PATENT DOCUMENTS

OTHER PUBLICATIONS
References Cited

OTHER PUBLICATIONS


References Cited

OTHER PUBLICATIONS

Yang, Y.T., et al., “The genome and occlusion bodies of marine Peneaus monodon nudivirus(PmNV, also known as MBV and PenMVNPV) suggest that it should be assigned to a new nudivirus genus that is distinct from the terrestrial nudivirus,” BMC Genomics, 2014, 15:628, 24 pgs., PMID: 25063321.
FIG 1.

Wild-type HzNV-2, 231,621 bp
Direct Repeats:

ORF2
ORF1
ORF7, juvenile hormone esterase

ORF55
ORF56

ORF92
ORF90

ORF113

pg-1

Wild-type
KS-3
KS-45
KS-51
FIG 2.

Percentage of gonadal F1 female progeny

Virus used to infect female moths

- OviD2
- OviD3
FIG 3.

Virus used to infect female moths
Females were infected and eggs were counted 1-4 days later.
FIG 5.

![Bar graph showing percent of agonadal females with different inoculation methods and genotypes.](image)
FIG 6.

<table>
<thead>
<tr>
<th>DNA: Primers</th>
<th>WT HzNV-2 YFP</th>
<th>PAG1</th>
<th>ORF78</th>
<th>yfp-puc57 YFP</th>
<th>PAG1</th>
<th>ORF78</th>
<th>yfp HzNV-2 YFP</th>
<th>PAG1</th>
<th>ORF78</th>
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[Image of gel electrophoresis]
adapt to insecticides, resistance to Bt toxins was predicted in insect pests. For example, data-products/adoption-of-genetically-engineered-crops-in-highly-polyphagous and cause economically significant damage to many crops. Crops commonly damaged by Heliothine complex of lepidopteran moths include cotton, corn, soybean, sunflowers, tomato, sorghum, cucumber, melon, lettuce, cauliflower, and cabbage. Since the commercial introduction of Bt crops in 1996, they have been adopted around the world and have been grown on more than one billion acres worldwide. In the US, 81% of corn and 84% of cotton express one or more Bt toxins. (http://www.ers.usda.gov/data-products/adoption-of-genetically-engineered-crops-in-the-us/recent-trends-in-ge-ado­ptio­n.aspx, 2015 report.) Unfortunately, due to the remarkable ability of insects to adapt to insecticides, resistance to Bt toxins was predicted and reports of field-evolved resistance and reduced efficacy are increasing. Such resistance is a threat to the sustainability of important Bt crops, in the US and elsewhere. Thus, there is a continuing need to develop new methods to control insect pests. For example, Helicoverpa zea (H. zea, commonly known as the corn earworm), is a major polyphagous moth pest in the Heliothine complex in the United States and causes millions of dollars of damage to corn and cotton plants each year. A number of pests in the Heliothine complex of moths, notably H. zea H. armigera and Heliothis virescens are highly polyphagous and cause economically significant damage to many crops. Crops commonly damaged by H. zea include cotton, corn, soybean, sunflowers, tomato, sorghum, strawberry, peppers, beans, aubergine, okra, peas, millet, cucumber, melon, lettuce, cauliflower, and cabbage. Because H. zea attacks a wide variety of plants and, in many instances, is developing resistance to Bt crops, farmers rely heavily on pesticides to control this pest insect. The need for pest management, such as in field, fruit and vegetable crops, is a need in the art, which will only become more critical as resistance to Bt expands. Further, there is a need for pest management that does not involve the use of conventional pesticides or transgenic technologies such as in organic cropping systems. The instant invention addresses one or more aforementioned needs in the art.

BRIEF SUMMARY

Disclosed are genetically modified nudiviruses capable of being sexually transmitted by an insect useful for controlling pest populations. The genetically modified nudiviruses are capable of causing sterility in a target population of insects. Also disclosed are insects infected with the disclosed genetically modified nudiviruses, methods of making the genetically modified nudiviruses, and methods of using the genetically modified nudiviruses to control an insect pest population.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1. Schematic of nudivirus genome showing genes known to be involved or implicated in sterilizing mutations.

FIG. 2. Percentage of agonaladal female F1 progeny. Wild-type (WT) and mutant HzNV-2 generated by chemical mutagenesis (KS-3, KS-38, KS-39, KS-45, KS-51, and KS-52) were injected into adult female moths on the day of emergence, and eggs were collected on oviposition days 2 (OviD2) and 3 (OviD3). Female F1 progeny were reared to adult moths and evaluated for the presence of a viral plug indicating an agonaladal pathology (OviD2-WT n=17, KS-3 n=24, KS-38 n=23, KS-39 n=26, KS-45 n=19, KS-51 n=14, KS-52 n=18; OviD3-WT n=15, KS-3 n=16, KS-38 n=22, KS-39 n=16, KS-45 n=19, KS-51 n=18, KS-52 n=23). FIG. 3. Occurrence of complete sterility in agonaladal female F1 progeny. Wild-type (WT) and mutant HzNV-2 (KS-3, KS-38, KS-39, KS-45, KS-51, and KS-52) were injected into adult female moths on the day of emergence, and offspring eggs were collected on oviposition days 2 (OviD2) and 3 (OviD3). Female F1 progeny were reared to adult moths and evaluated for ability to lay viable eggs. Failure to lay eggs or lay viable eggs indicates complete sterility (OviD2-WT n=17, KS-3 n=24, KS-38 n=23, KS-39 n=26, KS-45 n=19, KS-51 n=14, KS-52 n=18; OviD3-WT n=15, KS-3 n=16, KS-38 n=22, KS-39 n=16, KS-45 n=19, KS-51 n=18, KS-52 n=23). This illustrates that these mutant HzNV-2 causes decreased egg production and sterility.

FIG. 4. Effect of viral titer on H. zea egg production. Female adult moths (7) were injected with 100 µl wt HzNV-2 (high dose: 4x10⁴ pfu/ml; low dose: 40 pfu/ml) or yfp recombinant HzNV-2 (high dose: 1x10⁵ pfu/ml; low dose: 1x10⁴ pfu/ml isolated from cell culture and mated with uninfected male moths (9)). Eggs were collected on oviposition days 2-5 and counted. Uninfected females were mated with uninfected males as a control.

FIG. 5. Direct inoculation of insect larvae causes high numbers of agonaladal moths. Wild-type (WT) HzNV-2 and mutant KS3 were amplified in SO insect cell cultures and injected into third instar larvae via an insulin syringe. WT HzNV-2 and mutant yfp HzNV-2 virus isolated from viral plugs of agonaladal female moths were used to infect third instar larvae via a pre-sterilized pin. After both types of infections, larvae were reared to adult moths, and females were examined for the presence of a viral plug, an indicator of virus infection and agonaladal pathology (Syringe, WT n=20, KS3 n=25; Pin, WT n=20, yfp HzNV-2 n=21).

FIG. 6. 1.5% agarose gel showing KS51 that yfp HzNV-2 is a pag1 mutant. Wild-type (WT) HzNV-2 (control) and yfp HzNV-2 viral DNA and yfp-pUC57 (control), the plasmid used for homologous recombination to make the yfp HzNV-2 virus, were used as DNA templates in the PCR reactions. If present, yfp primers were used to amplify the yellow fluorescent protein gene (547 bp); pag1 primers were used to amplify pag1 DNA; ORF78 primers were used to amplify hypothetical gene ORF78 (403 bp) that the DNA is from HzNV-2.

DETAILED DESCRIPTION

As used herein and in the appended claims, the singular forms “a,” “an,” and “the” include plural referents unless
A sexually transmitted insect virus, *Helicoverpa zea* nudo-virus 2 (HzNV-2, accession number NC_004156.), is known to cause approximately 33% of infected *H. zea* to be sterile. (Raina 1995). Wildtype (WT) HzNV-2, however, is not a potential biological control agent due to the high proportion of asymptomatic carrier moths. Applicant has found that HzNV-2 can be modified so that extremely high percentages, for example, up to 100%, or greater than about 90%, of the infected *H. zea* become sterile. As such, the mutant HzNV-2 may be an important tool in controlling various insect pests by causing collapse in the target insect population. In turn, this modified virus can be used to infect a target insect, and control an insect population without the use of traditional pesticides, or, alternatively, can be used in combination with traditional pesticides such that the amount of the pesticide used is minimized. Such a technology may have particular utility in control of populations of Bt resistant insects and invasive insect populations for which traditional pesticides are ineffective. Applicant’s approach allows for pest control via release of insects infected with a sexually transmitted virus that can be transmitted by mating in the targeted farming area. The approach developed by Applicant is effective for both transgenic and/or non-transgenic crops and is capable of targeting pest species in which the virus replicates and is sexually transmitted.

Attempts to control insect populations via genetic manipulation of crops is currently limited due to the ability of insects to rapidly develop resistance to the genetically added toxins, and is further limited by the costs to producers to use such modified crops. For example, crops expressing the *Bacillus thuringiensis* (Bt) toxins were introduced twenty years ago to control caterpillar pests. Since then, they have been adopted worldwide, planted on more than one billion acres and have become one of the most successful and rapidly adopted agricultural technologies since the ‘green revolution’ of the mid-20th century (James, 2012). As of 2015 in the US, 81% of corn and 84% of cotton express one or more Bt toxins. However, the widespread adoption of Bt technology carries the significant risk that overuse will inevitably lead to development of insect resistance to Bt toxins and crop failures, which threatens the technology’s continued viability (Carriere et al., 2010, Tabashnik et al., 2013; Tabashnik et al., 2009). This risk, which always has been recognized by regulators, industry, and researchers, has been managed by resistance monitoring and the use of refuge strategies to delay resistance. These refuge strategies, which have been mandated by the EPA in the USA with similar mandates in other countries, entail the planting of nearby non-transgenic plants to maintain susceptible insect populations (EPA, 1998; Huang et al., 2011). Unfortunately, this practice is not always followed due to cost to producers, and is not always effective because of the remarkable ability of insects to evolve resistance to insecticides. Increasing insect resistance to Bt plants is reported, and some insects exhibit resistance traits that are genetically dominant (Campagne et al., 2013). To summarize, Bt-resistant insects represent an ongoing and increasingly important threat to the continued efficacy of Bt crops, and to food and fiber production in the US and worldwide.

One insect pest threatening Bt crops is the corn earworm, *Helicoverpa zea*, a lepidopteran moth. *H. zea* is found throughout North America, for example, where it is the second most costly crop pest (Fitt, 1989), and is also found in Central America, the Caribbean, and South America. *H. zea*, which feeds on many different plants and has several common names (e.g., corn earworm, cotton budworm, tomato fruitworm) has some strains that are 1000-times
more resistant to Bt toxin than susceptible insects (Ali and Luttrell, 2007; Ali et al., 2006).

Applicant has developed a new approach to suppress insect pest populations. In a further aspect, Applicant has developed a new approach to managing Bt resistance, which relies upon engineering or mutating a sexually-transmitted insect virus that sterilizes infected insects (including complete or partial sterility). Insects containing the mutant virus may be released in areas where Bt resistance is present in H. zea populations, thereby suppressing these targeted populations and preserving the utility of the Bt transgenic plants and/or non-transgenic plants. Similarly, the susceptible pest insects are commonly invasive across the world and the disclosed methods may be used to reduce and eliminate the invasive pest populations. The viruses developed by Applicant are mutant and recombinant forms of a naturally-occurring (i.e., wild-type) virus, Helicoverpa zea nudivirus 2 (HzNV-2), which infects H. zea. HzNV-2 is the only lepidopteran insect virus which has been shown to be sexually transmitted and causes sterility in both males and females. In one aspect, the infected insect may have partial sterility, defined as when a female H. zea moth lays less than 30 viable eggs each day due to damage to her reproductive organs. In one aspect, the infected insect may have complete sterility, defined as the inability of a female moth to lay viable eggs due to damage to her reproductive organs.

In one aspect, disclosed is a genetically modified nudivirus of a wild type virus. The genetically modified nudivirus contemplated herein is generally capable of being sexually transmitted by an insect and capable of causing sterility in an insect at a rate of greater than about 50%, or from about 50% to about 100%, or from about 80% to about 100% following infection of said insect with said nudivirus comprising a genetic modification resulting from the modification, wherein said viral regulatory associated transcript and has been shown to be involved in the establishment of latent infections of HzNV-1. In one aspect, the genetic modification may be a mutation in one or more sequences selected from dr1 (atagaactcagaactgatcggactgac, SEQ ID NO: 14), dr2 (gaacactctaaactaaggtgaccaactaagca, SEQ ID NO: 15), dr3 (ataaaaaagcgacgacgagaagctgctgctgcaaaagccaaagctg, SEQ ID NO: 16), dr4 (ttataccagagagcaagccagaaa, SEQ ID NO: 17), dr5 (acctaaagttgaatctaaagtagtggaaccacctaaagcggaatctaaacaacagcaatacttataaactaatgtag, SEQ ID NO: 18), dr6 (agctgctgctgcaaaagccgaggctga, SEQ ID NO: 19), or a combination thereof. In one aspect, the genetic modification may be a mutation in dr3 (SEQ ID NO: 16), for example, KS-3 in which there is a 1 bp insertion at 175,550 and KS-45, 80 bp insertion at 175,650. In one aspect, the genetic modification may be a mutation in dr6 (SEQ ID NO: 19), for example, KS-51, having a 29 bp deletion at 180,270-180,299.

In a further aspect, the genetic modification is one in which an increase in activity of a viral regulatory gene results from the modification, wherein said viral regulatory gene is hhi-1 (SEQ ID NO: 8). In certain aspects, the identification of a genetic modification of interest can be determined via detection of increased hhi-1 activity.

In one aspect, the genetically modified nudivirus may be obtained via chemical mutagenesis. In another aspect, the genetically modified nudivirus may be obtained via recombinant DNA technology. Exemplary, non-limiting methods are disclosed herein. In a further aspect, the genetically modified nudivirus may be obtained using gene editing technology as is known in the art.

In one aspect, the genetically modified nudivirus, may be obtained using gene editing technology as is known in the art. In one aspect, a method of reducing a population of lepidopteran moths is disclosed. The method may comprise the step of introducing an insect infected with a genetically modified nudivirus as disclosed herein into the population of interest. In one aspect, infected insects of a single sex may be introduced into a target population, for example an all-male or all-female population of insects. In another aspect, a mixed population of infected insects may be introduced.

In one aspect, an insect infected with a virus as described above is disclosed. The insect may be a lepidopteran moth. In further aspects, the insect may be Helicoverpa zea (H. zea) H. armigera, H. assulta, Heliothis virescens, Agrotis ipsilon, Spodoptera frugiperda, Spodoptera exigua or a closely-related moth, for example, a closely related moth, or noctuid moths. The insect may be a female or a male.

In one aspect, a method of making an insect capable of transmitting a genetically modified nudivirus as disclosed herein to a population of insects is disclosed. The method may comprise the step of introducing an insect with a genetically modified nudivirus as described herein. In one aspect, the insect is a lepidopteran moth. The insect may be Helicoverpa zea (H. zea) H. armigera, H. assulta, Heliothis virescens, Agrotis Ipsilon, Spodoptera frugiperda, Spodoptera exigua or a closely related moth or noctuid moth. The method may utilize male insects, female insects, or both. In one aspect, the genetically modified nudivirus may be derived from a viral plug. The genetically modified nudivirus may be administered orally to the insect. In other aspects, the genetically modified nudivirus may be administered to an insect via direct inoculation of insect larvae or adult moths by puncturing the cuticle of the insect with a pin containing viral inoculum derived from a viral plug. In a further aspect, the genetically modified nudivirus may be administered to the insect via direct hypodermic injection into third instar larvae or moths.
In one aspect, a method of protecting a crop susceptible to a moth pest from moth pest damage is disclosed. In this aspect, the method may comprise the step of introducing insects infected with a genetically modified nudivirus as described herein, into a crop of interest. The crop may be any crop threatened by the pest, and may include, for example, the following non-limiting list of crops: corn, cotton, soybeans, tomatoes, sorghum, artichoke, asparagus, cabbage, cantaloupe, collard, cowpea, cucumber, eggplant, lettuce, lime bean, melon, okra, pea, pepper, potato, pumpkin, snap bean, spinach, squash, sweet potato, and watermelon, alfalfa, clover, cotton, flax, oat, millet, rice, sorghum, soybean, sugarcane, sunflower, tobacco, vetch, and wheat, avocado, grape, peaches, pear, plum, raspberry, strawberry, carnation, geranium, gladiolus, nasturtium, rose, snapdragon, zinnia, and combinations thereof (see http://edis.ifas.ufl.edu/in302). In certain aspects, the crop may be a Bacillus thuringiensis (Bt) toxin producing crop. The insect used may be any insect as described above.

In a further aspect, a method of sterilizing an insect population is disclosed. The method may include the step of introducing a genetically modified nudivirus as described herein into a target insect population. This may include an invasive insect population, and may further include an insect population that is Bt resistant. One such example insect is the lepidopteran moth, which may further include Helicoverpa zea (H. zea), H. armigera, H. assulta, Heliothis virescens, Agrotis ipsilon, Spodoptera frugiperda, Spodoptera exigua and closely related moths or noctuid moths.

In one aspect, a method of making a genetically modified nudivirus via chemical modification is disclosed. The method may comprise the steps of:

a) incubating a population of insect cells infected with a virus with about 0.05 mM to about 0.1 mM 1,3-butadiene diepoxide (or 1,2,3,4-Diepoxybutane or “DEB”) for at least 1 hour and up to five hours at a temperature range of about 26 to about 28°C, wherein the population of infected insect cells may comprise an Sf9 insect cell, for example, further wherein the insect cell may be infected with a virus having at least 80% identity, or at least 85% identity, or at least 90% identity, or at least 95% identity, or at least 99% identity to a wild-type HzNV-2 virus (SEQ ID NO: 1), and wherein the incubation is sufficient to induce one or more mutations in the HzNV-2 virus;

b) purifying the virus, wherein the purifying step includes the steps of:

i. culturing the population of insect cells infected with a virus in a DEB-free media, wherein the population of infected insect cells are isolated and washed prior to the culturing step;

ii. collecting a supernatant from DEB-free media to obtain a DEB-exposed virus population;

iii. amplifying and collecting the mutated virus from the DEB-exposed virus population, wherein the collection step may comprise selecting virus from a plaque having a large plaque phenotype.

Exemplary methods making a genetically modified nudivirus via chemical modification are provided below.

EXAMPLES

The present invention may be understood more readily by reference to the following detailed description of the preferred embodiments of the invention and the Examples included herein and to the Figures and their previous and following description. Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, the preferred methods, devices, and materials are now described. All references, publications, patents, patent applications, and commercial materials mentioned herein are incorporated herein by reference for the purpose of describing and disclosing the materials and/or methodologies which are reported in the publications which might be used in connection with the invention. Nothing herein is to be construed as an admission that the invention is not entitled to antedate such disclosure by virtue of prior invention.

Method—Generating a Recombinant HzNV-2 Virus

To generate a yfp insert mutant virus using recombinant DNA technology, Applicant replaced the pagl gene with a gene encoding yellow fluorescent protein (yfp) by homologous recombination. pagl expresses a microRNA that suppresses the expression of the viral transcription factor, hli-1, an RNA intermediate necessary to maintain latency in HzNV-2 (Chao, 1998; Ww and Wu, 2011). To inactivate the pagl gene, a pUC57-based transfer vector, yfp-pUC57, was designed and synthesized with the yfp gene controlled by the Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus immediate early 2 (OpIE2) promoter, and flanked by 1.2 kb of viral HzNV-2 sequences upstream and downstream of pagl.

The yfp HzNV-2 recombinant virus was generated by homologous recombination of yfp/pagl-pUC57 plasmid with WT HzNV-2 genomic DNA after transfection into Sf9 insect cells. The mutant virus was plaque purified, screened for YFP fluorescence using a Zeiss observer A1 fluorescent microscope and the AxioVision Rel. 4.6 program, and amplified in Sf9 cells in nudivirus media (lx Supplemented Grace’s Media, 7% FBS, 1% Penicillin/streptomycin) in 25 cm² tissue culture flasks. Viral DNA was isolated from the cell culture supernatant using DNAzol (ThermoFisher Scientific #1994881). PCR results confirmed deletion of pagl and presence of the yfp gene using internal pagl (F 5’-GTGCTCACATTCGAGATGTAC-3’, R 5’-GGGTCGACTGGGACATGTCG-3’) and yfp (F 5’-CTGAGGATCCCATCTGAGGATCC-3’, R 5’-CAGGATCCGTCGAGGATCC-3’) primers, respectively (FIG. 6). Subsequent PCR reactions detected pagl DNA indicating that the yfp HzNV-2 virus is a yfp insertional mutant rather than a complete replacement of this gene. Nevertheless, inactivation of pagl was sufficient to produce a virus that caused sterility in up to 100% of infected insects. Primers to the HzNV-2 open-reading frame ORF78 (F 5’-GCACCATATGACATCAGGATCT-3’, R 5’-GACAGATCGTGACTTGCTAG-3’) were used as a control for detecting the HzNV-2 genome.

Method of Targeting Mutations in a Nudivirus Genome

Applicant has developed a novel method using diepoxide (DEB) to produce deletions in nudivirus genomes by chemical mutagenesis. DEB is known to crosslink DNA and lead to deletions of multiple bases (from ~50 bases to several kilobases), often within a single gene (Reardon et al., 1997; Wijen et al., 2001). DEB tends to cause mutations within regions of DNA that are actively transcribed. However, published protocols for DEB mutagenesis do not teach mutating a nudivirus as it infects an insect cell so that genes involved in establishing viral lysogeny are preferentially mutated. In the literature, DEB mutagenesis usually involves feeding DEB to insects (Reardon et al., 1997, Genetics 115:323-331; Kimble et al., 1990 Genetics. 1990 December; 126(4):991-1005; Olsen and Green 1982 Mutat Res. 1982

US 9,770,033 B2
February 22; 92(1-2):107-15, or exposing DNA directly to the mutagen (Yazaki et al., J Virol Methods. 1986 November; 14(3-4):275-83). See also Gherezghiher et al. (J Proteome Res 2013, 12(5):2151-2164), Kempf et al. (Biosci Rep 1990 10(4):363-374), “Methods of identifying anti-viral agents” U.S. Pat. No. 7,476,499, which relate to chemical mutagenesis, but which do not describe methods for targeting viral mutations to selective classes of viral genes as disclosed herein. The art does not teach the use of DEB to mutate nuidivirus genomes during an infection or methods to target viral genes by synchronizing chemical exposure with stages of the virus infection process in cells. Disclosed herein is a novel method that addresses one or more of the following objectives: 1) efficient mutation in early expressed genes in the HzNV-2 genome, 2) introducing a mutation while avoiding viral DNA damage to a level that compromises virus replication, 3) introducing a mutation while avoiding killing the virus-infected host Sf9 insect cell, and 4) allowing recovery of virus mutants before host cells lyse and the virus becomes unstable (typically in less than 48 h).

Applicant established an efficient protocol, wherein Sf9 cells were infected with WT HzNV-2 at a multiplicity of infection (MOI) of 1 for 1.5 hrs. The 1.5 hr incubation time was chosen because previous literature illustrated that 2 h was enough time for the related HzNV-1 virus (SEQ ID NO: 2) to enter Sf21 insect cells and to transcribe the pag1 gene (Chao et al., 1992. J Virol 66(3):1442-1448). Applicant found that one barrier to an effective method was allowing sufficient time for the virus to enter into the target cell (the insect cell) and start viral transcription. Without intending to be limited by theory, Applicant found that about 1.5 hours was sufficient to achieve this objective. In other aspects, the infection time may be about 45 minutes or more, or about one hour to about two hours. Following this step, 0.1 mM DEB is added to the culture. Applicant found that, at higher concentrations of DEB (equal to and greater than about 0.5 mM), the host cell (for example, Sf9 cells) could not survive. A range of from about 0.05 mM to about 0.1 mM DEB is considered sufficient to carry out the protocol. The cells were harvested by centrifugation after a three hr incubation and re-suspended in fresh medium. Applicant found that three hours was sufficient to cause mutagenesis but not kill host insect cells. In other aspects, the infection time may be about four to five hours.

Plaque assays are performed to isolate mutated viruses, which are then amplified in Sf9 cells and evaluated for cell lysis. A mutation in a locus required for the virus latent phase (MOI) of 1 for 1.5 hrs. Without intending to be limited by theory, Applicant found that at about 1.5 hours was sufficient to cause mutagenesis but not kill host insect cells. In other aspects, the infection time may be about four to five hours.

Increased lysis of virus-infected cells could be evident from observations of viral plaque morphology in which lytic virus infection (MOI) of 1 for 1.5 hrs. The 1.5 hr incubation time was chosen because previous literature illustrated that 2 h was enough time for the related HzNV-1 virus (SEQ ID NO: 2) to enter Sf21 insect cells and to transcribe the pag1 gene (Chao et al., 1992. J Virol 66(3):1442-1448). Applicant found that one barrier to an effective method was allowing sufficient time for the virus to enter into the target cell (the insect cell) and start viral transcription. Without intending to be limited by theory, Applicant found that about 1.5 hours was sufficient to achieve this objective. In other aspects, the infection time may be about 45 minutes or more, or about one hour to about two hours. Following this step, 0.1 mM DEB is added to the culture. Applicant found that, at higher concentrations of DEB (equal to and greater than about 0.5 mM), the host cell (for example, Sf9 cells) could not survive. A range of from about 0.05 mM to about 0.1 mM DEB is considered sufficient to carry out the protocol. The cells were harvested by centrifugation after a three hr incubation and re-suspended in fresh medium. Applicant found that three hours was sufficient to cause mutagenesis but not kill host insect cells. In other aspects, the infection time may be about four to five hours.

Mutation frequencies are determined by inoculating cell cultures containing DEB-treated viral plaques with Sf9 insect cells seeded at an estimated approximate viral titer from the procedure is 1.5x10^6 pfu/ml. To isolate the WT HzNV-2 from infected female moths, the viral plug from an infected female moth is first extracted from the body and moved to a 1.5 ml-microcentrifuge tube. 100 µl 1xPBS is added and the plug is homogenized manually with a pipette tip to release the virus. The large fragments of insect cuticle and tissue are then removed. This viral solution is termed unfiltered viral plug extract (UVPE). The filtered viral plug extract (FVPE) is a filtered solution (with a 0.22 µm filter) of 1x supplemented Grace’s media, 2% unfiltered viral plug extract, and 5% penicillin/streptomycin antibiotics.

Controls for this mutagenesis are performed in parallel. Controls included uninfected Sf9 culture, uninfected Sf9 culture treated with DEB, and virus-infected Sf9 culture. These cultures are prepared the same way and at the same time as the mutagenized culture described herein.

The infected Sf9 insect culture is incubated at 27°C. for 1.5 hours.

Chemical Mutagenesis

In a fume hood, DEB (other names 1,3-butadiene diepoxide or 1,2,3,4-Diepoxybutane) is added at a 0.1 mM final concentration to the culture. The culture is then incubated at 27°C. for 3 hours.

After the 3 h incubation, the culture is moved to the fume hood. A cell scraper is used to detach cells from the 25 cm² flask. The cells and supernatant are moved to a 50 ml-conical tube and centrifuged at 900xg for 10 min at 4°C. The supernatant is removed to a specified waste container. Cells are washed with 10 ml PBS, incubated in fume hood for 5 min, then spun down at 900xg for 10 min at 4°C. The wash supernatant is removed to a specified waste container. The cell pellet is then resuspended in 5 ml nuidivirus media and moved to a new 25 cm² tissue culture flask, which is now considered DEB-free. Culture is incubated at 27°C. for 2 d.

After 2 days, the cell culture medium containing DEB-exposed HzNV-2 is collected after culture centrifugation at 900xg for 10 min and filter sterilization using a 0.22 µm filter. 2 ml of the virus stock is added to a new 25 cm² tissue culture flask containing Sf9 insect cells that were seeded at 1x10^6 cells/ml in a 5 ml total volume with nuidivirus media. The virus-infected culture is incubated at 27°C. for 7 d.
To purify and amplify the virus to a suitable volume for insect infection, the virus-containing medium was collected after centrifugation (3000 rpm, 10 min, 4°C), filter sterilized using a 0.22 μm filter, and stored in 1 ml aliquots at -80°C. The titer of the virus is approximately 1x10^9 pfu/ml. While HzNV-2 has been shown to infect several lepidopteran cell lines including SF-9 and TN-368 cells, Applicant found that it is difficult to pass the virus in insect cells due to the virus causing quick cellular lysis. The disclosed methods allow for amplification of the virus to a volume that allows for both amounts sufficient virus for storage and also virus suitable for insect infection.

Viruses were isolated using a traditional plaque assay, described in, for example, Anderson, D., Harris, R., Polayes, D., Ciccaroni, V., Donahue, R., Gerard, G., and Jesse, J. (1996) Rapid Generation of Recombinant Baculoviruses and Expression of Foreign Genes Using the Bac-To-Bac® Baculovirus Expression System. Focus 17, 53-58. Large plaques, referred to as the p0 viruses, were further amplified.

For p0 to p1 amplification, Sf9 insect cells were seeded at 5x10^5 cells/ml in a final 2 ml volume with nudivirus media in 12-well culture plates and incubated at 27°C for 1 h. Afterwards, viral plaques were picked using a large bore pipette tip and transferred to one well. Plates were incubated at 27°C for 5 d. Medium containing DEB-treated HzNV-2 virus is collected after culture centrifugation (900xg for 10 m at 4°C) and filter sterilized using a 0.22 μm filter.

For p1 to p2 amplification, Sf9 insect cells were seeded at 8x10^5 cells/ml in a final 2 ml volume with nudivirus media in 6-well culture plates and incubated at 27°C for 1 h. Afterwards, 600 µl p1 virus was added to one well using a serological pipet. Plates were incubated at 27°C for 4 d. Medium containing DEB-mutated HzNV-2 was then collected after culture centrifugation (900xg for 10 m at 4°C).

For p2 to p3 amplification, Sf9 insect cells were seeded at 1x10^6 cells/ml in 5 ml with nudivirus media in 25 cm^2 tissue culture flask with no incubation. ~1.5 ml (or all) p2 virus was added to one flask using a serological pipet. Flasks were incubated at 27°C for 4 d. Medium containing DEB-mutated HzNV-2 is then collected after culture centrifugation (900xg for 10 min at 4°C) and filter sterilization using a 0.22 μm filter. p3 virus is stored in 1 ml aliquots at -80°C.

p3 virus was used to infect 3rd instar larvae via the direct inoculation method. Each mutant virus caused an infection in the insect leading to formation of a viral plug found in virus-infected female moths and then injected into new healthy female moths 2 days after emergence. The eggs laid on oviposition day 3 were collected and the F1 progeny female adults were analyzed for sterility as indicated by the presence of a viral plug and number of eggs laid (Table 2). Both female groups infected with mutants yfp HzNV-2 and KS-3 laid few or no eggs and had a much higher percentage of agonal females than the WT-infected group. Thus, the viruses obtained using the described methods are suited for use in sterilizing populations of pests susceptible to infection by the described viruses, and may be utilized to control pest populations.

<table>
<thead>
<tr>
<th>Virus</th>
<th>Plugs</th>
<th>Eggs laid</th>
</tr>
</thead>
<tbody>
<tr>
<td>WT HzNV-2</td>
<td>34%</td>
<td>many</td>
</tr>
<tr>
<td>KS3</td>
<td>95%</td>
<td>a few</td>
</tr>
<tr>
<td>yfp HzNV-2</td>
<td>100%</td>
<td>none</td>
</tr>
</tbody>
</table>

In a similar experiment, WT and 9 chemical mutant viruses were evaluated for the ability to cause agonal deaths. Briefly, adult female moths were injected with 100 μl of 10^8 pfu/ml of virus isolated from viral plugs on the day of emergence. Eggs laid on oviposition days 2 and 3 were collected and reared to adult moths. The F1 progeny female moths were evaluated for the ability to lay eggs and the presence of a viral plug. Four mutants (KS-3, KS-45, KS-52, KS-51) caused viral plug formation in 100% of the F1 female progeny (FIG. 2). No eggs were laid by F1 female progeny of female moths infected with the three mutants (indicative of an agonal phenotype (KS3, KS45, KS51) (FIG. 3). F1 female progeny of female moths infected with another mutant KS52 laid fewer eggs than F1 female progeny of female moths infected with WT virus on oviposition day 2 and no eggs on oviposition day 3.

The functional mutations defined by the applicant, KS-3, KS-45 and
KS-51, identify and localize to ORFs that have several unrelated direct repeated sequences ranging from 24 to 81 bp in size and having these sequence repeated from 4 to 12 times. These repeated sequences were identified by Burand et al., (2012). Such repeated sequences may have structural as well as coding roles and with some functions of repeated sequences involving recognition sites for DNA proteins and directing conformational changes of DNA that can promote DNA replication, DNA recombination and/or RNA transcription as examples. A similar repeated sequence exists in ORF 2 (direct repeat 1; Table 2; Burand et al., 2012) and is claimed herein as an identified sequence, region and ORF that is susceptible to mutation and such mutations are likely to impact DNA replication and recombination and the function of the virus relative to its effects on viral lysogeny and increased sterility among H. zea infected with mutations that alter ORF2 (SEQ ID NO: 3). It is notable that the 3 mutations defined by the applicant localize to ORFs 90 and 92 which contain 4 of the 6 repeated sequences in the HzNV2 genome. ORF 2 and ORF 91 contain the only other large repeated sequences in the viral genome and are thus obvious candidates for mutagenesis with an expectation that it would impact HzNV2 replication and recombination.

Table 2 shows additional data that compares genetically engineered and chemical mutant viruses. Progeny female moths developing from female moths infected with the genetically engineered recombinant virus, yfp HzNV-2 did not lay eggs and all F1 female progeny had viral plugs indicating their sterility. Similarly, essentially all F1 progeny of female moths infected with the chemical mutant viruses KS3, KS45, KS51, and KS52 had viral plugs and exhibited sterility (Table 2, FIGS. 2 and 3). By contrast, much smaller percentages (~33%) of insects infected with WT virus were agonadal (had plugs) with most moths infected with the WT HzNV-2 being fertile and laying many eggs (Table 2, FIG. 3). Similar results are seen on other oviposition days, although the number of female sterile moths in the F1 progeny of female moths injected with WT HzNV-2 increases at later oviposition days as reported in the literature (Hanmi et al., 1996; Burand 2013). These results support the hypothesis that inactivation of several nudivirus genes, for example, pg1 (SEQ ID NO: 6), ORF90 (SEQ ID NO: 4), and ORF92 (SEQ ID NO: 5) can cause sterility in essentially 100% of infected insects.

While it is to be recognized that viruses capable of being sexually transmitted among an insect pest species, can be mutated and selected using the described protocols without knowledge of specific genes involved in the phenotype of the resulting virus (for example, using the DUB protocol described above), some genes associated with increased sterility following viral infection have been identified by the Applicant. For example, the pg1, ORF 90, and ORF92 genes have been found by Applicant to be associated with increased sterility in virus-infected insects.

Infection of an Insect Using Modified HzNV-2

Published nudivirus literature describes various techniques for infecting and sterilizing H. zea moths with WT HzNV-2 but are lacking in various aspects such that a meaningful protocol can be carried out. Applicant has developed protocols that efficiently 1) infect the adult moth, 2) infect the moth offspring, and 3) mimic natural infections of moth populations in the field.

Method of Sterilizing the Offspring of Adult Moths. A Protocol for Producing Agonadal Infections with WT HzNV-2

To infect adult moths, the virus is injected into the abdomen of adult moths using an insulin syringe. In such experiments, WT virus collected from a viral plug effectively infected female adult moths and F1 progeny mimicking natural infected moth populations (i.e. 20-50% agonadal) (Table 3). Virus is collected by removing the plug from the abdominal area and suspending the plug in 100 µl PBS; this is called the unfiltered viral plug extract (UVPE). The virus is then diluted to 2% in 1x Grace’s media and filtered through a 0.22 micron filter to sterilize; this is called the filtered viral plug extract (FVPE). Applicant determined there was no difference in the percentage of agonadal F1 progeny when using either UVPE or FVPE for injections. (Table 3.) Applicant used FVPE for most experimentation.

### Table 3

<table>
<thead>
<tr>
<th>Oviposition day</th>
<th>Virus type</th>
<th># Females evaluated for plug</th>
<th>F1 progeny females with plug</th>
</tr>
</thead>
<tbody>
<tr>
<td>3</td>
<td>UVPE</td>
<td>46</td>
<td>33%</td>
</tr>
<tr>
<td>3</td>
<td>FVPE</td>
<td>25</td>
<td>36%</td>
</tr>
<tr>
<td>4</td>
<td>UVPE and FVPE</td>
<td>35</td>
<td>74%</td>
</tr>
</tbody>
</table>

Developing the Protocol to Generate a High Number of Agonadal Moths

Subsequent experimentation determined that injecting virus extracted from viral plugs results in a higher percentage of agonadal F1 progeny than injecting virus produced from infections of Sf9 cells in culture. Briefly, adult female moths were injected with 50-60 µl of either FVPE or virus amplified in cell culture. Eggs were collected on oviposition day 3 and reared to adults. F1 female progeny were evaluated for the presence of a plug. Almost all of the F1 female progeny developed a plug if F0 female moths were injected with viral plug extract, whereas only 10% of F1 progeny developed a plug if injected with virus collected from infected Sf9 cells. (Table 4).

### Table 4

<table>
<thead>
<tr>
<th>Virus type</th>
<th>Virus strain</th>
<th># Females evaluated for a plug</th>
<th>F1 female progeny females with plug</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cell culture</td>
<td>yfp HzNV-2</td>
<td>11</td>
<td>9%</td>
</tr>
<tr>
<td>Cell culture</td>
<td>KS-3</td>
<td>20</td>
<td>10%</td>
</tr>
<tr>
<td>Plug virus</td>
<td>yfp HzNV-2</td>
<td>26</td>
<td>100%</td>
</tr>
<tr>
<td>Plug virus</td>
<td>KS-3</td>
<td>20</td>
<td>95%</td>
</tr>
</tbody>
</table>

Thus, the titer of virus amplified in cell culture used for infection of adult moths was not optimal. Titer is an important factor in developing a method for creating high volumes of sterile insects. The optimal viral titer will be as low as possible but sufficient to cause agonadal adults. To assess the effects of virus titer, adult female moths were injected with either 10^7, 10^8, or 10^9 pfu/ml virus (WT or yfp HzNV-2) and mated with uninfected males. Eggs were collected on oviposition days 3-5, and reared to the adult stage. Moths were evaluated for the presence of a viral plug and egg production. Virus titer of 10^8 pfu/ml led to a high number of agonadal F1 progeny on oviposition day 5 (Table 5) indic-
cating that the virus replication in the host moth was important for effective transmission of the virus to the offspring eggs.

### TABLE 5

<table>
<thead>
<tr>
<th>Virus group</th>
<th>Virus dose</th>
<th>F1 progeny collected on oviposition day</th>
<th># females evaluated</th>
<th># eggs laid with plugs</th>
<th>F1 females with plugs</th>
</tr>
</thead>
<tbody>
<tr>
<td>Uninfected</td>
<td></td>
<td>Day 3</td>
<td>7</td>
<td>~30%</td>
<td>0%</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Day 4</td>
<td>6</td>
<td>14%</td>
<td>0%</td>
</tr>
<tr>
<td>WT-infected</td>
<td></td>
<td>Day 5</td>
<td>5</td>
<td>0%</td>
<td>0%</td>
</tr>
<tr>
<td></td>
<td>10&lt;sup&gt;7&lt;/sup&gt; pfu/ml</td>
<td>Day 4</td>
<td>5</td>
<td>~30%</td>
<td>0%</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Day 5</td>
<td>5</td>
<td>64%</td>
<td>22%</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Day 3</td>
<td>6</td>
<td>8%</td>
<td>0%</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Day 4</td>
<td>5</td>
<td>10%</td>
<td>20%</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Day 4</td>
<td>5</td>
<td>0%</td>
<td>100%</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Day 3</td>
<td>4</td>
<td>4%</td>
<td>0%</td>
</tr>
<tr>
<td></td>
<td>10&lt;sup&gt;7&lt;/sup&gt; pfu/ml</td>
<td>Day 4</td>
<td>4</td>
<td>0%</td>
<td>0%</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Day 5</td>
<td>2</td>
<td>5%</td>
<td>0%</td>
</tr>
<tr>
<td></td>
<td>10&lt;sup&gt;7&lt;/sup&gt; pfu/ml</td>
<td>Day 5</td>
<td>1</td>
<td>0%</td>
<td>0%</td>
</tr>
</tbody>
</table>

Injection of the recombinant virus into naïve male moths, followed by mating with healthy females, does not significantly reduce the number of eggs laid by female moths although the infection can be transmitted in this manner. However, when newly emerged female moths were injected with recombinant yfp HzNV-2 and mated with healthy males, the egg number was dramatically reduced (FIG. 4). This effect was dose-dependent as a viral dose of 1x10<sup>6</sup> pfu exhibited fewer eggs compared to a viral dose of 1x10<sup>7</sup> pfu. The total number of eggs laid by female moths injected with WT HzNV-2 was not reduced relative to media injected controls; this effect is only observed with the mutant and recombinant viruses.

Methods of Sterilizing Adult Moths by Injecting the Insects with Virus at the Larval Stage

An alternative protocol for inducing sterility is to inject virus into 3rd instar larval larvae such that the injected insects exhibit the sterile pathology as adults. While this is not the normal mode of transmission, larval injections are much faster, amenable to automation and likely mimic the activation of viral replication (Rallis et al., 2002-a). Applicant has created two protocols for inducing sterility in 3<sup>rd</sup> instar larval larvae: syringe injection and direct inoculation.

**Infection Using Syringe Injection**

Injecting supernatants from cultures of virus-infected cells into adult moths does not produce high numbers of gonadal offspring (Table 4). To determine if virus produced from infected, cultured insect cells effectively initiated productive virus infections when injected into larvae, Applicant injected virus-containing tissue culture medium into 3<sup>rd</sup> instar larvae. 3<sup>rd</sup> instar larvae (83 larvae per group) were injected using an insulin syringe with either WT HzNV-2, yfp HzNV-2, or KS-3 virus (25-50 µl) or not injected. Larvae were reared to adults. Surprisingly, none of the yfp HzNV-2-injected larvae pupated and eventually died (Table 6). However, ~95% of female larvae infected with either WT HzNV-2 or KS-3 virus produced a viral plug as adults (FIG. 5). Applicant concluded that while injecting virus amplified in tissue culture into adult moths does not produce many gonadal offspring, injecting virus amplified in tissue culture into 3<sup>rd</sup> instar larvae was an effective method as almost all moths became gonadal.

### TABLE 6

<table>
<thead>
<tr>
<th>Insects survived injection and pupation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Group</td>
</tr>
<tr>
<td>-------------</td>
</tr>
<tr>
<td></td>
</tr>
</tbody>
</table>

Injection of viral plug extract into 3<sup>rd</sup> instar larvae with an insulin syringe was also evaluated. Briefly, WT HzNV-2 and yfp HzNV-2 FVPE was diluted to 7x10<sup>5</sup> pfu/ml and 25 µl was injected into 3<sup>rd</sup> instar larvae. Larvae were reared to adults and female moths were evaluated for the presence of a plug. Female moths that were injected as larvae with a titer of 10<sup>5</sup> pfu/ml developed a viral plug, whereas only ~80% of those injected with 10<sup>2</sup> pfu/ml developed a viral plug (Table 7). Applicant concluded that injecting 3<sup>rd</sup> instar larvae with viral plug extract was also highly effective at developing agonal adult, but titer should be around 10<sup>5</sup> pfu/ml.

### TABLE 7

<table>
<thead>
<tr>
<th>Infection group</th>
<th>Virus titer (pfu/ml)</th>
<th>Females with plugs</th>
</tr>
</thead>
<tbody>
<tr>
<td>Uninfected</td>
<td>0</td>
<td>0%</td>
</tr>
<tr>
<td>W T-infected</td>
<td>1 x 10&lt;sup&gt;7&lt;/sup&gt;</td>
<td>50%</td>
</tr>
<tr>
<td>K3-infected</td>
<td>1 x 10&lt;sup&gt;7&lt;/sup&gt;</td>
<td>100%</td>
</tr>
<tr>
<td>yfp-HzNV2-infected</td>
<td>4 x 10&lt;sup&gt;7&lt;/sup&gt;</td>
<td>100%</td>
</tr>
</tbody>
</table>

**Infection Using Direct Inoculation Using a Pin**

Direct injection of third instar larvae or moths are efficient methods for infecting HzNV-2 in the laboratory, but feeding is a preferred method.

**Infecting H. zea with WT HzNV-2 via an oral route of infection is possible.** Raina et al. (2006) fed WT HzNV-2 to 1<sup>st</sup> instar larvae for 1-3 days and found that 9-17% (varies based on gender and duration of feeding) of adults became agonal. Hamm et al. (1996) fed WT HzNV-2 to adult moths in an aqueous solution and from 60-100% of the offspring adults were agonal. The HzNV-2 genome also encodes genes related to four baculovirus genes (p74, pif-1, pif-2, and pif-3) whose protein products are involved in viral entry per os (Burand, Kim, Afonso et al. 2012). Although the natural route of infection for HzNV-2 is through mating and/or transovarial transmission, other methods for infecting insects include direct inoculation and feeding of both larvae and adults.

**A direct inoculation method for transmitting the virus to 3<sup>rd</sup> instar larvae (Table 8) was developed and may be amenable to automation. This method is similar to that used by Hamm et al., (1996) to infect 1<sup>st</sup> instar larvae with viral
plug extract with 9 of 10 larvae becoming agonadal as adults. Direct inoculation is a rapid means to introduce virus into H. zea larvae in which a sterile pin is dipped into the viral solution and then used to prick larvae between the head capsule and abdomen with sufficient force to penetrate the cuticle and enter the insect’s body cavity. WT HzNV-2 (A, B) virus obtained from two different cell culture infections (A and B) were used for direct inoculation. The pricked larvae were reared to adult moths, and female moths were evaluated for the presence of a plug. 57% (WT A) and 16% (WT B) of moths were agonadal.

To test virus isolated from plugs, ~10^8 pfu/ml of WT HzNV-2 or recombinant yfp HzNV-2 viruses were isolated, filter sterilized and used in direct inoculation experiments. The inoculated larvae were reared to adult moths and mated. All female moths developing from larvae inoculated with recombinant yfp HzNV-2 were sterile (no eggs laid; plugs in 100% of females). Upon dissection, all male moths examined were found to be agonadal.

For larvae inoculated with WT HzNV-2, 90% of female moths had a viral plug with the number of eggs laid commensurately reduced relative to controls (Table 8). In summary, the direct inoculation method not only was as efficient as injecting the virus into larvae, it also was much faster.

**TABLE 8**

<table>
<thead>
<tr>
<th>Group</th>
<th># of eggs laid</th>
<th>% Female moths with plugs</th>
<th>State of reproductive organs in male moths* **</th>
</tr>
</thead>
<tbody>
<tr>
<td>Unpricked</td>
<td>High</td>
<td>0</td>
<td>0% agonadal</td>
</tr>
<tr>
<td>Medium control</td>
<td>High</td>
<td>0</td>
<td>0% agonadal</td>
</tr>
<tr>
<td>WT HzNV-2</td>
<td>Low</td>
<td>0</td>
<td>0% agonadal</td>
</tr>
<tr>
<td>yfp HzNV2</td>
<td>None</td>
<td>100</td>
<td>100% agonadal</td>
</tr>
</tbody>
</table>

*large >700 eggs; low <200 eggs; **determined by dissecting reproductive organs of H. zea males.

To investigate effects of titer on the direct inoculation method WT HzNV-2 isolated from a viral plug was diluted to 10^6 pfu/ml and used to inoculate 3rd instar larvae. Only 18% of WT-HzNV-2 pricked females were agonadal with the 10^5 pfu/ml inoculum. Many females, termed carriers, are infected with virus but have inactive or latent infections. Moths having latent infections have intact, functional reproductive tracts but can transmit the virus horizontally and vertically to their offspring. PCR using a primer set to the HzNV-2 ORF78 was performed, and all 20 of the females without viral plugs tested were carriers. Applicant concluded that use of direct inoculation with a lower titer of 10^6 pfu/ml to infect 3rd instar larvae created a carrier population.

Method of Protecting a Crop from Pest Insects

The instant disclosure addresses a method for control of lepidopteran pest moths by rendering them sterile from infection with mutant or transgenic HzNV-2. The delivery of HzNV-2 or a mutant form thereof in accordance with the disclosed methods and compositions to the targeted population may be through established methods for release of moths for sterile insect control. In one aspect, the moths or other pest infected with a mutant virus as disclosed herein, are released at point locations and permitted to disperse over a range. The range may be, for example, about 800 meters from the release site or released aerially from planes, helicopters or drones. Moths infected with mutant or recombinant HzNV-2 may be released after infection using one or more of the disclosed methods at ratios from 0.1 infected moths/WT moth in the field population. Targeted release at lower ratios may rely on generational transmission of the infection for control and may require supplemental release on virus-infected adult moths.

**REFERENCES**


CABI 2015 http://www.cabi.org/isc/datasheet/26776


Capinera 2000, revised 2007 UF/IFAS Extension http://entomology.ifas.ufl.edu/creatures.


U.S. Pat. No. 7,476,499: “Methods of identifying anti-viral agents” (use of DEB as mutagen)


What is claimed is:

1. A genetically modified *Helicoverpa zea* nudivirus 2 (HzNV-2) virus, having a mutation in a region selected from Open Reading Frame 90 (ORF90), Open Reading Frame 92 (ORF92), Persistence-associated Gene (pag1), or a combination thereof, to disrupt expression of the gene product encoded by said mutant region, wherein said mutation increases the rate of an agonadal phenotype in a progeny of a *Helicoverpa zea* (*H. zea*) moth infected with said genetically modified HzNV-2 as compared to a progeny of a *H. zea* moth infected with a wild-type HzNV-2 virus.

2. The genetically modified nudivirus of claim 1, wherein said genetically modified HzNV-2 virus is achieved via chemical mutagenesis.

3. The genetically modified nudivirus of claim 1, wherein said genetically modified HzNV-2 virus is achieved via recombinant DNA technology.

4. The genetically modified nudivirus of claim 1, wherein said genetically modified HzNV-2 virus is achieved via gene editing technology.

5. An insect infected with the virus of claim 1.

6. The insect of claim 5, wherein said insect is *H. zea*.

7. A method of protecting a crop susceptible to *H. zea* moth crop damage, comprising the step of introducing an *H. zea* moth infected with the genetically modified nudivirus of claim 1 into said crop.

* * * * *