Title: 1143-51B INSECTICIDAL COTTON

Abstract: The present application relates an insect resistant transgenic cotton plant. In particular, it relates to a specific event, designated 1143-51B. The application also relates to polynucleotides which are characteristic of the 1143-51B event, plants comprising said polynucleotides, and methods of detecting the 1143-51B event.
1143-51B INSECTICIDAL COTTON

The present invention relates to *inter alia*, polynucleotides and methods of use thereof and in particular to cotton plants comprising said polynucleotides. Specifically, the invention relates to a cotton event designated 1143-51B which comprises a Cry1Ab gene. The invention also relates to methods of identifying specific cotton events which contain a gene capable of conferring insect resistance on said cotton plants.

Plant pests are a major factor in the loss of the world’s important agricultural crops. About $8 billion is lost every year in the U.S. due to infestations of plants by non-mammalian pests including insects. In addition to losses in field crops, insect pests are also a burden to vegetable and fruit growers, to producers of ornamental flowers, and to home gardeners.

Insect pests are mainly controlled by intensive applications of chemical pesticides, which are active through inhibition of insect growth, prevention of insect feeding or reproduction, or cause death. Good control of insect pests can thus be reached, but these chemicals can sometimes also affect other, beneficial insects. Another problem resulting from the wide use of chemical pesticides is the appearance of resistant insect varieties. This has been partially alleviated by various resistance management practices, but there is an increasing need for alternative pest control agents. Biological pest control agents, such as *Bacillus thuringiensis* strains expressing pesticidal toxins like δ-endotoxins, have also been applied to crop plants with satisfactory results, offering an alternative or compliment to chemical pesticides. The genes coding for some of these δ-endotoxins have been isolated and their expression in heterologous hosts has been shown to provide another tool for the control of economically important insect pests. In particular, the expression of the insecticidal toxin Cry1Ac from *Bacillus thuringiensis* in transgenic plants, has provided efficient protection against selected insect pests, and transgenic plants expressing this toxin have been commercialised, allowing farmers to reduce applications of chemical insect control agents.

Cry1Ac is one of a large family of insecticidal toxins produced by different strains of *Bacillus thuringiensis*. Each toxin in the family has a unique spectrum of insecticidal activity.
The cotton family, genus Gossypium, a member of the Malvaceae, consists of 39 species, of which *Gossypium hirsutum* is the most commonly cultivated species. Three other species are also cultivated: *G. arboreum*, *G. barbadense*, and *G. herbaceum*. These cultivated species are grown primarily for the seed hairs that are made into textiles. Cotton is suitable as a textile fibre because the mature dry hairs twist in such a way that fine strong threads can be spun from them. Other products, such as cottonseed oil, cake, and cotton linters are by-products of fibre production.

Damage to cotton crops by insect pests throughout the world results in a significant yield loss each year. Effective control of these pests to minimise yield loss is of great economic importance. Examples of insect pests of cotton include Beet armyworm (*Spodoptera exigua*), Boll weevil (*Anthonomus grandis grandis*), Cabbage looper (*Trichoplusia ni*), Clouded plant bug (*Neurocolpus nubilus*), Cotton aphid (*Aphis gossypii*), Cotton bollworm (*Helicoverpa zea*), Cutworms (*Feltia subterranea, Peridroma saucia, Agrotis ipsilon*), European corn borer (*Ostrinia nubilalis*), Fall armyworm (*Spodoptera frugiperda*), Pink boll worm (*Pectinophera gossypiella*), Seedling thrips (*Frankliniella* spp.), Soybean looper (*Pseudoplusia includens*), Stink bugs (*Nezara viridula, Acrosternum hilare, Euschistus servus*), Tarnished plant bug (*Lygus lineolaris*), Tobacco budworm (*Heliothis virescens*) and Whiteflies (*Trialeurodes abutilonea, Bemisia tabaci*).

Transformation and regeneration of cotton plants is now a well-established procedure, typically based on *Agrobacterium tumefaciens* mediated transfer of foreign DNA into cotton plant parts and regeneration of said plant parts in tissue culture into fully fertile, transgenic cotton plants.

There exists a requirement to generate a new cotton plant that is insect resistant so that yield loss through damage to cotton crops by insect pests is reduced. An insect resistant cotton plant could reduce the need to apply chemical pesticides, which may be detrimental to other, beneficial insects and the environment. In particular, it is desirable to provide an alternative insect resistant plant to transgenic plants comprising the Cry1Ac gene from *Bacillus thuringiensis*. 
The present invention provides, *inter alia*, a specific cotton event (referred to hereinafter as “1143-51B”) and methods for the identification thereof. This specific event has been selected based on, *inter alia*, its agronomic performance, efficacy and molecular characteristics. It is believed that the characteristics of this event are far superior to like transformants based upon, *inter alia*, the integration site of the transgene during the transformation process.

“1143-51B event” in the context of this application refers to the original insecticidal transgenic cotton plant described herein and any plant material derived therefrom, including seeds. “Insecticidal” as used herein refers to any inhibitory effect on an insect, including but not limited to reduced feeding, retarded growth, reduced fecundity, paralysis or death. “Fecundity” comprises all aspects related to reproduction such as reproductive ability, reproductive frequency and number of offspring. Also embraced by this invention is any plant material derived from the 1143-51B event, including seeds.

The 1143-51B event exhibits a novel genotype comprising at least one expression cassette. The cassette comprises a suitable promoter for expression in plants operably linked to a gene that encodes a Cry1Ab insecticidal toxin, useful in controlling a wide spectrum of lepidopteran insect pests, and a suitable polyadenylation signal. Suitable promoters may be isolated from, *inter alia*, plants. Numerous plant promoters have been isolated and characterised including constitutive, switchable and/or tissue specific promoters. Suitable promoters may be selected from the following, non-limiting group: CaMV35S, FMV35S, Ubiquitin, Act2, NOS, OCS, Cestrum yellow leaf curl virus promoter, Patatin, E9, alcA/alcR switch, GST switch, RMS switch, oleosin, Gelvin, ribulose bisphosphate carboxylase-oxygenase small sub-unit, actin 7, MR7 promoter (maize), Gos 9 (rice), GOS2 promoters, MasOcs (or super promoter), RolD promoter (*Agrobacterium rhizogenes*), SuperMAS promoter, and Suc2 promoter (*Arabidopsis*). In one embodiment of the present invention, the promoter is the Actin promoter, ACT2, from *Arabidopsis thaliana*.

Additional elements such as enhancer sequences may also be incorporated into the expression cassette in order to boost levels of gene expression, for example transcriptional or translational enhancers, such as tobacco etch virus (TEV) translation activator, CaMV35S enhancer, and FMV35S enhancer. Alternatively it may be desirable to include a targeting sequence, for example, to direct transportation of the Cry1Ab toxin to a
particular cellular compartment. For example, if it is desired to provide the protein outside of the cell then an extracellular targeting sequence may be ligated to the polynucleotide encoding the Cry1Ab protein. Other examples of targeting include targeting to a specific intracellular organelle or compartment, for example to the endoplasmic reticulum using a ‘KDEL’ retention sequence. Numerous polyadenylation signals have been isolated and characterised. Examples of suitable polyadenylation signals functional in plants include that from the nopaline synthase gene (nos) of Agrobacterium tumefaciens, from the proteinase inhibitor II gene and from the alpha-tubulin gene (EP-A 652,286). In one embodiment of the present invention, the polyadenylation signal is that from the nos gene of Agrobacterium tumefaciens.

The polynucleotide encoding the Cry1Ab protein may be codon-optimised or otherwise altered to enhance for example, translation once it is incorporated into plant material. Such codon optimisation may also be used to alter the predicted secondary structure of the RNA transcript produced in any transformed cell, or to destroy cryptic RNA instability elements present in the unaltered transcript, thereby increasing the stability and/or availability of the transcript in the transformed cell (Abler and Green (1996) Plant Molecular Biology (32) pp.63-78). Codon optimisation may also be employed to alter a heterologous DNA coding sequence so that it more closely resembles the coding sequence of a gene of the host. For example, a bacterial gene can be codon optimised to increase the ratio of cytosine and guanine bases to adenine and thymine bases so that it more closely resembles a plant (e.g. cotton or maize) gene, yet encodes the same protein. Such codon optimisation may be performed in accordance with standard codon usage tables.

In a precursor to the 1143-51B event, a second cassette is present that comprises a gene which, when expressed, can be used as a selectable marker. Numerous selectable markers have been characterised, including some that confer tolerance to antibiotics and others that confer tolerance to herbicides. Examples of suitable selectable marker genes include those that confer tolerance to hygromycin, kanamycin or gentamycin. Further suitable selectable markers include genes that confer resistance to herbicides such as glyphosate-based herbicides or resistance to toxins such as eutypine. Other forms of selection are also available such as hormone based selection systems such as the Multi Auto Transformation (MAT) system of Hiroyrasu Ebinuma et al. (1997) PNAS Vol. 94 pp.2117-2121; visual
selection systems which use the known green fluorescence protein, β glucuronidase; and any other selection system such as mannose isomerase (Positech™), xylose isomerase and 2-deoxyglucose (2-DOG). In one embodiment of the present invention, the selectable marker gene is one that confers tolerance to hygromycin. This second expression cassette is useful for selecting transformants during and following plant transformation. Optionally, it may be segregated away from the 1143-51B event precursor after transformation to leave the 1143-51B event itself. The 1143-51B event per se does not comprise a selectable marker cassette. Further expression cassettes are optionally comprised in the 1143-51B event. For example these may provide genes encoding different insecticidal toxins such as VIP3A. Alternatively, these may provide other desirable benefits such as herbicide resistance.

The expression cassettes may be introduced into the plant on the same or different plasmids. If the expression cassettes are present on the same plasmid and introduced into the plant via an Agrobacterium-mediated transformation method, they may be present within the same or different T-DNA regions. In one embodiment of the present invention, two expression cassettes are present on different T-DNA regions within different plasmids. According to the present invention there is provided a polynucleotide which comprises the sequence depicted as SEQ ID NO: 1.

In a further embodiment said polynucleotide comprises a region which can be amplified by an amplification reaction which reaction uses the primers depicted as SEQ ID NO: 3 and 4. In a still further embodiment said polynucleotide comprises a still further region which encodes a Cry1Ab gene from Bacillus thuringiensis. In a still further embodiment said polynucleotide comprises a region which provides for the Arabidopsis actin promoter operably linked to said Cry1Ab gene.

In a further aspect of the invention there is provided a polynucleotide which comprises at least 18 contiguous nucleotides of the sequence depicted as SEQ ID NO: 2. Still further provided is a polynucleotide which comprises at least 20 contiguous nucleotides of the sequence depicted as SEQ ID NO: 2. Still further provided is a polynucleotide which comprises at least 25 contiguous nucleotides of the sequence depicted as SEQ ID NO: 2.
Still further provided is a polynucleotide which comprises the sequence depicted as SEQ ID NO: 2.

Still further provided is a polynucleotide which comprises at least 35 contiguous nucleotides of the sequence depicted as nucleotides 145 to 204 of SEQ ID NO: 1. Still further provided is a polynucleotide comprising at least 40 contiguous nucleotides of the sequence depicted as nucleotides 145 to 204 of SEQ ID NO: 1. Still further provided is a polynucleotide comprising at least 50 contiguous nucleotides of the sequence depicted as nucleotides 145 to 204 of SEQ ID NO: 1. Still further provided is a polynucleotide comprising the sequence depicted as nucleotides 145 to 204 of SEQ ID NO: 1.

Still further provided is a polynucleotide comprising at least 50, 100, 150, 200, 300, 400 or 500 contiguous nucleotides of SEQ ID NO: 1, said polynucleotide containing the nucleotide junction between nucleotides 174 and 175 of SEQ ID NO: 1. Still further provided is a polynucleotide which comprises the sequence depicted as SEQ ID NO: 1.

Still further provided is a sequence which is the complement of a sequence described above.

In a further embodiment there is provided a cotton plant which comprises a polynucleotide described above. In a still further embodiment there is provided a cotton seed which comprises the polynucleotide as described above. In a further embodiment, said plant is an insecticidal cotton plant which is a precursor to the 1143-51B event, the 1143-51B event per se, or a plant derived therefrom that still comprises a polynucleotide as described above. In a further embodiment said plant comprises a second expression cassette. In one embodiment said second expression cassette encodes a VIP3A insecticidal toxin. In another embodiment, said second expression cassette encodes a protein that provides resistance to a herbicide which comprises glyphosate acid or an agriculturally acceptable salt thereof.

The skilled man is familiar with plant transformation methods. In particular, two principal techniques have been characterised across a wide range of plant species: transformation by Agrobacterium and transformation by direct DNA transfer.
*Agrobacterium*-mediated transformation is a commonly used method for transformation of dicotyledonous plants. The foreign DNA to be introduced into the plant is cloned into a binary vector in between left and right border consensus sequences. This is the T-DNA region. The binary vector is transferred into an *Agrobacterium* cell, which is subsequently used to infect plant tissue. The T-DNA region of the vector comprising the foreign DNA is inserted into the plant genome. The marker gene cassette and trait gene cassette may be present on the same T-DNA region, different T-DNA regions in the same vector, or even different T-DNA regions in different vectors. In one embodiment of the present invention, the cassettes are present on different T-DNA regions on different vectors.

Alternatively, direct DNA transfer can be used to introduce the DNA directly into a plant cell. One suitable method of direct transfer may be bombardment of plant cells with a vector comprising the DNA for insertion using a particle gun (particle-mediated biolistic transformation); another established method, ‘whiskers’, involves coating the DNA onto silicon carbide fibres onto which cells are impaled. Other methods for transforming plant cells include protoplast transformation (optionally in the presence of polyethylene glycols); sonication of plant tissues, cells or protoplasts in a medium comprising the polynucleotide or vector; micro-insertion of the polynucleotide or vector into plant material (optionally employing the known silicon carbide “whiskers” technique), electroporation and the like.

Following transformation, transgenic plants are regenerated from the transformed plant tissue, and progeny possessing the foreign DNA selected using an appropriate marker such as resistance to hygromycin. The skilled man is familiar with the composition of suitable regeneration media. The selectable marker can be segregated away from transgenic events by conventional plant breeding methods, thus resulting in, for example, the 1143-51B event.

A plant of the invention, as described herein, has an insecticidal effect on insects from one or more species from the group comprising *Heliothis* sp. and *Helicoverpa* sp. which may infest it. “Infest” as used herein refers to attack, colonisation, feeding or damage in any way by one or more insects. Thus, for example, the plant of the present invention will provide a self-defence mechanism against infestation by pest insects such as *Helicoverpa*
zea (cotton boll worm). As a result, a reduced number of insecticide sprays are required during the cultivation of said plant compared to a non-transgenic cotton plant of the same variety and yield loss through insect pests is kept at a minimal level.

The present invention is not limited to the 1143-51B event itself, but is further extended to include any plant material derived therefrom, including seeds in so far as they contain at least one of the present inventive polynucleotides. The present invention includes, but is not limited to plants that are derived from a breeding cross with the 1143-51B event or a derivative therefrom by conventional breeding or other methods. The invention also includes plant material derived from the 1143-51B event that may comprise additional, modified or fewer polynucleotide sequences compared to the 1143-51B event or exhibit other phenotypic characteristics. For example, it may be desirable to transform plant material derived from the 1143-51B event to generate a new event that possesses an additional trait, such as a second insect resistance gene. This process is known as gene stacking. The second insect resistance gene may encode, for example insecticidal lectins, insecticidal protease inhibitors and insecticidal proteins derived from species of the Bacillus thuringiensis, Xenorhabdus nematophilus, or Photorhabdus luminescens. In one aspect, the second insect resistance gene encodes an insecticidal gene from Bacillus thuringiensis. Preferably, the second insect resistance gene encodes a VIP gene from the bacterium Bacillus thuringiensis, which VIP gene produces a toxin with a different mode of action or binding site in the insect gut to Cry1Ab for the control of different insect species. The VIP gene may, for example, be VIP3A.

The present invention further provides plant material derived from the 1143-51B event which possesses an additional trait such as herbicide resistance, nematode resistance or fungal resistance. In one embodiment, said additional trait is herbicide resistance. The herbicide resistance trait may be provided, for example, by a herbicide degradation enzyme, or a target-site specific resistant enzyme. In a further embodiment, said herbicide resistance trait provides resistance to a herbicide which comprises glyphosate acid or an agriculturally acceptable salt thereof. In a further embodiment still, said herbicide resistance trait is provided by a gene encoding EPSP synthase or a mutant thereof.
The present invention further provides a method of controlling insects comprising providing the 1143-51B event or plant material derived from the 1143-51B event at a locus where said insects feed. The invention yet further provides a method of controlling insects comprising providing the 1143-51B event or plant material derived from the 1143-51B event at a locus where said insects feed, and applying other agrochemicals to said plant material such as herbicides, fungicides and other insecticidal compounds including other insecticidal proteins. Examples of possible insecticidal compounds include insecticidal lectins, insecticidal protease inhibitors and insecticidal proteins derived from species of the Bacillus thuringiensis, Xenorhabdus nematophilus, or Photorabdus luminescens.

Examples of possible chemicals include pyrethroids, carbamates, imidacloprid, organochlorines, and macromolecules such as spinosad, abamectin or emamectin.

The present invention further provides a method for detecting plant material which is derived from the 1143-51B event, said method comprising: (a) preparing a sample containing the genomic DNA of the plant material to be tested; (b) obtaining a pair of primers which are suitable for use in an amplification reaction to amplify a sequence comprising at least 18 contiguous nucleotides of the sequence depicted as SEQ ID NO: 2 or the complement thereof; (c) adding said pair of primers to said sample and the means for performing an amplification reaction; (d) performing an amplification reaction; and (e) visualising the thus amplified sequence.

There are many amplification methods that may be used in accordance with the methods of the invention. The underlying principle, a known technique to those skilled in the art, is the polymerase chain reaction (PCR). The amplification product from a PCR reaction may be visualised by staining with ethidium bromide and excitation with UV light, typically after size separation using agarose gel electrophoresis. In a particular embodiment of the invention variations of the PCR principle such as TaqMan™ may be used. Such techniques involve labelling at least one of the primers involved in the amplification process with a fluorescent dye. When unbound, the primer adopts a conformation such that no fluorescence can be detected. However, when the primer is bound to a piece of DNA, the conformation changes and fluorescence can be detected. In this way, the amplification process can be monitored in real-time, the intensity of fluorescence corresponding directly to the level of amplification.
TaqMan™ analysis may be useful for example, for detecting the presence of the 1143-51B event in a background of wild type cotton, or for detecting the adventitious presence of 1143-51B in other germplasm. Further embodiments of the present invention include, but are not limited to, RACE PCR.

A further embodiment of the present invention involves the use of multiplex PCR for distinguishing between homozygous 1143-51B plant material and heterozygous 1143-51B plant material. This is known to those skilled in the art as zygosity testing, and involves the use of three PCR primers which bind to specific parts of the cotton genome and / or inserted DNA. The presence or absence of each of two amplification products of particular sizes indicates whether the test sample is hemizygous or homozygous for 1143-51B.

The present invention further provides a method for detecting a plant which contains the polynucleotide depicted as SEQ ID NO: 1 said method comprising: (a) preparing a sample containing the genomic DNA of the plant to be tested; (b) obtaining a pair of primers which are suitable for use in an amplification reaction to amplify a sequence comprising at least 18 contiguous nucleotides of the sequence depicted as SEQ ID NO: 2 and the complement thereof; (c) adding said pair of primers to said sample and the means for performing an amplification reaction; (d) performing an amplification reaction; and (e) visualising the thus amplified sequence.

The present invention further provides a method as described above wherein said primers are suitable for use in an amplification reaction to amplify a sequence comprising at least 20 contiguous nucleotides of the sequence depicted as SEQ ID NO: 2 and the complement thereof. In a still further embodiment said primers are suitable for use in an amplification reaction to amplify a sequence comprising at least 25 contiguous nucleotides of the sequence depicted as SEQ ID NO: 2 and the complement thereof. In a still further embodiment said primers are suitable for use in an amplification reaction to amplify a sequence comprising the sequence depicted as SEQ ID NO: 2 and the complement thereof.

The present invention still further provides a method as described above wherein the sequence to be amplified by said amplification reaction comprises a sequence containing
the nucleotide junction of genomic sequence-transgene cassette insert (t-a) provided as nucleotides 174/175 of SEQ ID NO: 1. The person skilled in the art will appreciate that this junction can be used to characterise and thus identify the event and so it is well within the ambit of said skilled person to design and produce oligonucleotide primer sequences that are suitable for use in an amplification reaction to amplify the sequence which comprises the aforesaid junction. The person skilled in the art will also appreciate that the primer sequences suitable for use in an amplification reaction may be designed based on the genomic sequence which is 5' i.e. upstream of nucleotide number 1 of SEQ ID NO: 1 and the insert or genomic sequence which is 3' i.e. downstream of nucleotide number 589 of SEQ ID NO: 1.

The present invention further provides a method for detecting a plant which contains the polynucleotide depicted as SEQ ID NO: 1 said method comprising: (a) preparing a sample containing the genomic DNA of the plant to be tested; (b) obtaining a pair of primers which are suitable for use in an amplification reaction to amplify a sequence comprising at least 35 contiguous nucleotides of the sequence depicted as nucleotides 145 to 204 of SEQ ID NO: 1 and the complement thereof; (c) adding said pair of primers to said sample and the means for performing an amplification reaction; (d) performing an amplification reaction; and (e) visualising the thus amplified sequence. In a further embodiment said primers are suitable for use in an amplification reaction to amplify a sequence comprising at least 40 contiguous nucleotides of the sequence depicted as nucleotides 145 to 204 of SEQ ID NO: 1. In a further embodiment said primers are suitable for use in an amplification reaction to amplify a sequence comprising at least 50 contiguous nucleotides of the sequence depicted as nucleotides 145 to 204 of SEQ ID NO: 1. In a further embodiment said primers are suitable for use in an amplification reaction to amplify a sequence comprising the sequence depicted as nucleotides 145 to 204 of SEQ ID NO: 1.

In a still further embodiment said primers are suitable for use in an amplification reaction to amplify a sequence comprising at least 50, 100, 150, 200, 300, 400 or 500 contiguous nucleotides of SEQ ID NO: 1 said sequence containing the nucleotide junction between nucleotides 174 and 175 of SEQ ID NO: 1. The primers referred to above are suitable for use in an amplification reaction to amplify the sequences mentioned above and the complementary sequences thereof.
The present invention still further provides a sequence which is the amplification product of the method described above.

The present invention still further provides a sequence which is the complement of a sequence described above.

The present invention still further provides a method as mentioned above wherein the thus amplified product comprises a sequence as described above.

The present invention still further provides a method as described above wherein said pair of primers comprise a forward primer which comprises a sequence which when read in the 5'→3' direction is identical to a region of the sequence depicted as nucleotides 1 to 174 of SEQ ID NO: 1 and a reverse primer which comprises a sequence which when read in the 5'→3' direction is identical to a region of the reverse complement of the sequence depicted as nucleotides 175 to 589 of SEQ ID NO: 1. The person skilled in the art will recognise that a number of primers suitable for use in the methods of the invention may be created based on the sequences provided herein and the complementary sequences thereto. In addition to this, as mentioned above, such primer sequences may be based on the sequence 5' and 3' (upstream and downstream) of the sequences depicted as SEQ ID NO: 1 and it is well within the capability of the skilled person to identify such 5' and 3' sequence.

In a particular embodiment of the invention said pair of primers comprise the sequences depicted as SEQ ID NO: 3 and 4.

The present invention still further provides a method for detecting plant material derived from the 1143-51B event, said method comprising: (a) preparing a sample containing the genomic DNA of the plant to be tested; (b) obtaining a probe which is capable of hybridising to a sequence comprising at least 18 contiguous nucleotides of the sequence depicted as SEQ ID NO: 2; (c) adding the probe to said sample under conditions which allow said probe to hybridise with a complementary nucleic acid within said sample; (d) removing substantially non-hybridised probe by washing; and (e) detecting the thus hybridised probe to identify if the sample is from the 1143-51B event.
The present invention further provides a method for detecting a plant which contains the polynucleotide depicted as SEQ ID NO: 1 said method comprising (a) preparing a sample containing the genomic DNA of the plant to be tested; (b) obtaining a probe which is capable of hybridising to a sequence comprising at least 18 contiguous nucleotides of the sequence depicted as SEQ ID NO: 2; (c) adding the probe to said sample under conditions which allow said probe to hybridise with a complementary nucleic acid within said sample; (d) removing substantially non-hybridised probe by washing; and (e) detecting the thus hybridised probe to identify if the sample contains said polynucleotide.

In a particular embodiment of the methods described above said probe comprises at least 20 contiguous nucleotides. In a still further embodiment of said method, said probe comprises at least 50, 100, 150, 200, 300, 400 or 500 contiguous nucleotides of SEQ ID NO: 1, said probe containing the nucleotide junction between nucleotides 174 and 175 of SEQ ID NO: 1. In a still further embodiment of the invention, said probe may comprise a fragment of a relevant polynucleotide described within this specification. In particular, said probe may comprise a polynucleotide sequence which is capable of hybridising with a sequence which characterises the event described in the present application. In a still further embodiment of said method, said washing takes place under high stringency conditions. Said probe may be generated and labelled using techniques well known to the person skilled in the art.

The probe may be, for example, a PCR product or restriction digestion fragment. In a further embodiment, the probe as described herein may be tagged with a fluorescent, radioactive, enzymatic or other suitable label to enable hybridisation to be detected.

In a still further embodiment of the present invention there is provided a method of hybridising a probe to the complementary nucleic acid within the sample under stringent conditions and detecting whether the probe has hybridised. High stringency hybridisation conditions are well known to the skilled person and comprise, for example: hybridisation at a temperature of about 65°C in a solution containing 6 x SSC, 0.01% SDS and 0.25% skimmed milk powder, followed by rinsing at the same temperature in a solution containing 0.2 x SSC and 0.1% SDS. The skilled person may alternatively select the following hybridisation conditions, viz., hybridisation at a temperature of between 60°C
and 65°C in 0.3 strength citrate buffered saline containing 0.1% SDS followed by rinsing 
at the same temperature with 0.3 strength citrate buffered saline containing 0.1% SDS. 
The person skilled in the art may also select further hybridisation conditions that are 
equally understood to be “high stringency” conditions. Suitable techniques for detecting 
plant material derived from the event described herein based on the hybridisation principle 
include, but are not limited to Southern Blots, Northern Blots and in-situ hybridisation. 
The skilled person is familiar with these techniques. Typically, they involve incubating a 
probe with a sample, washing to remove unbound probe, and detecting whether the probe 
has hybridised. Said detection method is dependent on the type of tag attached to the 
probe – for example, a radioactively labelled probe can be detected by exposure to and 
development of x-ray film. Alternatively, an enzymatically labelled probe may be detected 
by conversion of a substrate to effect a colour change. 

In a still further aspect there is provided a method for identifying a plant comprising the 
1143-51B event, said method comprising (a) preparing a sample containing the genomic 
DNA of the plant to be tested; (b) digesting said DNA via a restriction enzyme; (c) 
separating the digested DNA fragments and transferring the thus separated fragments to a 
membrane; (d) probing the thus bound fragments with a probe, designed as described 
above, which probe has be labelled to allow its visualisation; (e) removing substantially 
non-hybridised probe; and (f) detecting the thus hybridised probe wherein said event can 
be characterised by said probe hybridising to fragments having a particular size. 

In a further aspect there is provided a cotton event which is capable of being identified by a 
method according to the invention. In a particular embodiment said method is the one 
according to the preceding paragraph. 

The present disclosure also includes a method for detecting a plant which contains a 
protein capable of being encoded by a polynucleotide depicted as SEQ ID NO: 5, said 
method comprising: (a) preparing a protein-extract of the plant to be tested; (b) providing 
an antibody which is capable of binding to a Cry1Ab protein from Bacillus thuringiensis; 
(c) adding said antibody to said extract under conditions which allow said antibody to bind 
to said protein within said extract; and (d) detecting the thus bound antibody to identify if 
the extract contains said protein.
The present disclosure also includes a method for detecting a plant which comprises a Cry1Ab gene from *Bacillus thuringiensis* said method comprising: (a) preparing a protein-extract of the plant to be tested; (b) providing an antibody which is capable of binding to a Cry1Ab protein from *Bacillus thuringiensis*; (c) adding said antibody to said extract or said extract to said antibody under conditions which allow said antibody to bind to said Cry1Ab protein within said extract; and (d) detecting the thus bound antibody to identify if the extract contains said Cry1Ab protein. This method is useful for distinguishing between plants expressing Cry1Ab, such as plants comprising 1143-51B, and plants not-expressing Cry1Ab.

Suitable methods of detecting plant material derived from the event described herein which methods are based on said antibody binding include, but are not limited to Western Blots, Enzyme-Linked ImmunoSorbent Assays (ELISA) and SELDI mass spectrometry. The skilled person is familiar with these and further immunological techniques. Typical steps include incubating a sample with an antibody that binds to the said protein, washing to remove unbound antibody, and detecting whether the antibody has bound. Many such detection methods are based on enzymatic reactions - for example the antibody may be tagged with an enzyme such as horseradish peroxidase, and on application of a suitable substrate, a colour change detected. Suitable antibodies may be monoclonal or polyclonal.

The present disclosure also includes a method of detecting plant material derived from an event described herein said method comprising obtaining a sample for analysis; making a protein extract of the sample; providing a test strip or dipstick designed to detect the presence of a said protein present within the sample; incubating the test strip or dipstick with the sample; and detecting whether said protein is present.

This method may be an antibody-based detection method for the events referred to herein and uses test strips or dipsticks. Typical steps include incubating a test strip or dipstick with a sample and observing the presence or absence of coloured bands on the test strip or dipstick. The coloured bands are indicative of the presence of a protein in the sample. Such test strip or dipstick tests are usually protein specific, and may be used for rapid testing of samples in the field.
In one embodiment, the immunological method or dipstick utilises an antibody or antibodies, or fragment/fragments thereof, specific for the Cry1Ab gene from *Bacillus thuringiensis* as encoded by SEQ ID NO: 5. Antibody fragments include, but are not limited to, Fab, modified Fab, diFab, Fab’, F(ab’)2 or FV fragment, immunoglobulin light chain or heavy chain monomer, single chain FV (scFV) or nanobody. The antibody or fragment thereof may be monoclonal or polyclonal. In a particular embodiment, the antibody is an antibody secreted by cell lines selected from the group consisting of DSM ACC2723 and DSM ACC2724 (both deposited on 12 May 2005 at Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH, Mascheroder Weg 1b, 38124 Braunschweig, Germany) or an antibody which is capable of inhibiting the binding to the Cry1Ab of an antibody secreted by cell lines selected from the group consisting of DSM ACC2723 and DSM ACC2724. It is noted that methods for producing both monoclonal and polyclonal antibodies and fragments thereof are well known in the art.

Suitable test strips or dipsticks and materials for their use are described in PCT application WO 02/27322 and are, for example, lateral-flow immunostrips comprising a detection membrane of cellulose acetate, cellulose, nitrocellulose or nylon, supported on a plastic backing. Such an immunostrip may be produced using membranes and filters through which a liquid sample is drawn by capillary action. The protein in the sample reacts with the antibodies contained in the immunostrip as it moves the length of the strip and is captured at a line that becomes visible. Suitable means of detection are, for example, colloidal gold and coloured latex beads.

In a particular embodiment, a line of specific anti-Cry1Ab antibody, as described above, is sprayed on a test strip, which is suitably made from nitrocellulose supported on a plastic backing. A reagent control line of anti-mouse antibody is sprayed in parallel above the first antibody line. The membrane is flanked on the top by an absorption pad and on the bottom by a pad containing dried colloidal gold labelled anti-Cry1Ab antibody. In a preferred embodiment, the colloidal gold-labelled anti-Cry1Ab antibody is different from the first antibody sprayed as the test line. In a particular embodiment, the colloidal gold-labelled anti-Cry1Ab antibody is the antibody secreted by cell line DSM ACC2723 and the antibody sprayed at the test line is the antibody secreted by cell line DSM ACC2724. A
sample application pad flanks the colloidal gold pad. In use, the sample application pad is placed in a sample of extracted tissue or this sample is applied to the pad in another way, for example, by pipette. Any Cry1Ab protein contained within the sample flows up the strip and becomes bound by the colloidal gold labelled-anti-Cry1Ab antibody. As it continues up the strip, the protein also becomes bound by the anti-Cry1Ab antibody at the test line. Excess gold conjugate is captured at the reagent control line. In a positive test, that is, if Cry1Ab is present in the sample, a double red line appears: the lower line indicates the presence of Cry1Ab while the upper line is the control line signalling a properly working device.

In a still further aspect of the invention there is provided a kit of parts which comprises a pair of primers as described above and instructions for performing the method as described above and means for performing an amplification reaction and optionally means for preparing the sample to be tested. In a still further embodiment there is provided a kit of parts which comprises an antibody as described above and instructions for performing the method as described above and means for performing the method as described above and optionally means for preparing the sample to be tested. In a still further embodiment of the present invention, said kit of parts may comprise DNA amplification-detection technology such as PCR or TaqMan™. In a still further embodiment of the present invention, said kit of parts may comprise probe hybridisation-detection technology such as Southern Blots, Northern Blots or in-situ Hybridisation. In another embodiment of the present invention, said kit of parts may comprise antibody binding-detection technology such as Western Blots, ELISA’s, SELDI mass spectrometry, test strips or dipsticks. In a further embodiment of the present invention, said kit of parts may comprise any combination of the aforementioned detection technologies. In a still further embodiment, said kit of parts may comprise in the form of instructions one or more of the methods described above.

In a still further aspect there is provided a plant or seed according to the invention which is used in a method of breeding. For example, the plants may be used to transfer the trait which provides for insect resistance into a plant of the same genus but having a different background germplasm. Such breeding into a different germplasm may be desired if the plant is to be grown in under conditions where an alternative germplasm is favourable.
Methods for breeding that can be used to transfer the trait into a different background germplasm are well known in the art.

In a still further aspect there is provided the use of a plant or seed according to the invention to generate explant material for use in a method of transformation of said explant with a further genetic trait. Once provided with the events that can be identified by the methods of the present invention it is well within the capabilities of the person skilled in the art to generate such explant material and use in further transformation procedures. Furthermore, once provided with the events that can be identified by the methods of the present invention it is well within the capabilities of the person skilled in the art to use said events in breeding methods as described herein.

According to the present invention, there is provided the use of one or more of the polynucleotides of the invention as described above for detecting the 1143-51B event. In one embodiment, said polynucleotides may be used in a method for detecting the 1143-51B event as described above.
EXAMPLES

The invention will be further apparent from the following non-limiting examples in conjunction with the associated sequence listings as described below:

SEQ ID NO 1: 1143-51B event: Insert – Genomic sequence
SEQ ID NO 2: 1143-51B event: Insert - Genomic sequence junction
SEQ ID NOs 3 - 4: 1143-51B event: Primers
SEQ ID NO 5: 1143-51B event: Cry1Ab gene sequence

Example 1: Cloning and Transformation

1.1 Vector cloning

Standard gene cloning techniques of restriction digestion and ligation of fragments from in-house vectors were used to construct the transformation vectors, pNOV1914 and pNOV4641. Vector pNOV1914 included a selectable marker cassette comprising a Ubiquitin (UBQ3) promoter, the UBQ3 intron, a gene sequence which encodes a protein conferring resistance to hygromycin, and a nos polyadenylation sequence. Vector pNOV4641 included the expression cassette of the target gene, which cassette comprised a Actin (ACT2) promoter, the ACT2 intron, a sequence encoding the Cry1Ab gene that had been codon optimised for expression in maize, and a nos polyadenylation sequence.

The vectors were transformed into *Agrobacterium tumefaciens* strain GV3101 using standard *Agrobacterium* transformation techniques, and transformed cells selected via antibiotic resistance.

1.2 Plant transformation

The 1143-51B event was produced by *Agrobacterium*-mediated transformation of *Gossypium hirsutum* L. cv Coker 312.

Coker 312 seeds were sown in the glasshouse. Tender petioles were cut from 3 to 5 weeks old plants, and sterilized by immersion in 70% ethanol. The petioles were then immersed in a 5% Clorox + 2ml/l Tween20 solution for 20 minutes. Petioles were washed 3 times in
ddH₂O. The ends of petioles were cut off, and petioles transferred to petiole pre-culture medium (4.3g/l MS salts, B5 vitamins (100mg/l myo-Inositol, 1mg/l nicotinic acid, 1mg/l pyridoxine HCl, 10mg/l thiamine HCl), 30g/l glucose, 2.4g/l phytagel, pH 7.0) and allowed to pre-culture in the light at 30°C for 3 days.

2 ml cultures of Agrobacterium containing the pNOV1914 and pNOV4641 constructs were grown overnight in appropriate antibiotics and then diluted with liquid MMS1 medium (4.3g/l MS salts, B5 vitamins (100mg/l myo-Inositol, 1mg/l nicotinic acid, 1mg/l pyridoxine HCl, 10mg/l thiamine HCl), 0.05mg/l 2,4-D, 0.1mg/l kinetin, 30g/l glucose, pH 6.5) to an OD₆₆₀ of between 0.1 and 0.2.

The ends were cut off the petioles and placed in 10 to 20ml of bacterial solution in a sterile petri dish. Once in the solution, the petioles were cut lengthwise and then cut into 2cm sections. After the petiole explants had soaked in bacterial solution for 5 to 10 minutes, they were transferred to co-culture plates (same recipe as MMS1 liquid with the addition of 2.4g/l Phytagel) overlaid with sterile filter papers, and allowed to co-culture at 24°C for 48 to 72 hours under low light intensity. Co-cultured explants were transferred to MMS1 medium (recipe as for MMS1 liquid medium, additionally with 2.4g/l phytagel) containing 500mg/l cefotaxime and 10mg/l hygromycin, and incubated at 30 °C under a light cycle of 16 hours light and 8 hours dark. Explants were transferred to fresh medium after 2 weeks, and every 4 to 6 weeks thereafter until callus was formed.

Once calli were the size of a garden pea, they were removed from the explants and transferred to fresh MMS1 medium containing 500mg/l cefotaxime and 10mg/l hygromycin, and maintained in tissue culture by subculturing every 4 weeks as appropriate.

1.5g callus tissue was broken up thoroughly and placed in a 50 ml Erlenmeyer flask containing 10 ml of liquid MMS2 medium (4.3g/l MS salts, B5 vitamins (100mg/l myo-Inositol, 1mg/l nicotinic acid, 1mg/l pyridoxine HCl, 10mg/l thiamine HCl), 1.9g/l KNO₃, 30 g/l glucose, pH 6.5). The suspended callus was shaken at 100 rpm in the light at 30°C for two weeks. The suspension culture cells were rinsed 3 times in MMS2 liquid medium, resuspended and plated onto solid MMS2 medium (recipe as per liquid MMS2 medium,
additionally with 2.4g/L phyto gel). Once plated, excess liquid MMS2 medium was removed, and the plates incubated at 30°C in the light. Plates were checked for somatic embryo development each week. Somatic embryos formed within 1 to 2 months. This step of liquid suspension could be repeated multiple times until embryogenic callus or somatic embryos were formed.

Somatic embryos were transferred to EG (embryoid germination) medium (2.65g/l MS salts modification No. 4 (Duchefa), 1.9g/l KNO₃, B5 vitamins (as before), 30g/l glucose, 1g/l glutamine and 0.5g/l asparagine, pH 6.5), and sub-cultured to fresh EG medium every 3 to 4 weeks.

Once somatic embryos turned green and were larger than 2cm, they were plated root down in EG medium. At all stages of regeneration, growing plantlets were prevented from reaching the lids or sides of their containers to prevent leaf drop. Germinated embryos with 1 to 2 true leaves were transferred to EG medium in 175ml Greiner containers.

Strong plantlets with true leaves were transferred to sterile peat plugs expanded with dH₂O in 175ml Greiners and transferred to peat in 3 inch pots. Plants were acclimatised in a plant propagator at high humidity in a growth cabinet under conditions of 14 hours daylight at 30°C and 10 hours darkness at 20°C. Once roots were seen growing through the drainage holes of the pot they were transferred to larger pots containing 50% John Innes No. 3 and 50% peat supplemented with Osmocote, and placed in the glasshouse.

1.3 Identification and selection of transgenics

Putative transgenic plants were screened by PCR for the presence of the Cry1Ab gene. Positive events were identified and screened using insect bioassays for insecticidal activity. Molecular characterisation of insecticidal lines was carried out by Southern Blot analysis. T1 seed from several events were observed in a field trial for insect resistance and agronomic quality. The 1143-51B event was chosen based on molecular characterisation, protein expression levels as identified by ELISA, insecticidal activity against Heliothis virescens and Spodoptera littoralis and field performance. The hygromycin selectable marker cassette was segregated away using conventional plant breeding to result in the 1143-51B event.
1.4 Verification of sequence of 1143-51B

Genomic DNA was isolated from the 1143-51B event. This was used in the sequencing of the right border junction of the DNA insertion site with the cotton genomic DNA in the 1143-51B event (SEQ ID NO: 1), using standard DNA sequencing techniques.

Example 2: 1143-51B event specific Detection via PCR

2.1 DNA extraction

DNA was extracted from leaf tissue using the Wizard™ Magnetic 96 DNA Plant System (Promega, #FF3760), according to the manufacturers instructions, with an additional step at the beginning of the protocol: following grinding of the leaf material, 0.9ml Cotton Extraction Buffer (0.2M Tris pH 8.0, 50mM EDTA, 0.25M NaCl, 0.1% v/v 2-mercaptoethanol, 2.5% w/v polyvinyl-pyrrolidone) was added to each well, the plant tissue resuspended and the plate centrifuged at 4,000 rpm (2755g) for 10 minutes. After aspirating and discarding the supernatant, 300ul Lysis Buffer A (Promega) was added and the manufacturers protocol was followed from this point. This procedure resulted in approximately 85ul of purified genomic DNA at a concentration of approximately 10ng/ul.

2.2 Event-specific PCR reactions

25ul PCR reactions were setup using a standard reaction mix comprising:

1x Jumpstart RED TaqPCR (Sigma, #P-1107)
0.5 uM primer 1 (SEQ ID NO: 3)
0.5 uM primer 2 (SEQ ID NO: 4)
10ng genomic DNA
ddH₂O

The PCR reactions were heated in a thermocycler at 94°C for 3 minutes, followed by 35 cycles as follows: 94°C for 30 seconds, 67°C for 30 seconds, 72°C for 45 seconds. The reaction was completed by heating at 72°C for 5 minutes.

PCR reactions were run on an agarose gel, and DNA bands visualised under UV light after staining with ethidium bromide. A band of 462 bp in size was obtained.
Example 3: 1143-51B Detection via Multiplex PCR Zygosity Test

3.1 Genomic DNA extraction

Genomic DNA from 1143-51B was extracted as described in Example 2.1.

3.2 Multiplex PCR

PCR primers for use in a multiplex PCR zygosity test are designed. A 20ul PCR reaction is set up for each sample to be tested as follows:

1x JumpState ReadyMix REDTaq PCR (Sigma P-1107)
0.5 uM primer 1
0.5 uM primer 2
0.5 uM primer 3
10 ng genomic DNA
ddH₂O

The PCR reactions are heated in a thermocycler, for example at 94°C for 3 minutes, followed by 35 cycles as follows: 94°C for 15 seconds, 55°C for 15 seconds, 72°C for 45 seconds. The reaction is completed by heating at 72°C for 5 minutes.

3.3 Analysis

PCR reactions are run on an agarose gel, and DNA bands visualised under UV light after staining with ethidium bromide. The banding pattern obtained is used to distinguish between samples from a 1143-51B heterozygote plant, a 1143-51B homozygote plant and a homozygote wild type cotton plant.

Example 4: 1143-51B Detection via Southern Blot

4.1 DNA extraction for use in Southern Blotting

Approximately 2 to 3g fresh weight of frozen young leaf tissue was ground in a chilled mortar and pestle to a fine powder and added to 15 ml of ice-cold Nuclei extraction buffer (0.35M glucose, 0.1M Tris-HCl pH8, 50mM Na₂EDTA, 2% Polyvinyl-pyrrolidone-10, 0.1% ascorbic acid, 0.2% B-mercaptoethanol) in a labelled tube. The sample was incubated on ice for 15-20 minutes. The tube was mixed gently and centrifuged at 2700g
for 20 minutes at 4°C. The supernatant was discarded and 8ml of nuclei lysis buffer
(0.14M sorbitol, 0.22M Tris-Cl pH8, 0.8M NaCl, 0.22M Na₂EDTA, 0.8%w/v CTAB, 1% Sarkosyl, 1% Polyvinyl-pyrrolidone-10, 0.1% ascorbic acid, 0.2% B-mercaptoethanol,
5µg/ml proteinase K) was added. After mixing, the tubes were incubated at 65°C for 30
minutes. 10ml chloroform was added, and the tube mixed gently by inversion until an
emulsion formed followed by centrifugation at 4600rpm for 10 minutes at room
temperature.

The aqueous layer was removed into a new tube containing 10µl RNase A (10mg sigma
R4642), and the tube incubated for 30 minutes at 37°C. The chloroform and centrifugation
steps were repeated once. The aqueous layer was removed into a new tube containing
10ml propan-2-ol. After approximately 15 minutes incubation at room temperature, a
gelatinous precipitate was observed in the middle of the tube. The tube was mixed gently
to precipitate out the DNA. The DNA was spooled out using a sterile loop into a falcon
tube containing 70% ethanol. The DNA was air-dried to remove the ethanol and
resuspended in 200-400µl TE.

4.2  Alternative method for DNA extraction

2-3 young cotton leaves (approximately 1g fresh weight) are ground to a paste in a mortar
and pestle at room temperature, with 2ml of grinding buffer (100mM NaOAc pH 4.8,
50mM EDTA pH8.0, 500mM NaCl, 2% PVP (10,000 MW), 1.4 % SDS) and a little sand.
The ground tissue is transferred to a 15ml falcon tube, and the remnants in the mortar
rinsed with 1 ml of grinding buffer into the tube. The sample is incubated at 65°C for 15
minutes, shaking occasionally. 4ml 10M ammonium acetate is added, and the sample
mixed well and incubated at 65°C for 10 minutes to precipitate proteins. The samples are
centrifuged at room temperature at 4600 rpm for 10 minutes. The aqueous phase is
transferred to a fresh 15ml tube.

0.6 volumes of cold isopropanol are added and the sample is incubated at room
temperature for approximately 30 minutes. After mixing by slowly inverting the tube
several times, the DNA is spooled out and dissolved in 500ul TE. 10ul of 10mg/ml RNAse
are added and incubated for 15 minutes at room temperature. Following extraction with
500μl of phenol: chloroform: isoamyl alcohol (25:24:1), the sample is mixed gently and centrifuged at 13000rpm for 5 min.

The supernatant is transferred to a fresh tube using a fine Pasteur pipette and re-extracted with chloroform: isoamyl alcohol (24:1) as above. The supernatant is transferred to fresh tubes, 1/10 volume 3M NaOAc (pH4.8) added and mixed, and then one volume cold isopropanol is added. The sample may be incubated at room temperature for up to 30 minutes to precipitate the DNA. The DNA is spooled out and resuspended in 70% ethanol. The DNA is air-dried to remove the ethanol and resuspended in 200μl water.

4.3 Restriction enzyme digests

The DNA was quantified using a spectrophotometer and running out on a gel. Suitable enzyme digests were prepared using 5μg DNA per digest in a total volume of 40μl. Digests including NcoI, MscI, HindIII/KpnI and NheI/AscI were used to detect copy number and insert integrity. Digests were incubated for 6 hours at the appropriate temperature for each enzyme.

4.4 Gel electrophoresis

Bromophenol blue loading dye was added to each sample from 4.3 above, and each sample loaded on a 0.8% TBE agarose gel. The gel was run at 50 volts overnight.

After running, the gel was washed in 0.25M HCl for 10 minutes to depurinate the DNA, incubated in denaturing solution (0.5M NaOH, 1.5M NaCl) with gentle agitation for 30 minutes, rinsed with distilled water and then incubated in neutralising solution (0.5M Tris, 1.5M NaCl) for 30 minutes.

A Southern Blot was prepared as follows: A glass plate was placed over a tray containing 20X SSC and a strip of 3M paper was placed onto the glass plate such that both ends dipped into the 20X SSC solution (to act as a wick). A piece of 3M paper the same size as the gel was placed on the wick, and the gel placed on this. Strips of nescofilm were laid around the edges of the gel to form a seal. A Hybond membrane was placed on top of the gel, followed by two further pieces of 3M paper. Throughout the assembly of the blot, care was taken to ensure that no air bubbles were trapped between the membrane, gel and
3M paper. A 5cm-10cm stack of absorbent paper towels was placed on top of the 3M paper and held in place with a weight.

The DNA was allowed to transfer to the Hybond membrane overnight. After transfer the Southern Blot stack was disassembled and the DNA was bound to the membrane via UV cross-linking.

4.5 Hybridisation

A suitable DNA probe was prepared by HindIII/KpnI restriction digestion of binary plasmid pNOV4641 and purification of the resulting fragment. 25ng probe DNA in 45ul TE was boiled for 5 minutes, placed on ice for 5 minutes then transferred to a Rediprime II (Amersham Pharmacia Biotech, #RPN1633) tube. After addition of 5ul 32P-labelled dCTP to the Rediprime tube, the probe was incubated at 37°C for 1 hour. The probe was purified by centrifugation through a microspin G-50 column (Amersham Pharmacia Biotech, #27-5330-01) according to the manufacturers instructions to remove unincorporated dNTPs. The activity of the probe was measured roughly by comparing the amount of radioactive component remaining in the column to the amount in the sample tube, with a ratio of at least 50:50 being acceptable. The Hybond membrane was pre-hybridised by wetting with 40 ml pre-warmed Rapid-Hyb buffer (Amersham-Pharmacia), at 65°C for 30 minutes. The labelled probe was boiled for 5 minutes, and placed on ice for 5 minutes. An appropriate amount of probe (1 million counts per 1ml pre-hybridisation buffer) was added to the pre-hybridisation buffer and hybridisation occurred at 65°C overnight. The following day, the hybridisation buffer was discarded, and following a rinse with 50ml 2xSSC/1%SDS solution the membrane washed in 150ml 2xSSC/1%SDS solution at 65°C for 30-45 minutes. This process was repeated twice with 0.1xSSC/1%SDS solution. The membrane was exposed to a phosphor screen or X-ray film to detect where the probe had bound.

Example 5: 1143-51B Detection via ELISA

5.1 Protein extraction

Cotton tissue for analysis was harvested and frozen at -70°C. Frozen tissue was ground to a fine powder and weighed into a labelled polypropylene tube. Extraction buffer (100mM Tris, 100mM Sodium Borate, 5mM MgCl, 0.05% Tween 20, 0.2% Sodium Ascorbate,
Water, pH 7.8, 1mM AEBSF, 0.001mM Leupeptin) was added to the sample in a ratio of 2:1 (volume extraction buffer : sample fresh weight) for frozen tissue or 30:1 (volume extraction buffer : sample dry weight) for lyophilised tissue. The sample was vortexed and homogenised using a Brinkman PT 10/35 Polytron equipped with a PTA 10TS foam-reducing generator, until the mixture became liquefied. Extracts were centrifuged at 10,000 x g for 15 minutes. The protein extract supernatant was stored at 2-8°C.

5.2 ELISA protocol

The ELISA procedure used standard techniques as follows. A 96-well plate was soaked in ethanol for 2 hours, and air-dried. The plate was coated with 50ul goat anti-Cry1Ab antibody per well and incubated overnight at 2-8°C. After washing three times with 1X ELISA wash solution (100mM Tris, 0.5% Tween-20, 75mM NaCl, pH8.5), the plate was dried briefly by tapping upside down on a paper towel. 150ul blocking solution (10mM NaPO₄, 140mM NaCl, 1% BSA, 0.02% Sodium Azide, titrated to pH7.4 with NaH₂PO₄ and Na₂HPO₄) was added to each well followed by incubation at room temperature for 45 minutes. The plate was washed 3 times as described above.

Cry1Ab standards and protein extract samples were applied to appropriate wells of the plate in triplicate, 50ul total volume per well. The plate was incubated at 2-8°C for 1 hour 30 minutes, followed by room temperature for a further 30 minutes. The plate was washed three times with ELISA wash solution, and then incubated at 35-39°C for 1 hour with 50ul rabbit anti-Cry1Ab antibody per well. The plate was washed three times with ELISA wash solution, and incubated at room temperature for 30 minutes with 50ul donkey anti-rabbit antibody conjugated with alkaline phosphatase per well. Following a further three washes with ELISA wash solution, 50ul phosphatase substrate solution was added per well and the plate incubated for 30 minutes at room temperature. The reaction was stopped by addition of 50ul 3M NaOH per well. The absorbance of the solution in each well was measured at 405nm using a Ceres 900C multiwell plate reader and the results analysed using KC3 Curve fitting software (Bio-Tek Instruments Inc.). The concentration of Cry1Ab in the samples was calculated by reference to the Cry1Ab protein standards.

Example 6: 1143-51B detection via DipStick

6.1 Protein extraction
A piece of leaf tissue approximately 0.2 cm$^2$ was placed in a tube containing extraction buffer. A plastic stirrer was used to extract protein from the tissue, by cutting into and macerating the tissue.

6.2 Dipstick test

A test strip was placed into the tube and incubated for 5 to 10 minutes for the result to develop. The test strip comprised a first band at which anti-Cry1Ab antibody was bound, and a second band at which a control antibody was bound. After incubation, a double red line in the result window of the test strip indicated that Cry1Ab was present. The lower line indicated the presence of Cry1Ab protein while the upper line was a control indicating that the assay was working correctly.

Example 7: Insecticidal efficacy of 1143-51B

7.1 Field trial design

Field trials were set up at 6 locations in the US to test the insect resistance of 1143-51B. At each location, duplicate trials were planted in a randomized complete block design, each comprising 4 replicates. Each trial consisted of a plot comprising 4 x 40 ft rows, planted at 3 plants per foot.

At each location, one trial was artificially infested with *Heliothis virescens* (tobacco budworm) larvae, and the other with *Helicoverpa zea* (cotton bollworm) larvae when the plants were actively squaring. The trials were subsequently assessed for percentage damage to bolls and squares. The artificial infestations were carried out by spraying eggs in a solution of xanthan gum onto the plants so that the neonate larvae hatched directly onto the plants. Infestations were designed to give approximately 3 eggs per plant.

7.2 Field trial results

The data presented in the table below are the mean of all assessments taken during the trials: multiple square damage and boll damage ratings have been averaged together to give a mean fruiting body damage rating, and data from all 6 locations has been averaged together.
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<th>% damaged fruiting bodies (average of squares and bolls, over 6 trial locations)</th>
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</tr>
<tr>
<td>1143-51B</td>
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</table>

The data clearly show that 1143-51B has excellent resistance to both *Heliothis virescens* and *Helicoverpa zea* when compared to the non-transgenic control designated Coker312.
CLAIMS

1. A polynucleotide which comprises the sequence depicted as SEQ ID NO: 1.

2. A polynucleotide which comprises:
   a) at least 18 contiguous nucleotides of the sequence depicted as SEQ ID NO: 3;
   b) at least 35 contiguous nucleotides of the sequence depicted as nucleotides 145 to 204 of SEQ ID NO: 1; or
   c) at least 50 contiguous nucleotides of the sequence depicted as SEQ ID NO: 1, said polynucleotide encompassing nucleotides 174 and 175 of SEQ ID NO: 1.

3. A cotton plant comprising a polynucleotide according to any one of claims 1 to 2.

4. Seed of the cotton plant according to claim 3 which comprises the polynucleotide according to any one of claims 1 to 2.

5. A method for detecting a plant which contains the polynucleotide depicted as SEQ ID NO: 1 said method comprising:
   a) preparing a sample containing the genomic DNA of the plant to be tested;
   b) obtaining a pair of primers which are suitable for use in an amplification reaction to amplify a sequence comprising at least 18 contiguous nucleotides of the sequence depicted as SEQ ID NO: 2 and the complement thereof;
   c) adding said pair of primers to said sample and the means for performing an amplification reaction;
   d) performing an amplification reaction; and
   e) visualising the thus amplified sequence.

6. A method according to claim 5 wherein said sequence comprises at least 20 contiguous nucleotides.
7. A method for detecting a plant which contains the polynucleotide depicted as SEQ ID NO: 1 said method comprising:
   a) preparing a sample containing the genomic DNA of the plant to be tested;
   b) obtaining a probe which is capable of hybridising to a sequence comprising at least 18 contiguous nucleotides of the sequence depicted as SEQ ID NO: 2;
   c) adding the probe to said sample under conditions which allow said probe to hybridise with a complementary nucleic acid within said sample;
   d) removing substantially non-hybridised probe; and
   e) detecting the thus hybridised probe to identify if the sample contains said polynucleotide.

8. A method according to claim 7 wherein said sequence comprises at least 20 contiguous nucleotides.

9. A method according to claim 7 or claim 8 wherein said substantially non-hybridised probe is removed by rinsing said probe under high stringency conditions.

10. A kit of parts which comprises a pair of primers as defined in claim 5, instructions for performing the method of claim 5, means for performing an amplification reaction, and optionally means for preparing the sample to be tested.

11. An anti Cry1Ab-antibody secreted by cell line DSM ACC2723 or DSM ACC2724.

12. A dipstick comprising
   a) a test line of specific anti-Cry1Ab antibody;
   b) a reagent control line of anti-mouse antibody;
   c) a pad containing dried colloidal gold labelled anti-Cry1Ab antibody; and
   d) a sample application pad.

wherein the anti-Cry1Ab antibody and the dried colloidal gold labelled anti-Cry1Ab antibody are independently selected from the group consisting of an antibody secreted by cell line DSM ACC2723 and an antibody secreted by cell line DSM ACC2724.
SEQUENCE LISTING

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Artificial sequence

1143-51B nucleotide motif

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1143-51B nucleotide motif

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Artificial sequence

1143-51B nucleotide motif

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Artificial sequence

DNA

DNA
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**INTERNATIONAL SEARCH REPORT**

**A. CLASSIFICATION OF SUBJECT MATTER**

INV. C12N15/02  C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

**B. FIELDS SEARCHED**

Minimum documentation searched (classification system followed by classification symbols)

C12N  C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ, EMBASE, FSTA, Sequence Search, CHEMABS Data

**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

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X See patent family annex.

Further documents are listed in the continuation of Box C.

- Special categories of cited documents:
  - "A" document defining the general state of the art which is not considered to be of particular relevance
  - "E" earlier document but published on or after the international filing date
  - "L" document which may throw doubts on the novelty or other special reason (as specified)
  - "O" document referring to an oral disclosure, use, exhibition or other means
  - "P" document published prior to the international filing date but later than the priority date claimed

- "Y" later document published after the international filing date on priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- "Y*" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- "X*" document member of the same patent family

**Date of the actual completion of the international search**

10 August 2006

**Date of mailing of the international search report**

1 1.10.2006

**Name and mailing address of the ISA/ Authorized officer**

European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Hilversum
Tel. (+31-70) 340-2040, Tx 31 691 epo nl, Fax (+31-70) 340-3016

Marchesini, Patrizia
**INTERNATIONAL SEARCH REPORT**

**Box II** Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. __☐__ Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:

2. __☐__ Claims Nos.: because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. __☐__ Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

**Box III** Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this International application, as follows:

```
see additional sheet
```

1. __☐__ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. __☐__ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. __☐__ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. __☒__ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the Invention first mentioned in the claims; it is covered by claims Nos.:

   1–10

Remark on Protest

- __☐__ The additional search fees were accompanied by the applicant's protest.
- __☐__ No protest accompanied the payment of additional search fees.

Form PCT/ISA/210 (continuation of first sheet (2)) (January 2004)
This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. claims: 1-10

   Relates to a polynucleotide which comprises the sequence depicted as SEQ ID No: 1

2. claims: 11-12

   Relates to an anti Cry1Ab antibody
# INTERNATIONAL SEARCH REPORT

Information on patent family members

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