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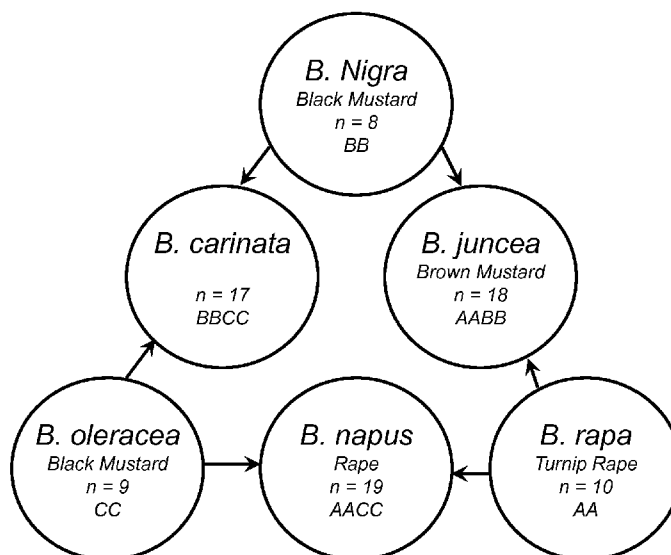
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[Continued on next page]

(54) Title: BRASSICA GENOMIC ASSAYS

FIG. 1



(57) Abstract: Methods and compositions for detecting, identifying, and quantifying Brassica A genomic DNA are described. The methods are specific to the Brassica A genome and do not cross-react with other Brassica species, crops or weedy relatives that could contribute to contamination of a canola field.



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BRASSICA GENOMIC ASSAYS

Field of the Disclosure

The present disclosure relates generally to plant molecular biology. More specifically, it relates to the detection of Brassica A genomic DNA.

Background of the Disclosure

Brassica species are used as a source of vegetable oil, animal feeds, vegetables and condiments. *Brassica* plants that are used for vegetable production include cabbage, cauliflower, broccoli, kale, kohlrabi, leaf mustard and rutabaga. However, on a world-wide basis, the most economically important use of *Brassica* species is for the production of seed-derived, vegetable oils. The predominant *Brassica* species grown for oil production is *B. napus*, followed by *B. juncea* and *B. rapa*. Seeds of *B. napus*, *B. juncea* and *B. rapa* are referred to as rapeseed. *Brassica* species that are grown primarily for oil production are often called oilseed rape. In North America, canola, a type of oilseed rape that has been selected for low levels of erucic acid and glucosinolates in seeds, is the predominant *Brassica* plant grown for the production of vegetable oil for human consumption.

Canola includes three oilseed *Brassica* species (*B. napus*, *B. rapa*, *B. juncea*) and is grown on over 80 million acres worldwide. Canola is a member of the *Brassica* genus which includes a wide variety of plant species that are under commercial cultivation.

Transgenic canola is currently being cultivated worldwide as a means to solve agricultural production problems. With the development of transgenic canola and other transgenic crops, various countries have instituted regulations to identify transgenic material and their derived products. Polymerase chain reaction (PCR) methods have generally been accepted as the method of choice for transgene detection because of its quantitative and qualitative reliability. This method usually requires amplification and detection of a transgene and a corresponding reference gene, and comparing the quantity of the transgene against the quantity of the reference gene. This system requires a set of two primers and a detection probe specific for the transgene and another set of species specific primers and a probe for an endogenous reference gene.

For the purpose of labeling and traceability, transgene detection assays are developed to meet the requirements of various countries. The European Union's Regulation 619/2011 specifies that the results of detection methods be expressed in transgenic mass fraction with respect to a taxon-specific reference system. The target for the "taxon" specific real-time PCR assay needs to not only be taxon specific, but also quantitatively stable in different genetic backgrounds in order to yield stable testing results.

In most crops, the target species for developing a specific PCR assay is unique, such as for *Zea mays*, *Glycine max*, and *Oryza sativa*. For example, in maize (*Zea mays*) fields, there are no other closely-related *Zea* species likely to cross-contaminate a *Zea mays* field and therefore complicate quantification of maize transgenes. However, canola is quite different.

The Triangle of U (Figure 1) depicts the evolution and relationship between *B. napus*, *B. rapa*, *B. juncea* and three other Brassica species (Nagaharu U (1935) Genome analysis in Brassica with special reference to the experimental formation of *B. napus* and peculiar mode of fertilization. *Japan. J. Bot* 7: 389–452). Through evolution, the 3 base species (*B. nigra*, *B. oleracea* and *B. rapa*) have combined to form three allotetraploid species (*B. carinata*, *B. napus* and *B. juncea*). The three species where canola exists (*B. juncea*, *B. napus* and *B. rapa*) share the A-genome (Figure 1).

If an endogenous system can be proven to specifically detect the A-genome, it could provide an endogenous reference system for a variety of applications including the relative quantitation of transgenic canola in *B. juncea*, *B. napus* and *B. rapa*. For example, currently most commercial transgenic canola is *B. napus*, however, an A-specific endogenous reference system could be utilized in detection methods on future transgenics in the other two species (*B. rapa* and *B. juncea*). In addition to being able to detect a wide range of varieties of *B. rapa*, *B. napus* and *B. juncea*, the assay must not detect *B. nigra*, *B. carinata*, *B. oleracea*, and other related species that might contaminate a canola grain lot or other major crops, where such cross-detection reduces the accuracy of the assay. Even more, there are other closely-related *Brassica* relatives that could contaminate canola fields, including, but not limited to, *Camelina sativa*, *Thlaspi arvense*, *Erucastrum gallicum*, *Raphanus raphanistrum*, *Raphanus sativus*, and *Sinapis arvensis*. As such for canola, from a labeling and traceability viewpoint, the challenge is to identify a real-time PCR assay that will be specific to the species that constitute the canola crop.

Several endogenous reference systems currently exist for measuring the relative percentage of genetically modified canola using real-time PCR. However, these systems are not reliable endogenous reference systems (Wu et al., (2010) Comparison of Five Endogenous Reference Genes for Specific PCR Detection and Quantification of *Brassica napus*, *J. Agric. Food Chem*, 58: 2812-2817). They are not specific for the taxon or crop of interest, and they have not been shown to be stable across a globally representative sample within the taxon or crop.

This disclosure relates to methods of detection and quantification that are specific to the Brassica A-genome and does not significantly cross-react with other Brassica species, crops or weedy relatives that could contribute to contamination of a canola field. In addition this endogenous target is stable within each of the three A-genome species when tested on samples from multiple varieties from diverse geographical regions.

Summary

Compositions and methods for detecting, identifying, and quantifying Brassica A genomic DNA are provided herein.

A first aspect features a method of detecting and quantifying the amount of Brassica A genomic DNA in a sample. The method comprises specifically amplifying a genomic DNA fragment of the Brassica A genome, wherein the amplified DNA fragment comprises at least one of the nucleotide sequences of a genomic region selected from the group consisting of SEQ ID NOS: 25, 26, 27, 28, and 35; and, detecting and quantifying the Brassica A genome from the amplified fragment of the Brassica A genome.

In an embodiment, the amplified fragment of Brassica A genome comprises the nucleotide sequence of at least one of SEQ ID NOS: 29, 30, or 31 selected from the group consisting of nucleotide position from about 50 to about nucleotide position 400, 50 to about nucleotide position 100, 50 to about nucleotide position 350, 400 to about nucleotide position 350, 400 to about nucleotide position 200, and 400 to about nucleotide position 100.

In an embodiment, the amplified fragment of Brassica A genome comprises (i) the nucleotide sequence of at least one of SEQ ID NOS: 29, 30, or 31; or (ii) a nucleic acid fragment of at least one of SEQ ID NOS: 29, 30, or 31, wherein the nucleic acid fragment is

selected from the group consisting of nucleotide position from about 50 to about nucleotide position 400, 50 to about nucleotide position 100, 50 to about nucleotide position 350, 400 to about nucleotide position 350, 400 to about nucleotide position 200, and 400 to about nucleotide position 100 of SEQ ID NOS: 29, 30, or 31.

In an embodiment, the amplification is performed with a primer pair comprising nucleotide sequences selected from the group consisting of SEQ ID NOS: 17, 18, 19, 20, 21, 22, 23, and 24.

In an embodiment, the genomic DNA comprises a FatA gene.

In other embodiments, the amplification does not substantially amplify Brassica B and C genomic DNA.

Another aspect features a method of determining the relative amount of a Brassica transgenic event in a sample. The method comprises performing a Brassica A genome specific polymerase chain reaction, wherein the analysis includes specifically amplifying a genomic DNA fragment of the Brassica A genome, wherein the amplified DNA fragment comprises at least one of the nucleotide sequences of a genomic region selected from the group consisting of SEQ ID NOS: 25, 26, 27, 28, and 35; determining the total amount of Brassica A genomic DNA in the sample; performing an event specific assay for the transgenic event to determine the amount of the transgenic event in the sample; and, comparing the amount of the transgenic event DNA to the total amount of Brassica A genomic DNA in the sample.

In an embodiment, the amplified fragment of Brassica A genome comprises the nucleotide sequence of at least one of SEQ ID NOS: 29, 30, or 31 from nucleotide position about 50 to about 400.

In an embodiment, the amplification is performed with a primer pair comprising nucleotide sequences selected from the group consisting of SEQ ID NOS: 17, 18, 19, 20, 21, 22, 23, and 24.

In other embodiments, the genomic DNA comprises a FatA gene.

In an embodiment, the amplification does not substantially amplify Brassica B and C genomic DNA.

Another aspect features a method of determining adventitious presence of a Brassica transgenic event in a sample. The method comprises obtaining a sample suspected of containing

a Brassica transgenic event; performing a Brassica A genome specific polymerase chain reaction, with a primer, wherein the primer binds to a genomic region of the Brassica A genome, the genomic region selected from the nucleotide sequence of at least one of SEQ ID NOS: 29, 30, or 31 from nucleotide position about 50 to about 400; determining the total amount of Brassica A genomic DNA in the sample; performing an event specific quantitative assay for the transgenic event to determine the amount of the transgenic event DNA in the sample; and, comparing the amount of the transgenic event to the total amount of Brassica in the sample.

In an embodiment, the primer is selected from the group consisting of SEQ ID NOS: 17, 18, 19, 20, 21, 22, 23, and 24.

Another aspect features an amplicon comprising at least one of the nucleotide sequences of a genomic region selected from the group consisting of SEQ ID NOS: 25, 26, 27, 28, and 35 wherein the amplicon is not larger than 500 base pairs.

Another aspect features an oligonucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS: 17, 18, 19, 20, 21, 22, 23, and 24 wherein the oligo is about 15-500 nucleotides.

Another aspect features a detection kit comprising oligonucleotides comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS: 17, 18, 19, 20, 21, 22, 23, and 24 wherein the oligo is less than about 50 nucleotides and one or more reaction components to perform a quantitative reaction.

Another aspect features a method of determining trait purity of a Brassica trait. The method comprises obtaining a sample of a Brassica trait; and performing the Brassica A genome specific assay by specifically amplifying a genomic DNA fragment of the Brassica A genome, wherein the amplified DNA fragment comprises at least one of the nucleotide sequences of a genomic region selected from the group consisting of SEQ ID NOS: 25, 26, 27, 28, and 35; and, detecting and quantifying the Brassica A genome from the amplified fragment of the Brassica A genome.

In an embodiment, the trait is selected from the group consisting of RT73, RT200, MON88302, DP-073496, HCN92, T45 (HCN28), 23-18-17, 23-198, OXY-235, MS1, MS3, MS6, MS8, RF1, RF2, RF3, and Topas 19/2.

In an embodiment, the determination comprises performing a quantitative polymerase chain reaction.

Another aspect features a method of establishing purity of a Brassica seed lot, the method comprising performing a polymerase chain reaction wherein the oligonucleotide primers or probes are capable of discriminating the Brassica A genome from the Brassica B and C genomes, wherein the oligonucleotide primers and/or probes bind to a target region of the Brassica A genome, the target region comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS: 25, 26, 27, 28, and 35.

In an embodiment, the oligonucleotide primers and/or probes comprise a nucleotide sequence selected from the group consisting of SEQ ID NOS: 19, 20, 21, 22, 23, and 24.

Another aspect features a method of quantifying the amount of a transgenic element in a Brassica sample. The method comprises performing a polymerase chain reaction wherein the oligonucleotide primers or probes are capable of discriminating the Brassica A genome from the Brassica B and C genomes, the oligonucleotide primers or probes bind to a target region of the Brassica A genome comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS: 29, 30, and 31; performing the transgenic element specific quantitative polymerase chain reaction; and, determining the amount of the transgenic element present in the canola sample by comparing to the amount of Brassica A genomic DNA in the sample.

A further aspect features a method of determining seed purity of a seed sample suspected of containing the Brassica A genome. The method comprises specifically amplifying a genomic DNA of the Brassica A genome, wherein the amplified DNA comprises at least one of the nucleotide sequences of a genomic region selected from the group consisting of SEQ ID NOS: 25, 26, 27, 28, and 35; and, determining the purity of the seed sample based on the presence or absence of the Brassica A genome.

In other embodiments, the seed sample contains at least one of broccoli, brussel sprouts, mustard seeds, cauliflower, collards, cabbage, kale, kohlrabi, leaf mustard, or rutabaga.

In other embodiments, the seed sample contains, but is not limited to, broccoli, brussel sprouts, mustard seeds, cauliflower, collards, cabbage, kale, kohlrabi, leaf mustard, or rutabaga.

Another aspect features a method of determining the presence and/or quantity of the Brassica A genome. The method comprises specifically hybridizing DNA of the Brassica A

genome with a probe, wherein the probe selectively binds to at least one of the nucleotide sequences of a genomic region selected from the group consisting of SEQ ID NOS: 25, 26, 27, 28, and 35, optionally under high stringency conditions; and, detecting the presence and/or quantity of the Brassica A genome.

In an embodiment, the probe binds the genomic region of the Brassica A genome selected from the nucleotide sequence of at least one of SEQ ID NOS: 29, 30, or 31 from nucleotide position about 50 to about 400.

In a further embodiment, the probe comprises the nucleotide sequences of SEQ ID NOS: 19, 20, 21, 22, 23, or 24.

Another aspect features a method of sequencing a region of the Brassica A genome. The method comprises obtaining a DNA sample; and, performing a sequencing reaction of the DNA sample wherein the sequenced region comprises at least one of the nucleotide sequences of a genomic region selected from the group consisting of SEQ ID NOS: 25, 26, 27, 28, and 35.

The methods and compositions disclosed herein discriminate detection of Brassica A genome as compared to detecting genomic DNA of other genomes (e.g., Brassica B and Brassica C genomes).

BRIEF DESCRIPTION OF FIGURES AND SEQUENCE LISTING

The disclosure can be more fully understood from the following detailed description and the accompanying drawings and Sequence Listing which form a part of this application. The Sequence Listing contains the one letter code for nucleotide sequence characters and the three letter codes for amino acids as defined in conformity with the IUPAC-IUBMB standards described in Nucleic Acids Research 13:3021-3030 (1985) and in the Biochemical Journal 219 (No. 2): 345-373 (1984), which are herein incorporated by reference in their entirety. The symbols and format used for nucleotide and amino acid sequence data comply with the rules set forth in 37 C.F.R. § 1.822.

Figure 1 shows the triangle of “U” which depicts the relationships between the different plant species of Brassica (Nagaharu U (1935) Genome analysis in Brassica with special reference to the experimental formation of *B. napus* and peculiar mode of fertilization. *Japan. J.*

Bot 7: 389–452). Number of chromosomes is represented by n. *B. nigra*, *B. oleracea* and *B. rapa* are three base species. Allotetraploid species are *B. carinata*, *B. juncea*, and *B. napus*.

Figure 2-A shows the evolutionary relationship of the six consensus sequences of FatA.

Figure 2-B shows the breakdown of the 53 sequenced varieties into the six consensus sequences.

Figure 3 shows an alignment of the FatA consensus sequences. The circles show regions or bases of A-specificity. The gray highlighted bases show location of the primers and probe for the FatA(A) real-time PCR assay. From left to right: the first, second and third highlighted regions represent the forward primer, the probe, and the reverse primer, respectively. The underline bases show where there are ambiguities within the consensus. The sequences that are aligned in the figure are the A1 sequence (SEQ ID NO: 29), A3 (SEQ ID NO: 31), A2 (SEQ ID NO: 30), B (SEQ ID NO: 32), C2 (SEQ ID NO: 34), and C1 (SEQ ID NO: 33).

The sequence descriptions and Sequence Listing attached hereto comply with the rules governing nucleotide and/or amino acid sequence disclosures in patent applications as set forth in 37 C.F.R. §1.821-1.825. The Sequence Listing contains the one letter code for nucleotide sequence characters and the three letter codes for amino acids as defined in conformity with the IUPAC-IUBMB standards described in *Nucleic Acids Res.* 13:3021-3030 (1985) and in the *Biochemical J.* 219 (2):345-373 (1984) which are herein incorporated by reference. The symbols and format used for nucleotide and amino acid sequence data comply with the rules set forth in 37 C.F.R. §1.822.

SEQ ID NO:1 is the FatA-A1 consensus nucleotide sequence from *Brassica napus*. Varieties used to create SEQ ID NO: 1 include 45H73, NS1822BC, 46A76, NS5536BC, 43A56, NW1717M, NW4219BC, NW4201BC. 436554, 458967, 531273, 458941, 469735, 458605, 305278, and 633153.

SEQ ID NO: 2 is the FatA-A1.2 consensus nucleotide sequence from *Brassica rapa*. Varieties used to create SEQ ID NO: 2 include Tobin, 257229, 163496, 649190, and 390962.

SEQ ID NO:3 is the FatA-A1.3 consensus nucleotide sequence from *Brassica juncea*. Varieties used to create SEQ ID NO: 3 include JS0917BC, JS0936BC, JS1056BC, JS1260MC, JS1432MC, 418956, 458942, 603011, and 649156.

SEQ ID NO:4 is the FatA-A2.1 consensus nucleotide sequence from *Brassica napus*. Varieties used to create SEQ ID NO:4 include 458954, 469735, and 311729.

SEQ ID NO:5 is the FatA-A2.2 consensus nucleotide sequence from *Brassica rapa*. Varieties used to create SEQ ID NO:5 include 163496, 347600, 346882, and 390962.

SEQ ID NO:6 is the FatA-A2.3 consensus nucleotide sequence from *Brassica rapa*. Varieties used to create SEQ ID NO:6 include Reward.

SEQ ID NO:7 is the FatA-A3.1 consensus nucleotide sequence from *Brassica rapa*. Varieties used to create SEQ ID NO:7 include Tobin, Klondike, Reward, 41P95, 257229, 649159, 163496, and 649190.

SEQ ID NO:8 is the FatA-B.1 consensus nucleotide sequence from *Brassica juncea*. Varieties used to create SEQ ID NO:8 include JS0879BC, JS0917BC, JS0936BC, JS1056BC, JS1260MC, JS1432MC, 418956, 458942, 603011, and 649156.

SEQ ID NO:9 is the FatA-B.2 consensus nucleotide sequence from *Brassica carinata*. Varieties used to create SEQ ID NO:9 include 649155 and 597822.

SEQ ID NO:10 is the FatA-B.3 consensus nucleotide sequence from *Brassica nigra*. Varieties used to create SEQ ID NO:10 include 273638 and 633142.

SEQ ID NO:11 is the FatA-C1.1 consensus nucleotide sequence from *Brassica napus*. Varieties used to create SEQ ID NO:11 include 45H73, NS1822BC, 46A76, NS5536BC, 46A56, NW1717M, NW4219BC, NW4201BC, 436554, 458967, 458954, 531273, 458941, 469735, 458605, 311729, 305278, and 633153.

SEQ ID NO:12 is the FatA-C1.2 consensus nucleotide sequence from *Brassica oleracea*. Varieties used to create SEQ ID NO:12 include 28888, 29800, 365148, 29790, 28852, and 30862.

SEQ ID NO:13 is the FatA-C1.3 consensus nucleotide sequence from *Brassica oleracea*. Varieties used to create SEQ ID NO:13 include 32550.

SEQ ID NO:14 is the FatA-C2.1 consensus nucleotide sequence from *Brassica oleracea*. Varieties used to create SEQ ID NO:14 include 249556, 29041, 29800, 30862, 30724, and 32550.

SEQ ID NO:15 is the FatA-C2.2 consensus nucleotide sequence from *Brassica carinata*. Varieties used to create SEQ ID NO:15 include 649155 and 597822.

SEQ ID NO:16 is the FatA-other consensus nucleotide sequence from *Brassica juncea*. Variety used to create SEQ ID NO:16 include JS1260MC.

SEQ ID NO:17 is the 09-0-2812 primer used to PCR an approximately 500 base product from several varieties from the six Brassica species in the Triangle of "U". 09-0-2812 corresponds to position 1500-1530 (5' to 3') for Genbank FatA sequence for *Brassica juncea* Accession No. AJ294419.

SEQ ID NO:18 is the 09-0-2813 primer used to PCR an approximately 500 base product from several varieties from the six Brassica species in the Triangle of "U". 09-0-2813 corresponds to position 2226-2197 (5' to 3') for Genbank FatA sequence for *Brassica juncea* Accession No. AJ294419.

SEQ ID NO:19 is the 09-0-3249 assay primer used in the A-specific real time PCR assay
SEQ ID NO:20 is the 09-0-3251 FatA A-genome specific real time PCR assay primer.
SEQ ID NO:21 is the 09-QP87 probe for the FatA A-genome specific real time PCR assay.

SEQ ID NO:22 is the 11-0-4046 FatA-A-genome specific gel based PCR assay primer. 11-0-4046 corresponds to position 1782-1813 (5' to 3') for Genbank FatA sequence for *Brassica napus* Accession No. X87842. 11-0-4046 corresponds to position 62-93 (5' to 3') for Genbank FatA sequence for *Brassica juncea* Accession No. AJ294419.

SEQ ID NO:23 is the 11-0-4047 FatA gel-based PCR assay primer. 11-0-4047 corresponds to position 2001-1971 (5' to 3') for the Genbank FatA sequence for *Brassica napus* Accession No. X87842). 11-0-4047 corresponds to position 279-252 (5' to 3') for GenBank FatA sequence for *Brassica juncea* Accession No. AJ294419.

SEQ ID NO:24 is the 11-0-4253 FatA gel-based PCR assay primer. 11-0-4253 corresponds to position 1918-1889 (5' to 3') for the Genbank FatA sequence for *Brassica napua* Accession No. X87842. 11-0-4253 corresponds to position 196-167 (5' to 3') for the Genbank FatA sequence for *Brassica juncea* Accession No. AJ294419.

SEQ ID NO:25 is a 14 nucleotide consensus region of SEQ ID NOS: 29, 30, and 31.

SEQ ID NO:26 is a 15 nucleotide consensus region of SEQ ID NOS: 29, 30, and 31.

SEQ ID NO: 27 is a 13 nucleotide consensus region of SEQ ID NOS: 29, 30, and 31.

SEQ ID NO:28 is a 15 nucleotide consensus region of SEQ ID NOS: 29, 30, and 31.

SEQ ID NO:29 is the A1 consensus sequence used for the alignment.
SEQ ID NO:30 is the A2 consensus sequence used for the alignment.
SEQ ID NO:31 is the A3 consensus sequence used for the alignment.
SEQ ID NO:32 is the B consensus sequence used for the alignment.
SEQ ID NO:33 is the C1 consensus sequence used for the alignment.
SEQ ID NO:34 is the C2 consensus sequence used for the alignment.
SEQ ID NO:35 is a 15 nucleotide consensus region of SEQ ID NOS: 29, 30, and 31.
SEQ ID NO: 36 is the CruA 09-O-2809 primer.
SEQ ID NO: 37 is the CruA 09-O-2811 primer.
SEQ ID NO: 38 is the HMG-I/Y 09-0-2807 primer.
SEQ ID NO: 39 is the HMG-I/Y 09-0-2808 primer.
SEQ ID NO: 40 is the CruA MDB510 forward primer.
SEQ ID NO: 41 is the MDB511 reverse primer.
SEQ ID NO: 42 is the CruA TM003 probe.
SEQ ID NO: 43 is the FatA FatA-F forward primer.
SEQ ID NO: 44 is the FatA FatA-R reverse primer.
SEQ ID NO: 45 is the FatA FatA-P probe.
SEQ ID NO: 46 is the HMG-I/Y hmg-F forward primer.
SEQ ID NO: 47 is the HMG-I/Y hmg-R reverse primer.
SEQ ID NO: 48 is the HMG-I/Y hmg-P probe.
SEQ ID NO: 49 is the BnACCg8 acc1 forward primer.
SEQ ID NO: 50 is the BnACCg8 acc2 reverse primer.
SEQ ID NO: 51 is the BnACCg8 accp probe.
SEQ ID NO: 52 is the PEP pep-F forward primer.
SEQ ID NO: 53 is the PEP pep-R reverse primer.
SEQ ID NO: 54 is the PEP pep-P probe.

DETAILED DESCRIPTION

Methods of detection and quantification that are specific to the Brassica A-genome and do not substantially cross-react with other Brassica species, crops or weedy relatives that could

contribute to contamination of a canola field are disclosed. An endogenous target that is detected is stable within each of the three A-genome species when tested on samples from multiple varieties from diverse geographical regions.

Units, prefixes, and symbols are denoted in their International System of Units (SI) accepted form. Unless otherwise indicated, nucleic acids are written left to right in 5' to 3' orientation; and amino acid sequences are written left to right in amino to carboxy orientation. Numeric ranges recited within the specification are inclusive of the numbers defining the range and include each integer within the defined range. Nucleotides may be referred to herein by their one-letter symbols recommended by the IUPAC-IUBMB Nomenclature Commission. The terms defined below are more fully defined by reference to the specification as a whole. Section headings provided throughout the specification are provided for convenience and are not limitations to the various objects and embodiments of the present disclosure.

The disclosure of each reference set forth herein is hereby incorporated by reference in its entirety, to the extent they relate to the materials and methods described herein.

As used herein and in the appended claims, the singular forms "a", "an", and "the" include plural reference unless the context clearly dictates otherwise. Thus, for example, reference to "a plant" includes a plurality of such plants, reference to "a cell" includes one or more cells and equivalents thereof known to those skilled in the art, and so forth.

As used herein, the term "comprising" means "including but not limited to."

"Plant" includes reference to whole plants, plant organs, plant tissues, plant propagules, seeds and plant cells and progeny of same. Plant cells include, without limitation, cells from seeds, suspension cultures, embryos, meristematic regions, callus tissue, leaves, roots, shoots, gametophytes, sporophytes, pollen, and microspores.

As used herein, the term "canola" refers to a type of *Brassica* having a low level of glucosinolates and erucic acid in the seed. Three canola quality *Brassica* species exist and include *B. napus*, *B. rapa*, *B. juncea*.

The terms "dicot" and "dicotyledonous plant" are used interchangeably herein.

The term "dicot" refers to the subclass of angiosperm plants also known as "dicotyledoneae" and includes reference to whole plants, plant organs (e.g., leaves, stems, roots, etc.), seeds, plant cells, and progeny of the same. Plant cell, as used herein includes, without

limitation, seeds, suspension cultures, embryos, meristematic regions, callus tissue, leaves, roots, shoots, gametophytes, sporophytes, pollen, and microspores.

The term "transgenic plant" refers to a plant that comprises within its genome a heterologous polynucleotide. Generally, the heterologous polynucleotide is stably integrated within the genome such that the polynucleotide is passed on to successive generations. The heterologous polynucleotide may be integrated into the genome alone or as part of a recombinant expression cassette. "Transgenic" is used herein to refer to any cell, cell line, callus, tissue, plant part or plant, the genotype of which has been altered by the presence of heterologous nucleic acid including those transgenic organisms or cells initially so altered, as well as those created by crosses or asexual propagation from the initial transgenic organism or cell. The term "transgenic" as used herein does not encompass the alteration of the genome (chromosomal or extra-chromosomal) by conventional plant breeding methods (i.e., crosses) or by naturally occurring events such as random cross-fertilization, non-recombinant viral infection, non-recombinant bacterial transformation, non-recombinant transposition, or spontaneous mutation.

A transgenic "event" is produced by transformation of plant cells with a heterologous DNA construct(s), including a nucleic acid expression cassette that comprises a transgene of interest, the regeneration of a population of plants resulting from the insertion of the transgene into the genome of the plant, and selection of a particular plant characterized by insertion into a particular genome location. An event is characterized phenotypically by the expression of the transgene(s). At the genetic level, an event is part of the genetic makeup of a plant. The term "event" also refers to progeny produced by a sexual outcross between the transformant and another variety that include the heterologous DNA. Even after repeated back-crossing to a recurrent parent, the inserted DNA and flanking DNA from the transformed parent is present in the progeny of the cross at the same chromosomal location. The term "event" also refers to DNA from the original transformant comprising the inserted DNA and flanking sequence immediately adjacent to the inserted DNA that would be expected to be transferred to a progeny that receives inserted DNA including the transgene of interest as the result of a sexual cross of one parental line that includes the inserted DNA (e.g., the original transformant and progeny resulting from selfing) and a parental line that does not contain the inserted DNA.

As used herein, "insert DNA" refers to the heterologous DNA within the expression cassettes used to transform the plant material while "flanking DNA" can comprise either genomic DNA naturally present in an organism such as a plant, or foreign (heterologous) DNA introduced via the transformation process which is extraneous to the original insert DNA molecule, e.g. fragments associated with the transformation event. A "flanking region" or "flanking sequence" as used herein refers to a sequence of at least 20, 50, 100, 200, 300, 400, 1000, 1500, 2000, 2500, or 5000 base pair or greater which is located either immediately upstream of and contiguous with or immediately downstream of and contiguous with the original foreign insert DNA molecule.

As used herein, a "probe" is an isolated polynucleotide to which is attached a conventional detectable label or reporter molecule, e.g., a radioactive isotope, ligand, chemiluminescent agent, enzyme, etc. Such a probe is complementary to a strand of a target polynucleotide, in the instant case, to a strand of isolated DNA from the target sample, from a sample that includes DNA e.g., from the trait of interest. Probes include not only deoxyribonucleic or ribonucleic acids but also polyamides and other probe materials that can specifically detect the presence of the target DNA sequence.

As used herein, "primers" are isolated polynucleotides that are annealed to a complementary target DNA strand by nucleic acid hybridization to form a hybrid between the primer and the target DNA strand, then extended along the target DNA strand by a polymerase, e.g., a DNA polymerase. Primer pairs refer to their use for amplification of a target polynucleotide, e.g., by the polymerase chain reaction (PCR) or other conventional nucleic-acid amplification methods. "PCR" or "polymerase chain reaction" is a technique used for the amplification of specific DNA segments (see, U.S. Pat. Nos. 4,683,195 and 4,800,159; herein incorporated by reference). Any combination of primers disclosed herein can be used such that the pair allows for the detection of Brassica A-genome.

Probes and primers are of sufficient nucleotide length to bind to the target DNA sequence and specifically detect and/or identify a polynucleotide of interest. It is recognized that the hybridization conditions or reaction conditions can be determined by the operator to achieve this result. This length may be of any length that is of sufficient length to be useful in a detection method of choice. Generally, 8, 11, 14, 16, 18, 20, 22, 24, 26, 28, 30, 40, 50, 75, 100, 200, 300,

400, 500, 600, 700 nucleotides or more, or between about 11-20, 20-30, 30-40, 40-50, 50-100, 100-200, 200-300, 300-400, 400-500, 500-600, 600-700, 700-800, or more nucleotides in length are used. Such probes and primers can hybridize specifically to a target sequence under high stringency hybridization conditions. Probes and primers according to embodiments may have complete DNA sequence identity of contiguous nucleotides with the target sequence, although probes differing from the target DNA sequence and that retain the ability to specifically detect and/or identify a target DNA sequence may be designed by conventional methods. Accordingly, probes and primers can share about 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity or complementarity to the target polynucleotide, or can differ from the target sequence by 1, 2, 3, 4, 5, 6 or more nucleotides. Probes can be used as primers, but are generally designed to bind to the target DNA or RNA and are not used in an amplification process.

Specific primers can be used to amplify an integration fragment to produce an amplicon that can be used as a "specific probe" or can itself be detected for identifying the polynucleotide of interest in biological samples. Alternatively, a probe can be used during the PCR reaction to allow for the detection of the amplification event (i.e., a Taqman probe or a MGB probe) (so called real time PCR). When the probe is hybridized with the polynucleotides of a biological sample under conditions which allow for the binding of the probe to the sample, this binding can be detected and thus allow for an indication of the presence of an event in the biological sample. Such identification of a bound probe has been described in the art. In an embodiment, the specific probe is a sequence which, under optimized conditions, hybridizes specifically to a region within the 5' or 3' flanking region of the desired location and also may comprise a part of the foreign DNA contiguous therewith. The specific probe may comprise a sequence of at least 80%, between 80 and 85%, between 85 and 90%, between 90 and 95%, and between 95 and 100% identical (or complementary) to a specific region of the target DNA.

As used herein, "amplified DNA" or "amplified fragment" or "amplicon" refers to the product of polynucleotide amplification of a target polynucleotide that is part of a nucleic acid template.

"Polynucleotide", "nucleic acid sequence", "nucleotide sequence", or "nucleic acid fragment" are used interchangeably and is a polymer of RNA or DNA that is single- or double-

stranded, optionally containing synthetic, non-natural or altered nucleotide bases. Nucleotides (usually found in their 5'-monophosphate form) are referred to by their single letter designation as follows: "A" for adenylate or deoxyadenylate (for RNA or DNA, respectively), "C" for cytidylate or deoxycytidylate, "G" for guanylate or deoxyguanylate, "U" for uridylate, "T" for deoxythymidylate, "R" for purines (A or G), "Y" for pyrimidines (C or T), "K" for G or T, "H" for A or C or T, "I" for inosine, and "N" for any nucleotide.

The term "single nucleotide polymorphism" or "SNP" is a DNA_{sequence} variation occurring when a single nucleotide — A, T, C, or G — in the genome (or other shared sequence) differs between members of a species (or between paired chromosomes in an individual). For example, two sequenced DNA fragments from different individuals, AAGCCTA to AAGCTTA, contain a difference in a single nucleotide. In this case we say that there are two alleles: C and T. Almost all common SNPs have only two alleles.

Alleles may be detected using various techniques (Nakitandwe et al., 2007; herein incorporated by reference).

"Polypeptide", "peptide", "amino acid sequence" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical analogue of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers. The terms "polypeptide", "peptide", "amino acid sequence", and "protein" are also inclusive of modifications including, but not limited to, glycosylation, lipid attachment, sulfation, gamma-carboxylation of glutamic acid residues, hydroxylation and ADP-ribosylation.

Probes and primers hybridize specifically to a target sequence under stringency hybridization conditions. Hybridization references include, but are not limited to, Herzer and Englert, 2002 Palmisano et al., 2005; herein incorporated by reference.

The term "under stringent conditions" means that two sequences hybridize under moderately or highly stringent conditions. More specifically, moderately stringent conditions can be readily determined by those having ordinary skill in the art, e.g., depending on the length of DNA. The basic conditions are set forth by Sambrook et al., Molecular Cloning: A Laboratory Manual, third edition, chapters 6 and 7, Cold Spring Harbor Laboratory Press, 2001 and include the use of a prewashing solution for nitrocellulose filters 5xSSC, 0.5% SDS, 1.0

mM EDTA (pH 8.0), hybridization conditions of about 50% formamide, 2xSSC to 6xSSC at about 40-50 °C (or other similar hybridization solutions, such as Stark's solution, in about 50% formamide at about 42 °C) and washing conditions of, for example, about 40-60 °C, 0.5-6xSSC, 0.1% SDS. Preferably, moderately stringent conditions include hybridization (and washing) at about 50 °C and 6xSSC. Highly stringent conditions can also be readily determined by those skilled in the art, e.g., depending on the length of DNA.

Generally, such conditions include hybridization and/or washing at higher temperature and/or lower salt concentration (such as hybridization at about 65 °C, 6xSSC to 0.2xSSC, preferably 6xSSC, more preferably 2xSSC, most preferably 0.2xSSC), compared to the moderately stringent conditions. For example, highly stringent conditions may include hybridization as defined above, and washing at approximately 65-68 °C, 0.2xSSC, 0.1% SDS. SSPE (1xSSPE is 0.15 M NaCl, 10 mM NaH₂PO₄, and 1.25 mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15 M NaCl and 15 mM sodium citrate) in the hybridization and washing buffers; washing is performed for 15 minutes after hybridization is completed.

It is also possible to use a commercially available hybridization kit which uses no radioactive substance as a probe. Specific examples include hybridization with an ECL direct labeling & detection system (Amersham). Stringent conditions include, for example, hybridization at 42 °C for 4 hours using the hybridization buffer included in the kit, which is supplemented with 5% (w/v) Blocking reagent and 0.5 M NaCl, and washing twice in 0.4% SDS, 0.5xSSC at 55 °C for 20 minutes and once in 2xSSC at room temperature for 5 minutes. As used herein, "amplified DNA" or "amplicon" refers to the product of nucleic acid amplification of a target nucleic acid sequence that is part of a nucleic acid template.

"Genome" as it applies to plant cells encompasses not only chromosomal DNA found within the nucleus, but organelle DNA found within subcellular components (e.g., mitochondrial, plastid) of the cell. Genomic regions refer to a portion of the genome that is targeted to be specifically detected for example, through an amplification reaction or by direct sequencing.

"Heterologous" with respect to sequence means a sequence that originates from a foreign species, or, if from the same species, is substantially modified from its native form in composition and/or genomic locus by deliberate human intervention.

The term “homologous” refers to nucleic acid sequences that are derived from a common ancestral gene through natural or artificial processes (e.g., are members of the same gene family), and thus, typically, share sequence similarity. Typically, homologous nucleic acids have sufficient sequence identity that one of the sequences or its complement is able to selectively hybridize to the other under selective hybridization conditions. The term “selectively hybridizes” includes reference to hybridization, under stringent hybridization conditions, of a nucleic acid sequence to a specified nucleic acid target sequence to a detectably greater degree (e.g., at least 2-fold over background) than its hybridization to non-target nucleic acid sequences and to the substantial exclusion of non-target nucleic acids. Selectively hybridizing sequences have about at least 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity with each other. A nucleic acid that exhibits at least some degree of homology to a reference nucleic acid can be unique or identical to the reference nucleic acid or its complementary sequence.

“Messenger RNA (mRNA)” refers to the RNA that is without introns and that can be translated into protein by the cell.

“cDNA” refers to a DNA that is complementary to and synthesized from a mRNA template using the enzyme reverse transcriptase. The cDNA can be single-stranded or converted into the double-stranded form using the Klenow fragment of DNA polymerase I.

“Isolated” refers to materials, such as nucleic acid molecules and/or proteins, which are substantially free or otherwise removed from components that normally accompany or interact with the materials in a naturally occurring environment. Isolated polynucleotides may be purified from a host cell in which they naturally occur. Conventional nucleic acid purification methods known to skilled artisans may be used to obtain isolated polynucleotides. The term also embraces recombinant polynucleotides and chemically synthesized polynucleotides.

“Recombinant” refers to an artificial combination of two otherwise separated segments of sequence, e.g., by chemical synthesis or by the manipulation of isolated segments of nucleic acids by genetic engineering techniques. “Recombinant” also includes reference to a cell or vector, that has been modified by the introduction of a heterologous nucleic acid or a cell derived from a cell so modified, but does not encompass the alteration of the cell or vector by

naturally occurring events (e.g., spontaneous mutation, natural transformation/transduction/transposition) such as those occurring without deliberate human intervention.

“Recombinant DNA construct” refers to a combination of nucleic acid fragments that are not normally found together in nature. Accordingly, a recombinant DNA construct may comprise regulatory sequences and coding sequences that are derived from different sources, or regulatory sequences and coding sequences derived from the same source, but arranged in a manner different than that normally found in nature.

“Regulatory sequences” refer to nucleotide sequences located upstream (5' non-coding sequences), within, or downstream (3' non-coding sequences) of a coding sequence, and which influence the transcription, RNA processing or stability, or translation of the associated coding sequence. Regulatory sequences may include, but are not limited to, promoters, translation leader sequences, introns, and polyadenylation recognition sequences. The terms “regulatory sequence” and “regulatory element” are used interchangeably herein.

“Promoter” refers to a nucleic acid fragment capable of controlling transcription of another nucleic acid fragment.

"Promoter functional in a plant" is a promoter capable of controlling transcription in plant cells whether or not its origin is from a plant cell.

“Tissue-specific promoter” and “tissue-preferred promoter” are used interchangeably, and refer to a promoter that is expressed predominantly but not necessarily exclusively in one tissue or organ, but that may also be expressed in one specific cell.

"Developmentally regulated promoter" refers to a promoter whose activity is determined by developmental events.

“Operably linked” refers to the association of nucleic acid fragments in a single fragment so that the function of one is regulated by the other. For example, a promoter is operably linked with a nucleic acid fragment when it is capable of regulating the transcription of that nucleic acid fragment.

“Expression” refers to the production of a functional product. For example, expression of a nucleic acid fragment may refer to transcription of the nucleic acid fragment (e.g.,

transcription resulting in mRNA or functional RNA) and/or translation of mRNA into a precursor or mature protein.

“Phenotype” means the detectable characteristics of a cell or organism.

“Introduced” in the context of inserting a nucleic acid fragment (e.g., a recombinant DNA construct) into a cell, means “transfection” or “transformation” or “transduction” and includes reference to the incorporation of a nucleic acid fragment into a eukaryotic or prokaryotic cell where the nucleic acid fragment may be incorporated into the genome of the cell (e.g., chromosome, plasmid, plastid or mitochondrial DNA), converted into an autonomous replicon, or transiently expressed (e.g., transfected mRNA).

A “transformed cell” is any cell into which a nucleic acid fragment (e.g., a recombinant DNA construct) has been introduced.

“Transformation” as used herein refers to both stable transformation and transient transformation.

“Stable transformation” refers to the introduction of a nucleic acid fragment into a genome of a host organism resulting in genetically stable inheritance. Once stably transformed, the nucleic acid fragment is stably integrated in the genome of the host organism and any subsequent generation.

“Transient transformation” refers to the introduction of a nucleic acid fragment into the nucleus, or DNA-containing organelle, of a host organism resulting in gene expression without genetically stable inheritance.

Amplification

In vitro amplification techniques are well known in the art. Examples of techniques sufficient to direct persons of skill through such *in vitro* methods, including the polymerase chain reaction (PCR), the ligase chain reaction (LCR), Q β -replicase amplification and other RNA polymerase mediated techniques (e.g., NASBA), are found in Berger, Sambrook and Ausubel (all *supra*) as well as Mullis et al. ((1987) U.S. Patent No. 4,683,202); PCR Protocols, A Guide to Methods and Applications ((Innis et al., eds.) Academic Press Inc., San Diego Academic Press Inc. San Diego, CA (1990) (Innis)); Arnheim & Levinson ((October 1, 1990) C&EN 36-47); The Journal Of NIH Research (1991) 3, 81-94; Kwoh et al. ((1989) Proc. Natl.

Acad. Sci. USA 86, 1173); Guatelli et al. ((1990) Proc. Natl. Acad. Sci. USA 87, 1874); Lomell et al. ((1989) J. Clin. Chem. 35, 1826); Landegren et al. ((1988) Science 241, 1077-1080); Van Brunt ((1990) Biotechnology 8, 291-294); Wu and Wallace ((1989) Gene 4, 560); Barringer et al. ((1990) Gene 89, 117), and Sooknanan and Malek ((1995) Biotechnology 13: 563-564). Improved methods of cloning *in vitro* amplified nucleic acids are described in Wallace et al., U.S. Pat. No. 5,426,039. Improved methods of amplifying large nucleic acids by PCR are summarized in Cheng et al. (1994) Nature 369: 684, and the references therein, in which PCR amplicons of up to 40kb are generated. One of skill will appreciate that essentially any RNA can be converted into a double stranded DNA suitable for restriction digestion, PCR expansion and sequencing using reverse transcriptase and a polymerase. *See*, Ausubel, Sambrook and Berger, *all supra*.

In an embodiment of the disclosure described herein, the amplified fragment of Brassica A genome comprises (i) the nucleotide sequence of at least one of SEQ ID NOS: 29, 30, or 31; or (ii) a nucleic acid fragment of at least one of SEQ ID NOS: 29, 30, or 31, wherein the nucleic acid fragment is selected from the group consisting of nucleotide position from about 50 to about nucleotide position 400, 50 to about nucleotide position 100, 50 to about nucleotide position 350, 400 to about nucleotide position 350, 400 to about nucleotide position 200, and 400 to about nucleotide position 100 of SEQ ID NOS: 29, 30, or 31. The amplified fragment of Brassica A genome comprises a nucleic acid fragment of at least one of SEQ ID NOS: 29, 30, or 31, wherein the nucleic acid fragment is selected from the group consisting of nucleotide position from about 50 to about nucleotide position 400. This may include, but is not limited to, any single numeric digit interval from about position 50 to about position 400. The nucleic acid fragment may comprise any amplified fragment between and including nucleotide position 50 to nucleotide position 400.

In an embodiment of the disclosure, the detection method comprises sequencing a biological sample containing genomic DNA of Brassica A genome, wherein the genomic DNA comprises (i) the nucleotide sequence of at least one of SEQ ID NOS: 29, 30, or 31; or (ii) a nucleic acid fragment of at least one of SEQ ID NOS: 29, 30, or 31, wherein the nucleic acid fragment is selected from the group consisting of nucleotide position from about 50 to about nucleotide position 400, 50 to about nucleotide position 100, 50 to about nucleotide position

350, 400 to about nucleotide position 350, 400 to about nucleotide position 200, and 400 to about nucleotide position 100 of SEQ ID NOS: 29, 30, or 31 or a complement thereof. The portion of the genomic DNA sequenced can be any region within one of SEQ ID NOS: 29, 30, or 31.

The amplicon produced by these methods may be detected by a plurality of methods.

Oligonucleotides for use as primers, e.g., in amplification reactions and for use as nucleic acid sequence probes, are typically synthesized chemically according to the solid phase phosphoramidite triester method described by Beaucage and Caruthers ((1981) Tetrahedron Lett. 22:1859), or can simply be ordered commercially.

DNA detection kits can be developed using the compositions disclosed herein and the methods well known in the art.

“Sequence identity” or “identity” in the context of two nucleic acid or polypeptide sequences refers to residues that are the same in both sequences when aligned for maximum correspondence over a specified comparison window.

“Percentage sequence identity” refers to the value determined by comparing two optimally aligned sequences over a comparison window. The percentage is calculated by determining the number of positions at which both sequences have the same nucleotide or amino acid residue, determining the number of matched positions, dividing the number of matched positions by the total number of positions in the comparison window, and multiplying the result by 100 to yield the percentage of sequence identity.

When percentage of sequence identity is used in reference to proteins it is recognized that residue positions that are not identical often differ by conservative amino acid substitutions, where amino acid residues are substituted for other amino acid residues with similar chemical properties (e.g., charge or hydrophobicity) and therefore do not change the functional properties of the molecule. Where sequences differ by conservative substitutions, the percent sequence identity may be adjusted upwards to correct for the conservative nature of the substitution. Sequences that differ by such conservative substitutions are said to have “sequence similarity” or “similarity”. Means for making this adjustment are well-known to those of skill in the art. Typically this involves scoring a conservative substitution as a partial rather than a full mismatch, thereby increasing the percentage sequence identity. Thus, for example, where an

identical amino acid is given a score of 1 and a non-conservative substitution is given a score of zero, a conservative substitution is given a score between zero and 1. The scoring of conservative substitutions is calculated, e.g., according to the algorithm of Meyers and Miller (1988) Computer Applic. Biol. Sci. 4:11-17, e.g., as implemented in the program PC/GENE (Intelligenetics, Mountain View, California, USA).

Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison may be conducted by the local homology algorithm of Smith and Waterman ((1981) Adv. Appl. Math. 2:482); by the homology alignment algorithm of Needleman and Wunsch ((1970) J. Mol. Biol. 48:443); by the search for similarity method of Pearson and Lipman ((1988) Proc. Natl. Acad. Sci. USA 85:2444); by computerized implementations of these algorithms, including, but not limited to: CLUSTAL in the PC/Gene program by Intelligenetics, Mountain View, California; GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), Madison, Wisconsin, USA; the CLUSTAL program is well described by Higgins and Sharp ((1988) Gene 73:237-244); Higgins and Sharp ((1989) CABIOS 5:151-153); Corpet et al. ((1988) Nucleic Acids Research 16:10881-90); Huang et al. ((1992) Computer Applications in the Biosciences 8: 155-65), and Pearson et al. ((1994) Methods in Molecular Biology 24:307-331).

The BLAST family of programs that can be used for database similarity searches includes: BLASTN for nucleotide query sequences against nucleotide database sequences; BLASTX for nucleotide query sequences against protein database sequences; BLASTP for protein query sequences against protein database sequences; TBLASTN for protein query sequences against nucleotide database sequences; and TBLASTX for nucleotide query sequences against nucleotide database sequences. See, e.g., Current Protocols in Molecular Biology, Chapter 19, Ausubel et al., Eds., (1995) Greene Publishing and Wiley-Interscience, New York; Altschul et al. (1990) J. Mol. Biol. 215:403-410; and, Altschul et al. (1997) Nucleic Acids Res. 25:3389-3402.

Software for performing BLAST analyses is publicly available, e.g., through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of

length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold. These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W , T , and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, $M=5$, $N=-4$, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (see, e.g., Henikoff & Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915).

In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin & Altschul (1993) Proc. Nat'l. Acad. Sci. USA 90:5873-5877). One measure of similarity provided by the BLAST algorithm is the smallest sum probability ($P(N)$), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance.

BLAST searches assume that proteins can be modeled as random sequences. However, many real proteins comprise regions of nonrandom sequences that may be homopolymeric tracts, short-period repeats, or regions enriched in one or more amino acids. Such low-complexity regions may be aligned between unrelated proteins even though other regions of the protein are entirely dissimilar. A number of low-complexity filter programs can be employed to reduce such low-complexity alignments. For example, the SEG (Wooten and Federhen (1993) Comput. Chem. 17:149-163) and XNU (Claverie and States (1993) Comput. Chem. 17:191-201) low-complexity filters can be employed alone or in combination.

Standard recombinant DNA and molecular cloning techniques used herein are well known in the art and are described more fully in Sambrook, J., Fritsch, E.F. and Maniatis, T. *Molecular Cloning: A Laboratory Manual*; Cold Spring Harbor Laboratory Press: Cold Spring Harbor, 1989 (hereinafter “Sambrook”).

Examples

The following experimental methods and results provide additional details regarding specific aspects of protocols and procedures relevant to the practice of the present disclosure. The examples, which are provided without limitation to illustrate the claimed invention, involve the application of protocols well known to those of skill in the art, and detailed in the references cited herein.

Example 1: Development of A-Genome Specific Endogenous Reference System

Selection of Plant Material

Seeds from various countries were selected from the six Brassica species that make up the Triangle of “U”: *B. carinata*, *B. juncea*, *B. napus*, *B. nigra*, *B. oleracea*, and *B. rapa* (as well as *B. rapa* subspecies) varieties (Figure 1). Brassica-related species that may be found in or around canola were also included in this study. This includes: *Camelina sitava*, *Erucastrum gallicum*, *Thlaspi arvense*, *Sinapis alba* and *Sinapis arvensis* (as well as *S. arvensis* subspecies). Seeds from other crops were also included: maize, rice, sorghum, tomato, cotton, soybean. The majority of seeds were received from Pioneer Hybrid Inc. in Georgetown, Ontario, Canada and also from USDA (United States Department of Agriculture) in Ames, IA and Geneva, NY. Table 1 shows the source of seeds used. For those seeds obtained from the USDA, the USDA Accession Numbers (ACNO) are included.

Table 1. Seed Sources. Italicized text denotes seed varieties used for sequencing. ACNO represents accession number for seeds acquired from USDA. ACNO=Accession Number; Note: Sequences from ACNO 633153 were assigned to both the A and C contigs, suggesting this variety may actually be a *B. napus* (AACC) variety (see Example 3 herein). Two *B. nigra* varieties (ACNO 633142 and ACNO 649156) were assigned to two different consensuses suggesting that these two varieties are not the same species (see Example 3 herein).

Species	Source	ACNO (seeds from USDA); Variety name (seeds from Pioneer)
B. napus	Pioneer	45H73
	Pioneer	NS1822BC
	Pioneer	46A76
	Pioneer	NS5536BC
	Pioneer	43A56
	Pioneer	NW1717M
	Pioneer	NW4219BC
	Pioneer	NW4201BC
	USDA (Ames, IA)	436554
	USDA (Ames, IA)	458967
	USDA (Ames, IA)	458954
	USDA (Ames, IA)	531273
	USDA (Ames, IA)	458941
	USDA (Ames, IA)	469735
	USDA (Ames, IA)	458605
	USDA (Ames, IA)	311729
	USDA (Ames, IA)	305278
B. rapa	Pioneer	Tobin
	Pioneer	Klondike
	Pioneer	Reward
	Pioneer	41P95
	USDA (Ames, IA)	257229
	USDA (Ames, IA)	633153
	USDA (Ames, IA)	649159
	USDA (Ames, IA)	163496
B. rapa ssp dichotoma	USDA (Ames, IA)	347600
B. rapa ssp oleifera	USDA (Ames, IA)	649190
B. rapa ssp trilocularis	USDA (Ames, IA)	346882
B. rapa var. parachinensis	USDA (Ames, IA)	390962
B. juncea	Pioneer	JS0879BC
	Pioneer	JS0917BC

	Pioneer	<i>JS0936BC</i>
	Pioneer	<i>JS1056BC</i>
	Pioneer	<i>JS1260MC</i>
	Pioneer	<i>JS1432MC</i>
	USDA (Ames, IA)	<i>418956</i>
	USDA (Ames, IA)	<i>458942</i>
	USDA (Ames, IA)	<i>603011</i>
B. oleracea var. alboglabra	USDA (Geneva, NY)	<i>249556</i>
B. oleracea var. botrytis	USDA (Geneva, NY)	<i>28888</i>
B. oleracea var. capitata	USDA (Geneva, NY)	<i>29041</i>
B. oleracea var. costata	USDA (Geneva, NY)	<i>29800</i>
B. oleracea var. gemmifera	USDA (Geneva, NY)	<i>365148</i>
B. oleracea var. gongylodes	USDA (Geneva, NY)	<i>29790</i>
B. oleracea var. italica	USDA (Geneva, NY)	<i>28852</i>
B. oleracea var. medullosa	USDA (Geneva, NY)	<i>30862</i>
B. oleracea var. ramosa	USDA (Geneva, NY)	<i>30724</i>
B. oleracea var. viridis	USDA (Geneva, NY)	<i>32550</i>
B. nigra	USDA (Ames, IA)	<i>273638</i>
	USDA (Ames, IA)	<i>633142</i>
	USDA (Ames, IA)	<i>649156</i>
	USDA (Ames, IA)	<i>193960</i>
	USDA (Ames, IA)	<i>271444</i>
	USDA (Ames, IA)	<i>633143</i>
	USDA (Ames, IA)	<i>220282</i>
	USDA (Ames, IA)	<i>649154</i>
	USDA (Ames, IA)	<i>280638</i>
	USDA (Ames, IA)	<i>357369</i>
	USDA (Ames, IA)	<i>633147</i>

	USDA (Ames, IA)	131512
	USDA (Ames, IA)	597829
	USDA (Ames, IA)	649155
B. carinata	USDA (Ames, IA)	613124
	USDA (Ames, IA)	597822
	USDA (Ames, IA)	360879
	USDA (Ames, IA)	596534
	USDA (Ames, IA)	2779
	USDA (Ames, IA)	193460
	USDA (Ames, IA)	633076
	USDA (Ames, IA)	390133
	USDA (Ames, IA)	209023
	USDA (Ames, IA)	360882
Sinapis alba	USDA (Ames, IA)	19266
	USDA (Ames, IA)	305276
	USDA (Ames, IA)	311724
	USDA (Ames, IA)	458960
	USDA (Ames, IA)	409025
	USDA (Ames, IA)	633274
Sinapis arvensis	USDA (Ames, IA)	21449
	USDA (Ames, IA)	597863
	USDA (Ames, IA)	633374
Sinapis arvensis subsp. arvensis	USDA (Ames, IA)	296079
	USDA (Ames, IA)	407561
	USDA (Ames, IA)	633411
Erucastrum gallicum	USDA (Ames, IA)	22990
Raphanus raphanistrum	USDA (Geneva, NY)	271456
Raphanus sativus	USDA (Geneva, NY)	268370
Camelina sativa	USDA (Ames, IA)	650165
Thlaspi arvense	USDA (Ames, IA)	633414
	USDA (Ames, IA)	29118
Arabidopsis thaliana Columbia type	Pioneer	
Gossypium hirsutum	Pioneer	
Helianthus annuus	USDA (Ames, IA)	7451
	USDA (Ames, IA)	29348

	USDA (Ames, IA)	592319
<i>Solanum lycopersicum</i>	USDA (Geneva, NY)	645248
<i>Glycine max</i>	Pioneer	
<i>Oryza sativa</i>	Grocery store (USA)	
<i>Sorghum bicolor</i>	Pioneer	
<i>Zea mays</i>	Pioneer	

Genomic DNA Extraction from Seeds

For consistency, all genomic DNA was extracted from seeds using the same DNA extraction method: a CTAB-based lysis method with passage of the precipitated DNA through a Qiagen Genomic Tip (Qiagen Inc, Valencia, CA) for further purification. This DNA extraction protocol was validated in-house for *Zea mays*, *Glycine max*, and *Brassica napus*. All DNA samples were quantified using a PicoGreen assay (Molecular Probes; Eugene, OR). For the Specificity Comparison of assays, most of the DNAs were tested in a total of 9 reactions (i.e. 3 runs in triplicate). The exceptions are listed in Table 2.

Table 2. Exceptions (DNA tested in less than 9 replicates)

ACNO or Variety name	Species	BnACCg8	FatA	FatA(A)	HMG-I/Y	PEP
	<i>Arabidopsis thaliana</i> Columbia type	6	4	7	4	4
<i>JS0879BC</i>	<i>Brassica juncea</i>		6			
<i>JS0917BC</i>	<i>Brassica juncea</i>		6			
<i>NW4219BC</i>	<i>Brassica napus</i>		6			
<i>469735</i>			6			
193960	<i>Brassica nigra</i>	4	2	2	2	2
220282		2	2	5	2	2
357369		2	7	7	7	4
597829			6			
22990	<i>Erucastrum gallicum</i>	6	4	7	4	4
633374	<i>Sinapis arvensis</i>	6	6	6	6	6
633414	<i>Thlaspi arvense</i>	6				

Primers and Probes

The primers used herein were synthesized by Integrated DNA Technologies (Coralville, Iowa), and the probes were synthesized by Applied Biosystems (Carlsbad, CA). The sequences of all primers used for generating PCR products for sequencing are listed in Table 3; and the sequences for all primers and probes for the Specificity Testing are listed in Table 4. All probes were labeled as described in the relevant references, except the HMG-I/Y probe 9. Since the SDS2.3 software does not have a detector for HEX, the HMG-I/Y probe was labeled with VIC instead of HEX, since the VIC dye fluoresces in wavelength similar to the HEX dye.

Table 3. Primers Used for Generating PCR Products. *B. carinata* or *B. nigra* sequences were not found for CruA, FatA, or HMG-I/Y genes in Genbank.

Genbank Accession numbers						
Gene	Primer/Probe	Sequence (5' to 3')	<i>B. napus</i> (position of forward (f) and reverse (r) primers; amplicon size)	<i>B. rapa</i>	<i>B. juncea</i>	<i>B. oleracea</i>
FatA	09-O-2809	AGCTCAATGCAC TGGAGCCGTCAC AC (SEQ ID NO: 36)	X1455 (f:809-834; r:1555-1528; 747 bp)	KBrHO42K14F	n/a	BOGK18 6TF
	09-O-2811	GGTGGCTGGCTA AATCGAGGACG GAAAC (SEQ ID NO: 37)				
CruA	09-O-2812	GACACAAGGCG GCTTCAAAGAGT TACAGATG (SEQ ID NO: 17)	X87842 (f: 1721- 1751; r: 2226-2197; 506 bp)	n/a	BJU278479, AJ294419	n/a
	09-O-2813	ACAATGTCATCT TGCTGGCATTCT CTTCTG (SEQ ID NO: 18)				
HMG-I/Y	09-0-2807	AACGACGCGAA CGGTTGCAACAA GAC (SEQ ID NO: 38)	AF127919 (f: 176- 201; r: 678-649; 503 bp)	KBrB123C07R, KBrB078D23F, KBrB026F21R , CT012477	n/a	OEG82B0 5.B1, BOMRW 66TR, BONPC3 2TF
	09-0-2808	CGTCAACTTTAG CAACCAACAGG CACCATC (SEQ ID NO: 39)				

Table 4. Real-time PCR Primers and Probes. Asterisk notes that all probes were labeled as described in the reference, except the HMG-I/Y probe; VIC-TAMRA was used instead of HEX-TAMRA. Double asterisk notes that FatA(A) describes the A-genome specific assay disclosed herein.

Gene	Primer/Probe*	Sequence (5' to 3')	Final conc. (nM) in real-time PCR	Reference
uA	MDB510	GGCCAGGGTTTCCGTGAT (SEQ ID NO 40)	200	1
	MDB511	CCGTCGTTGTAGAACCATTGG (SEQ ID NO 41)	200	
	TM003	VIC- AGTCCTTATGTGCTCCACTTTCTGGTGC A-TAMRA (SEQ IN NO 42)	200	
tA	FatA-F	GGTCTCTCAGCAAGTGGGTGAT (SEQ ID NO 43)	150	2
	FatA-R	TCGTCCCGAACTTCATCTGTAA (SEQ ID NO 44)	150	
	FatA-P	FAM- ATGAACCAAGACACAAGGCGGCTTCA- TAMRA (SEQ ID NO 45)	50	
(A)**	09-0-3249	ACAGATGAAGTTCGGGACGAGTAC (SEQ ID NO 19)	300	Described in this patent application.
	09-0-3251	CAGGTTGAGATCCACATGCTTAAATAT (SEQ ID NO 20)	900	
	09-QP87	FAM-AAGAAGAATCATCATGCTTC-MGB (SEQ ID NO 21)	150	
G-I/Y	hmg-F	GGTCGTCCTCCTAAGGCGAAAG (SEQ ID NO 46)	500	3
	hmg-R	CTTCTTCGGCGGTTCGTCCAC (SEQ ID NO 47)	500	
	hmg-P**	VIC-CGGAGCCACTCGGTGCCGCAACTT- TAMRA (SEQ ID NO 48)	300	
CCg8	acc1	GGTGAGCTGTATAATCGAGCGA (SEQ ID NO 49)	300	4
	acc2	GGCGCAGCATCGGCT (SEQ ID NO 50)	300	
	accp	VIC- AACACCTATTAGACATTTCGTTCCATTGG TCGA-TAMRA (SEQ ID NO 51)	200	
EP	pep-F	CAGTTCTTGAGCCGCTTGAG (SEQ ID NO 52)	300	5
	pep-R	TGACGGATGTGAGCTTCACA (SEQ ID NO 53)	300	
	pep-P	FAM- ACAGACCTACAGCCGATGGAAGCCTGC- TAMRA (SEQ ID NO 54)	200	

References in Table 4:

1. EURL method for detection of: 1) T45 (http://gmo-crl.jrc.ec.europa.eu/summaries/T45_validated_RTPCR_method.pdf), 2) MS8 (http://gmo-crl.jrc.ec.europa.eu/summaries/Ms8_validated_Method_Corrected%20version%201.pdf), 3) RF3 (http://gmo-crl.jrc.ec.europa.eu/summaries/Rf3_validated_Method.pdf), and 4) RT73 (http://gmo-crl.jrc.ec.europa.eu/summaries/RT73_validated_Method.pdf)
2. Wu, Y., Wu, G., Xiao, L., Lu, C. Event-Specific Qualitative and Quantitative PCR Detection Methods for Transgenic Rapeseed Hybrids MS1 x RF1 and MS1 x RF2; J. Agric. Food Chem. 2007, 55, 8380-8389
3. Weng, H.; Yang, L.; Liu, Z.; Ding, J.; Pan, A.; Zhang, D. Novel reference gene, *High-mobility-group protein I/Y*, used in qualitative and real-time quantitative polymerase chain reaction detection of transgenic rapeseed cultivars J. AOAC Int. 2005, 88, 577-584
4. Hernandez, M.; Rio, A.; Esteve, T.; Prat, S.; Pla, M. A rapeseed-specific gene, *Acetyl-CoA Carboxylase*, can be used as a reference for qualitative and real-time quantitative PCR detection of transgenes from mixed food samples. J. Agric. Food Chem. 2001, 49, 3622-3627.
5. Zeitler, R.; Rietsch, K.; Vaiblinger, H. Validation of real-time PCR methods for the quantification of transgenic contaminations in rapeseed; Eur Food Res Technol (2002) 214:346-351.

CruA, HMG I/Y and FatA PCR design and selection of template DNAs

In order to design an A-genome specific endogenous real-time PCR assay, three genes were selected: CruA, HMG-I/Y and FatA. Amplification and sequencing of an approximately 500 bp region from these genes from multiple varieties of the six species in the Triangle of "U" was performed. Primers were designed in the identified conserved regions in the available sequences from the six members of the Triangle of "U". Although sequences were not available from all six of the Brassica species for all three genes, alignments were made and primers were designed in the conserved regions of the available sequences. Seeds from several varieties (N=38) were selected from various geographical regions in order to capture sequence diversity of the A-genome species (*B. rapa*, *B. napus*, and *B. juncea*) to develop the assays. The number

of varieties sequenced from the remaining 3 species (*B. olearcea*, *B. carinata*, and *B. nigra*) were less (N=15).

Primer design for PCR/cloning/sequencing regions of FatA, CruA and HMG genes

GenBank sequences of FatA, CruA and HMG from the Triangle of “U” species were selected and aligned to find conserved sequences for designing primers and to amplify an approximate 500 bp region from each of these genes. Table 3 shows the Genbank accession number of the sequences used in the alignment, as well as the position and amplicon size of the selected primers (on the *B. napus* accession). No GenBank sequences were available for *B. carinata* and *B. nigra* for these three genes.

Primers were selected to PCR, clone and sequence a region of each gene. For CruA, the selected primers (09-O-2809/ 09-O-2811) encompass the referenced real-time assay (MDB410, MDB511, TM003), extending 599 bases 5’ and 47 bases 3’ of the real-time PCR amplicon. For HMG-I/Y the selected primers (09-O-2807/ 09-O-2808) encompass the referenced real-time assay (hmg-F, hmg-R, hmg-P), extending 273 bases 5’ and 131 bases 3’ of the real-time PCR amplicon. For FatA, the selected primers (09-O-2812/09-O-2813) are slightly downstream of the FatA assay (FatA-F, FatA-R, FatA-P), omitting 32 bases 5’ and extending 462 bases 3’ of the real-time PCR amplicon.

PCR, cleanup and cloning

Genomic DNA (100-120ng) isolated from 53 seed varieties (see italicized varieties in Table 1) was used as template for PCRing the region of interest to be cloned and sequenced. The selection of seeds consist of multiple varieties from various geographical regions for *B. napus* (N=17), *B. juncea* (N=9), *B. rapa* (N=12), *B. nigra* (N=3), *B. carinata* (N=2) and *B. oleracea* (N=10). The purified PCR products were cloned into PGEM-T Easy vector. Approximately 6 clones were selected for sequencing using the T7 and SP6 vector primers. In some cases more clones were isolated and sequenced to achieve coverage of both genomes in the allotetraploid species.

Sequence analysis and optimization of A-specific real-time PCR primers and probe

Sequencher v. 4.8 was used for sequence analysis of the cloned PCR products from the CruA, HMG and FatA genes. Alignments of the final contigs were made in Vector NTI. After the design of several primer/probe combinations to be specific to the A-genome of FatA, the optimum primer/probe combination was selected based on A-genome specificity, cycle threshold (Ct) values and PCR efficiency. The optimum primer and probe concentrations were selected based on Ct values, delta Rn values, and PCR efficiency.

Once the assay was optimized, a dilution series was prepared with *B. napus* genomic DNA. A 40 ng/ul dilution of genomic DNA was serially diluted 4 times at 1:2. This dilution series was tested in the optimized real-time assay, using 5 ul of the dilutions (input template DNA in the PCR ranged from 200ng to 12.5ng). PCR efficiency and R2 coefficient were evaluated.

Specificity testing with six endogenous real-time PCR assays

Six rapeseed endogenous real-time PCR assays were selected for the specificity testing, including the FatA (A) assay described herein. For consistency, all reactions included 15 ul of a mastermix (including primers, probes, water and 10 ul of Applied Biosystems TaqMan Universal PCR Master Mix w/o AmpErase UNG) and 5 ul of 20 ng/ul genomic DNA (=100ng genomic DNA) for a final reaction volume of 20 ul. The primer and probe concentrations were as described in the relevant references, and listed in Table 4.

The cycling parameters for the real-time PCR runs were as follows: initial denaturation at 95°C for 10 minutes; 40 cycles of 95°C for 15 seconds (denaturation) and 60°C for 60 seconds (annealing and extension). The real-time PCR runs were performed on 384-well plates in an Applied Biosystems 7900HT instrument. Data was analyzed using Applied Biosystems Sequence Detection Systems (SDS) v. 2.3. For most of the tested samples (see Table 1), the PCR was run in triplicate over three separate real-time PCR runs. Some of the DNA was in limited supply and was run in duplicate and/or less PCR runs. See Table 2 for description of the number of runs and replicates in each of the assays with the DNA that was in limited supply. Varieties NW4219BC, 469735, JS0879BC, JS0917BC, and 597829 had less replicates due to poor PCR results, not lack of DNA.

Example 2: Sequencing regions of CruA, HMG I/Y and FatA

The primers that were selected resulted in amplification in all six species. To maximize the likelihood that amplification would occur on both genomes within the allotetraploid species (*B. napus*, *B. juncea* and *B. carinata*), additional clones were selected.

Once the PCR products were cloned from the multiple varieties within the six species, several clones (≥ 6) were selected for sequencing in order to increase the chance of capturing all potential diversity from the resulting PCR products. For the allotetraploid species, the goal was to obtain sequences from both genomes.

Subsequent to sequence analysis, some additional clones were selected and sequenced in order to fill gaps in genome coverage for the allotetraploid species.

Example 3: Assigning sequence data into consensus representing genomes

The consensus sequences were assigned to various consensus groups, and based on overlap of the base species (*B. rapa*, *B. oleracea* and *B. nigra*) and the allotetraploid species (*B. napus*, *B. juncea* and *B. carinata*), these were further assigned to either the A, B or C genome. Due to genetic variation of the A, B and C genomes between the species, in some cases more than one consensus sequence was defined for each genome.

CruA

For the CruA sequencing project, two A and two C genome consensus were identified. However, defining a consensus for the B genome was difficult. The cloned PCR products from *B. juncea* (AABB) all fell within the A consensus. In addition, several of the *B. juncea* varieties were difficult to PCR. The two *B. carinata* (BBCC) varieties resulted in cloned PCR products from the C genome only. The difficulty in determining a B consensus may be due to poor binding of the primers to the B genome or the B sequence may not differ significantly from the A consensus. The limited number of varieties from *B. carinata* (BBCC) and *B. nigra* (BB) that were sequenced also may have contributed to difficulty in distinguishing a B consensus. Sequences from ACNO 633153 were assigned to both the A and C contigs, suggesting this variety was mis-typed, and is actually a *B. napus* (AACC) variety. Two *B. nigra* varieties (ACNO 633142 and ACNO 649156) were assigned to 2 different consensus: 633142 to a non-distinguishing consensus and 649156 to the A consensus, suggesting that these two varieties are

not the same species. Within the two A genome consensus from CruA, there was not a suitable conserved region for the design of a real-time assay.

HMG

For the HMG sequencing project, four A genome consensus, and one C genome consensus were identified. Again, a B consensus could not be identified, either because it could not be distinguished from the A and C consensus, or because it could not be amplified with the PCR primers. All sequences from the *B. juncea* varieties (AABB) were assigned to the A consensus, except ACNO 458942 which was assigned to the A and C. The *B. nigra* varieties (BB) were assigned to the A genome, and the *B. carinata* varieties (BBCC) were assigned to the C consensus. Inability to get a consensus for the B genome could be due to inefficient binding of the primers to the target on the B genome, or overlap with the A consensus. A small sample size of the *B. nigra* and *B. carinata* varieties were sequenced which may have made it more difficult to come up with a B consensus. As for CruA, ACNO 633153 grouped with sequences assigned to the A and C genome consensus. The two *B. nigra* species grouped into two different consensus: ACNO 633142 did not group in the A or C consensus and ACNO 649156 grouped into the A consensus. A conserved A-genome-specific region could not be identified from the sequenced region of HMG.

FatA

For FatA, there were six consensus sequences: three for the A-genome, two for the C genome, and one for the B genome. The sequence from ACNO 633153 grouped into the C1 and A1 contigs, verifying that it is a *B. napus* and not a *B. rapa* variety. In addition, ACNO 649156 sequence grouped within the A and B consensus, verifying that it is a *B. juncea* variety and not a *B. nigra*. The six consensus sequences from FatA were aligned in VNTI, and the presumed evolutionary relationship of the six sequences is displayed in Figure 2-A. Figure 2-B shows the distribution of the various species into the six consensus.

Example 4. Design and optimization of A-specific real-time PCR assay

Several real-time primers and probes were designed in regions conserved among FatA of all three A consensus, and divergent from the FatA of the B and C genomes. The primer/probe

set that gave the lowest Ct value and the highest PCR efficiency was selected for further analysis. The selected primers and probe are shown on the consensus alignment in Figure 3.

After a test for specificity on a smaller set, the real-time PCR assay was optimized. Three runs were performed on a dilution series of DNA from *B. napus* variety 45H73. The results of these runs are shown in Table 5.

Table 5. Slope and R2 from 3 real time PCR runs with the FatA(A) assay.

Run	Slope	R2	PCR Efficiency (%)
1	-3.39	0.997	97.2
2	-3.42	0.997	96.1
3	-3.41	0.996	96.5

Example 5. Specificity comparison of six rapeseed endogenous real-time PCR assays

To verify that the FatA(A) real-time PCR assay offers greater specificity than existing systems, a panel of DNAs were tested with the Fat(A) assay as well as five other rapeseed endogenous real-time PCR assays. The sources of DNA included: 1) the seed varieties used in the sequence analysis (ACNO 649156 was omitted); 2) additional varieties of *B. carinata* and *B. nigra*; 3) other species that may contaminate canola fields; and 4) seeds from various other crops. The real-time assays were run using the primers and probes (and final concentrations in the reactions) as described in references for the various assays described in Table 4. In most cases the real-time assay was run in triplicate over 3 separate PCR runs. Due to variation in DNA yields, some DNAs were in limited supply and had fewer replicates and/or runs (see Table 2). The average Ct values from this specificity testing is shown in Table 6.

With one exception (*B. nigra* variety ACNO 273638), the FatA(A) assay resulted in average Ct values of ≥ 35 for all DNAs tested except the Brassica species containing the A-genome: *B. napus*, *B. rapa* and *B. juncea* varieties. The average Ct value of the ACNO 273638 *B. nigra* variety in the FatA(A) assay is approximately 9 cycles later than the other A-genome samples, therefore it was possible that this *B. nigra* sample was contaminated with one of the A-genome species. The A genome was not detected during the sequencing of this variety, but if

the amplification is due to contaminating A genomic DNA, it is at a very low level based on the delayed Ct value.

All of the other assays tested showed less specificity than the FatA(A) assay; for example, cross reactivity with non-Brassica species and/or not specific to the A-genome. BnACCg8 detects the A and B genome and *Sinapis alba*, *Sinapis arvensis* (and *Sinapis arvensis* ssp. *arvensis*); PEP detects the A and C genome; and, and HMG detects primarily the A and B with some cross-reactivity with the C genome and cross reactivity with some of the *Sinapis arvensis* varieties. The CruA assay appears to detect all A, B, and C genomes as well as the related species *Thlaspi arvense*, *Erucastrum gallicum*, *Raphanus raphanistrum*, *Raphanus sativus*, *Sinapis alba*, and *Sinapis arvensis* (and the subspecies: *Sinapis arvensis* ssp. *arvensis*). The FatA assay detects the A, B and C genomes, as well as *Camelina sativa*, *Raphanus raphanistrum*, *Raphanus sativus*, *Sinapis alba*, *Sinapis arvensis* (and the subspecies: *Sinapis arvensis* ssp. *arvensis*) and *Arabidopsis thaliana*.

Table 6. Average Ct values with six endogenous real-time PCR systems. UDT represents undetermined, or not detectable in this assay.

Species	ACNO or Variety	FatA(A)	Average Ct values				
			BnACCg8	CruA	FatA	HMG	PEP
B. napus	45H73	21.2	21.9	21.9	20.3	21.5	20.1
	NS1822BC	21.8	22.9	22.6	20.9	22.2	20.6
	46A76	21.6	22.0	22.3	20.6	22.0	20.4
	NS5536BC	22.2	22.7	23.1	21.2	22.6	21.1
	43A56	22.5	23.1	23.4	21.5	23.9	21.8
	NW1717M	21.7	22.8	22.5	20.6	27.5	21.2
	NW4219BC	22.1	22.6	23.0	20.5	23.6	21.5
	NW4201BC	21.6	22.1	22.4	20.7	22.2	21.0
	436554	21.9	22.6	22.9	21.0	25.5	21.3

	458967	21.9	22.4	22.9	20.9	26.0	21.3
	458954	22.2	22.9	23.3	21.2	23.3	21.6
	531273	21.9	22.9	23.3	20.8	23.4	21.5
	458941	21.8	23.1	22.7	20.8	23.3	21.2
	469735	21.7	22.3	22.6	20.2	25.2	21.1
	458605	21.8	23.0	22.7	20.9	23.4	21.0
	311729	22.4	22.5	23.0	21.3	22.8	21.5
	305278	21.7	22.3	22.7	20.8	27.5	20.8
B. rapa	Tobin	22.1	22.6	22.9	21.1	22.8	21.7
	Klondike	21.0	21.3	23.0	21.8	22.4	21.1
	Reward	20.7	21.0	22.6	21.4	21.9	20.8
	41P95	21.1	21.2	23.1	21.7	22.1	21.2
	257229	21.6	21.7	23.6	22.5	22.7	21.8
	633153	21.1	22.5	23.2	22.2	23.1	21.5
	649159	21.5	21.9	23.4	22.3	22.2	22.1
	163496	21.2	21.7	23.4	22.0	22.4	22.1
B. rapa ssp dichotoma	347600	21.5	22.7	23.4	22.1	22.6	21.0
B. rapa ssp oleifera	649190	21.7	21.9	23.5	22.2	22.4	22.4
B. rapa ssp trilocularis	346882	21.1	23.0	23.3	21.7	22.1	20.9
B. rapa var. parachinensis	390962	21.2	23.1	23.2	22.0	21.9	22.2
B. juncea	JS0879BC	22.0	24.1	23.6	20.7	23.5	23.4
	JS0917BC	22.0	23.8	23.4	20.7	23.3	23.5
	JS0936BC	21.9	24.0	23.9	21.4	23.7	23.4
	JS1056BC	21.5	23.6	23.2	20.9	23.0	22.7
	JS1260MC	21.6	23.6	23.2	20.9	23.2	22.8
	JS1432MC	21.7	23.5	23.2	21.0	23.2	22.9

	418956	21.7	23.7	23.5	20.8	23.4	23.1
	458942	22.0	23.3	23.6	21.1	23.9	23.2
	603011	21.7	23.8	23.5	20.9	22.9	23.2
B. oleracea var. alboglabra	249556	UDT	UDT	23.1	20.4	33.2	21.7
B. oleracea var. botrytis	28888	UDT	37.5	22.8	21.1	32.7	21.5
B. oleracea var. capitata	29041	UDT	37.5	23.3	21.1	33.2	22.2
B. oleracea var. costata	29800	UDT	37.6	22.3	20.3	32.2	20.8
B. oleracea var. gemmifera	365148	UDT	37.5	22.5	20.6	31.9	21.1
B. oleracea var. gongylodes	29790	UDT	37.1	23.2	21.3	32.7	22.1
B. oleracea var. italica	28852	UDT	UDT	27.4	25.8	35.0	26.4
B. oleracea var. medullosa	30862	UDT	38.0	22.4	20.7	31.6	21.4
B. oleracea var. ramosa	30724	UDT	37.8	22.4	20.8	31.0	21.2
B. oleracea var. viridis	32550	UDT	38.7	22.8	20.7	30.8	21.8
B. nigra	273638	30.1	25.1	24.9	19.6	25.3	UDT
	633142	37.0	25.4	23.6	20.0	25.1	UDT
	193960	UDT	30.1	26.4	23.6	31.6	21.4
	271444	UDT	27.7	25.0	21.0	28.0	UDT
	633143	UDT	25.8	23.5	20.4	27.1	UDT
	220282	UDT	29.9	27.8	21.6	29.8	UDT
	649154	UDT	24.8	22.4	19.5	27.3	UDT
	280638	UDT	26.8	26.5	20.5	27.1	UDT
	357369	37.4	26.7	25.3	20.5	26.9	UDT
	633147	36.2	25.6	23.7	20.4	26.9	UDT

	131512	37.1	26.7	25.1	20.4	27.0	UDT
	597829	UDT	25.6	23.7	20.3	26.2	UDT
	649155	UDT	27.3	24.2	20.5	27.8	UDT
B. carinata	613124	UDT	26.7	23.1	20.7	27.8	22.3
	597822	UDT	26.4	23.2	20.1	27.3	21.7
	360879	UDT	25.6	25.6	19.9	26.5	UDT
	596534	UDT	26.6	22.6	20.0	27.6	21.5
	2779	UDT	27.0	23.7	20.7	27.9	22.2
	193460	UDT	26.7	23.4	20.8	28.5	23.0
	633076	UDT	27.3	23.5	20.8	28.0	22.3
	390133	UDT	26.9	22.8	20.5	27.2	22.2
	209023	UDT	26.9	23.4	20.4	27.7	21.9
	360882	UDT	27.1	23.5	21.0	26.8	22.5
Sinapis alba	19266	UDT	27.0	24.1	21.7	UDT	UDT
	305276	UDT	29.2	23.6	22.8	UDT	UDT
	311724	UDT	27.9	23.7	21.7	UDT	UDT
	458960	UDT	27.5	23.5	22.0	UDT	UDT
	409025	UDT	29.0	24.5	21.9	UDT	UDT
	633274	UDT	25.2	23.5	20.8	UDT	UDT
Sinapis arvensis	21449	UDT	26.6	23.1	24.0	UDT	UDT
	597863	UDT	27.5	23.6	23.7	UDT	30.5
	633374	UDT	27.1	24.4	24.6	29.5	UDT
Sinapis arvensis subsp. arvensis	296079	UDT	26.5	23.6	23.9	29.5	UDT
	407561	UDT	26.0	22.6	23.3	29.8	UDT
	633411	UDT	28.0	24.4	24.9	29.5	UDT
Erucastrum gallicum	22990	37.1	UDT	26.1	21.0	UDT	UDT

Raphanus raphanistrum	271456	UDT	37.0	27.8	24.1	UDT	UDT
Raphanus sativus	268370	UDT	35.6	27.9	24.0	UDT	UDT
	650165	UDT	UDT	UDT	22.8	39.1	UDT
Thlaspi arvense	633414	UDT	UDT	32.1	UDT	UDT	UDT
	29118	UDT	UDT	31.7	UDT	UDT	UDT
Arabidopsis thaliana Columbia type		UDT	UDT	UDT	29.8	UDT	37.7
Gossypium hirsutum		UDT	UDT	UDT	37.3	UDT	UDT
Helianthus annuus	7451	39.0	UDT	UDT	UDT	UDT	UDT
	29348	UDT	UDT	UDT	UDT	UDT	UDT
	592319	UDT	UDT	UDT	UDT	UDT	UDT
Solanum lycopersicum	645248	UDT	UDT	UDT	UDT	UDT	UDT
Glycine max		UDT	UDT	UDT	UDT	UDT	UDT
Oryza sativa		UDT	UDT	UDT	UDT	UDT	UDT
Sorghum bicolor		UDT	UDT	UDT	UDT	UDT	UDT
Zea mays		UDT	UDT	UDT	UDT	UDT	UDT

Example 6: Testing for heterogeneity within each A-genome species

In addition to specificity, a desirable endogenous reference system may not exhibit allelic variation among varieties. The FatA(A) assay recognizes the A-genome, and therefore three different species, with varying haploid genome sizes. Therefore, the stability measurements were restricted to the comparison of Ct values of the varieties within each species. By restricting the Ct comparison to those varieties within a species, it eliminates the Ct variation caused by the variation in genome size between the base species (*B. rapa*, AA) and the allotetraploid species (*B. juncea*/AABB and *B. napus*/AACC). The results of this analysis are shown in Table 7. For *B. napus*, the Ct values ranged from 21.6 to 22.5; for *B. rapa* the Ct

values ranged from 20.7 to 22.1, and for *B. juncea* the Ct values ranged from 21.5 to 22.0. In the *B. napus* and *B. juncea* species, the Ct range is within 1 Ct value; and for *B. rapa* the Ct range is within 1.4 Cts. In all cases the deviation from the mean is within 1 Ct value.

Table 7. Heterogeneity Test of FatA (A-genome specific) endogenous reference real-time PCR assay. Note: Sequences from ACNO 633153 were assigned to both the A and C contigs, suggesting this variety may actually be a *B. napus* (AACC) variety (see Example 3 herein).

Species	ACNO or Variety name	Mean	Mean (within species)	SD	CV(%)
B. napus	45H73	21.2	21.84	0.36	1.66
	NS1822BC	21.8			
	46A76	21.6			
	NS5536BC	22.2			
	43A56	22.5			
	NW1717M	21.7			
	NW4219BC	22.1			
	NW4201BC	21.6			
	436554	21.9			
	458967	21.9			
	458954	22.2			
	531273	21.9			
	458941	21.8			
	469735	21.7			
	458605	21.8			
	311729	22.4			
	305278	21.7			
	633153**	21.1			
B. rapa	Tobin	22.1	21.34	0.39	1.82
	Klondike	21			
	Reward	20.7			
	41P95	21.1			
	257229	21.6			
	649159	21.5			
	163496	21.2			
B. rapa ssp dichotoma	347600	21.5			

B. rapa ssp oleifera	649190	21.7			
B. rapa ssp trilocularis	346882	21.1			
B. rapa var. parachinensis	390962	21.2			
B. juncea	JS0879BC	22	21.79	0.19	0.88
	JS0917BC	22			
	JS0936BC	21.9			
	JS1056BC	21.5			
	JS1260MC	21.6			
	JS1432MC	21.7			
	418956	21.7			
	458942	22			
	603011	21.7			

While the foregoing has been described in some detail for purposes of clarity and understanding, it will be clear to one skilled in the art from a reading of this disclosure that various changes in form and detail can be made without departing from the true scope. For example, all the techniques, methods, compositions, apparatus and systems described above may be used in various combinations. All publications, patents, patent applications, or other documents cited in this application are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication, patent, patent application, or other document were individually indicated to be incorporated by reference for all purposes.

Claims

What is claimed is:

1. A method of detecting and quantifying the amount of Brassica A genomic DNA in a sample, the method comprising:
 - (a) specifically amplifying a genomic DNA fragment of the Brassica A genome, wherein the amplified DNA fragment comprises at least one of the nucleotide sequences of a genomic region selected from the group consisting of SEQ ID NOS: 25, 26, 27, 28, and 35; and
 - (b) detecting and quantifying the Brassica A genome from the amplified fragment of the Brassica A genome.
2. The method of claim 1, wherein the amplified fragment of Brassica A genome comprises (i) the nucleotide sequence of at least one of SEQ ID NOS: 29, 30, or 31; or (ii) a nucleic acid fragment of at least one of SEQ ID NOS: 29, 30, or 31, wherein the nucleic acid fragment is selected from the group consisting of nucleotide position from about 50 to about nucleotide position 400, 50 to about nucleotide position 100, 50 to about nucleotide position 350, 400 to about nucleotide position 350, 400 to about nucleotide position 200, and 400 to about nucleotide position 100 of SEQ ID NOS: 29, 30, or 31.
3. The method of claim 1, wherein the amplification is performed with a primer pair comprising nucleotide sequences selected from the group consisting of SEQ ID NOS: 17, 18, 19, 20, 21, 22, 23, and 24.
4. The method of claim 1, wherein the genomic DNA comprises a FatA gene.
5. The method of claim 1, wherein the amplification does not substantially amplify Brassica B and C genomic DNA.
6. A method of determining the relative amount of a Brassica transgenic event in a sample, the method comprising:

- (a) performing a Brassica A genome specific polymerase chain reaction, wherein the analysis includes specifically amplifying a genomic DNA fragment of the Brassica A genome, wherein the amplified DNA fragment comprises at least one of the nucleotide sequences of a genomic region selected from the group consisting of SEQ ID NOS: 25, 26, 27, 28, and 35;
 - (b) determining the total amount of Brassica A genomic DNA in the sample;
 - (c) performing an event specific assay for the transgenic event to determine the amount of the transgenic event in the sample; and
 - (d) comparing the amount of the transgenic event DNA to the total amount of Brassica A genomic DNA in the sample.
7. The method of claim 1 wherein the amplified fragment of Brassica A genome comprises the nucleotide sequence of at least one of SEQ ID NOS. 29, 30, or 31 from nucleotide position about 50 to about 400.
8. The method of claim 6, wherein the amplification is performed with a primer pair comprising nucleotide sequences selected from the group consisting of SEQ ID NOS: 17, 18, 19, 20, 21, 22, 23, and 24.
9. The method of claim 6, wherein the genomic DNA comprises a FatA gene.
10. The method of claim 6, wherein the amplification does not substantially amplify Brassica B and C genomic DNA.
11. A method of determining adventitious presence of a Brassica transgenic event in a sample, the method comprising:
- (a) obtaining a sample suspected of containing a Brassica transgenic event;
 - (b) performing a Brassica A genome specific polymerase chain reaction, with a primer, wherein the primer binds to a genomic region of the Brassica A genome,

- the genomic region selected from the nucleotide sequence of at least one of SEQ ID NOS: 29, 30, or 31 from nucleotide position about 50 to about 400;
- (c) determining the total amount of Brassica A genomic DNA in the sample;
 - (d) performing an event specific quantitative assay for the transgenic event to determine the amount of the transgenic event DNA in the sample; and
 - (e) comparing the amount of the transgenic event to the total amount of Brassica in the sample.
12. The method of claim 11 wherein the primer is selected from the group consisting of SEQ ID NOS: 17, 18, 19, 20, 21, 22, 23, and 24.
13. An amplicon comprising at least one of the nucleotide sequences of a genomic region selected from the group consisting of SEQ ID NOS: 25, 26, 27, 28, and 35 wherein the amplicon is not larger than 500 base pairs.
14. An oligonucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS: 17, 18, 19, 20, 21, 22, 23, and 24 wherein the oligo is about 15-500 nucleotides.
15. A detection kit comprising oligonucleotides comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS: 17, 18, 19, 20, 21, 22, 23, and 24 wherein the oligo is less than about 50 nucleotides and one or more reaction components to perform a quantitative reaction.
16. A method of determining trait purity of a Brassica trait, the method comprising:
- (a) obtaining a sample of a Brassica trait; and
 - (b) performing the Brassica A genome specific assay of Claim 1.

17. The method of any one of claims 6 and 11, wherein the trait is selected from the group consisting of RT73, RT200, MON88302, DP-073496, HCN92, T45 (HCN28), 23-18-17, 23-198, OXY-235, MS1, MS3, MS6, MS8, RF1, RF2, RF3, and Topas 19/2.
18. The method of any one of claims 1-17, wherein the determination comprises performing a quantitative polymerase chain reaction.
19. A method of establishing purity of a Brassica seed lot, the method comprising performing a polymerase chain reaction wherein the oligonucleotide primers or probes are capable of discriminating the Brassica A genome from the Brassica B and C genomes, wherein the oligonucleotide primers and/or probes bind to a target region of the Brassica A genome, the target region comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS: 25, 26, 27, 28, and 35.
20. The method of claim 19, wherein the oligonucleotide primers and/or probes comprise a nucleotide sequence selected from the group consisting of SEQ ID NOS: 19, 20, 21, 22, 23, and 24.
21. A method of quantifying the amount of a transgenic element in a Brassica sample, the method comprising:
 - (a) performing a polymerase chain reaction wherein the oligonucleotide primers or probes are capable of discriminating the Brassica A genome from the Brassica B and C genomes, the oligonucleotide primers or probes bind to a target region of the Brassica A genome comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS: 29, 30, and 31;
 - (b) performing the transgenic element specific quantitative polymerase chain reaction; and
 - (c) determining the amount of the transgenic element present in the canola sample by comparing to the amount of Brassica A genomic DNA in the sample.

22. A method of determining seed purity of a seed sample suspected of containing the Brassica A genome, the method comprising:
- (a) specifically amplifying a genomic DNA of the Brassica A genome, wherein the amplified DNA comprises at least one of the nucleotide sequences of a genomic region selected from the group consisting of SEQ ID NOS: 25, 26, 27, 28, and 35; and
 - (b) determining the purity of the seed sample based on the presence or absence of the Brassica A genome
23. The method of claim 22, wherein the seed sample contains at least one of broccoli, brussel sprouts, mustard seeds, cauliflower, collards, cabbage, kale, kohlrabi, leaf mustard, or rutabaga.
24. A method of determining the presence and/or quantity of the Brassica A genome, the method comprising:
- (a) specifically hybridizing DNA of the Brassica A genome with a probe, wherein the probe selectively binds to at least one of the nucleotide sequences of a genomic region selected from the group consisting of SEQ ID NOS: 25, 26, 27, 28, and 35, optionally under high stringency conditions, and;
 - (b) detecting the presence and/or quantity of the Brassica A genome.
25. The method of claim 24, wherein the probe binds the genomic region of the Brassica A genome selected from the nucleotide sequence of at least one of SEQ ID NOS: 29, 30, or 31 from nucleotide position about 50 to about 400.
26. The method of claim 24, wherein the probe comprises the nucleotide sequences of SEQ ID NOS: 19, 20, 21, 22, 23, or 24.
27. A method of sequencing a region of the Brassica A genome, the method comprising:

- (a) obtaining a DNA sample; and
- (b) performing a sequencing reaction of the DNA sample wherein the sequenced region comprises at least one of the nucleotide sequences of a genomic region selected from the group consisting of SEQ ID NOS: 25, 26, 27, 28, and 35.

FIG. 1

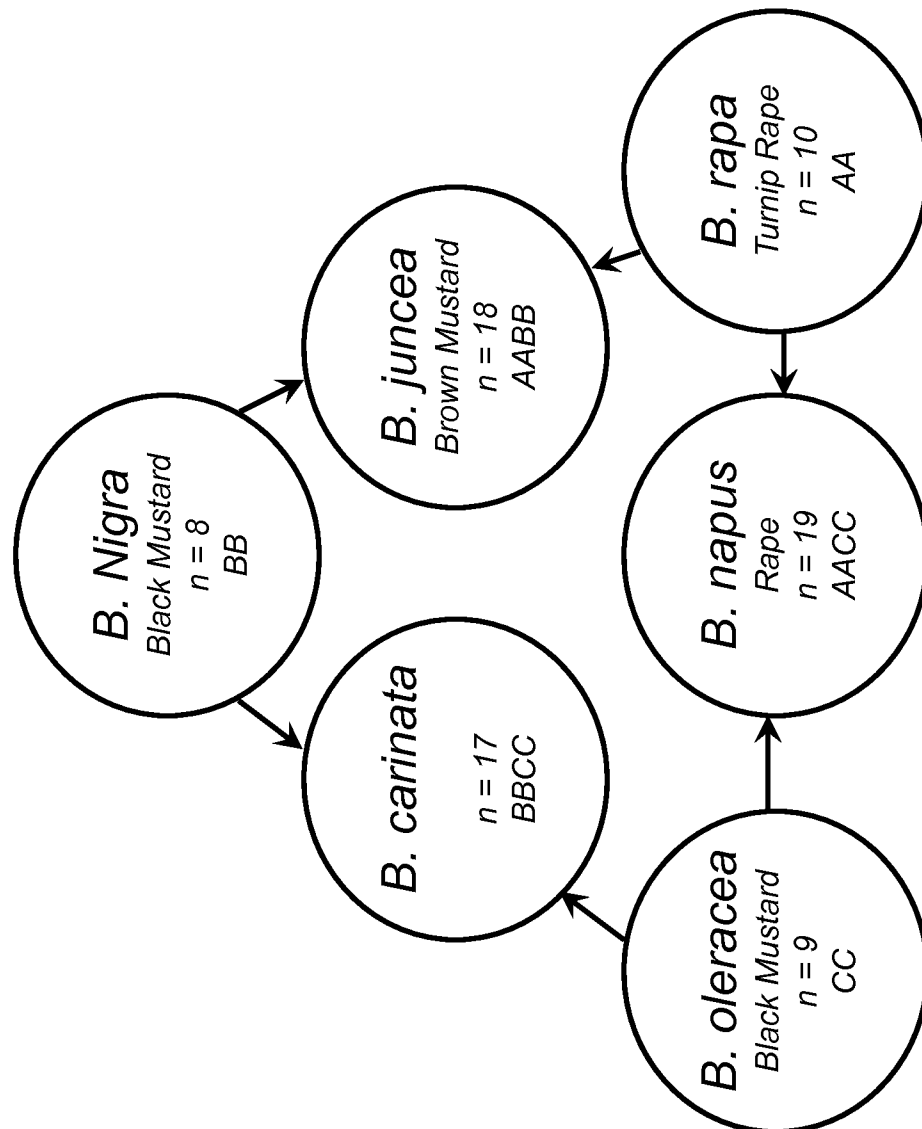


FIG. 2-A

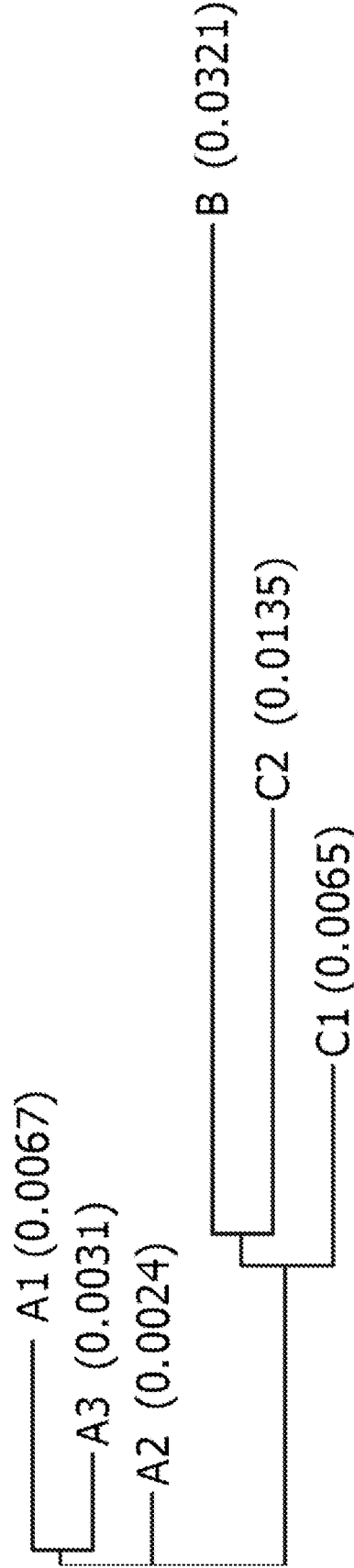


FIG. 2-B

	B. napus AACC n=18	B. rapa AA n=11	B. juncea AABB n=10	B. oleracea CC n=10	B. nigra BB n=2	B. carinata BBCC n=2
A1	15	-	10	-	-	-
A2	2	2	-	-	-	-
A3	-	3	-	-	-	-
A1 and A2	1	1	-	-	-	-
A1 and A3	-	3	-	-	-	-
A2 and A3	-	1	-	-	-	-
A1, A2 and A3	-	1	-	-	-	-
B	-	-	10	-	2	2
C1	18	-	-	4	-	-
C2	-	-	-	3	-	2
C1 and C2	-	-	-	3	-	-

[illegible]

INTERNATIONAL SEARCH REPORT

International application No
PCT/US2013/042470

A. CLASSIFICATION OF SUBJECT MATTER
INV. C12Q1/68
ADD.

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)
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 practicable, search terms used)

EPO-Internal, EMBL

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	CN 101 629 206 A (CHUNLIN LIU) 20 January 2010 (2010-01-20) abstract; claim 1 -----	1-10,13, 16-20, 22-27
Y	CN 102 433 379 A (UNIV HENAN SCIENCE & TECH) 2 May 2012 (2012-05-02) abstract -----	1-10,13, 16-20, 22-27
X	DATABASE Genbank [Online] EBI; 6 July 2007 (2007-07-06), "Brassica napus cDNA", XP002699929, Database accession no. EV080417 the whole document ----- -/--	14,15



Further documents are listed in the continuation of Box C.



See patent family annex.

* 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 application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation 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

"T" later document published after the international filing date or 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

"&" document member of the same patent family

Date of the actual completion of the international search

3 July 2013

Date of mailing of the international search report

14/10/2013

Name and mailing address of the ISA/

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Celler, Jakub

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2013/042470

Box No. 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 No. 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 fees, this Authority did not invite payment of additional fees.
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, 13-20, 22-27

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.
- ☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.
- ☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No

PCT/US2013/042470

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE Genbank [Online] EMBL; 27 August 2010 (2010-08-27), "Arabidopsis lyrata genomic sequence", XP002699930, Database accession no. HN196531 the whole document	14,15
Y	----- CHENG FENG ET AL: "Biased gene fractionation and dominant gene expression among the subgenomes of Brassica rapa.", PLOS ONE, vol. 7, no. 5, E36442, 2 May 2012 (2012-05-02), pages 1-9, XP002699931, ISSN: 1932-6203 abstract	1-10,13, 16-20, 22-27
X	----- WO 2011/075716 A1 (CARGILL INC [US]; ZHENG HONGGANG [US]; BRANDT KEVIN [US]; FLETCHER RIC) 23 June 2011 (2011-06-23) abstract; sequences 32,86, 310 -----	14,15

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. claims: 1-10, 13-20, 22-27

Subject matter of the above claims, as characterised by th group of SEQ ID NOs: 25, 26, 27, 28 and 35, and claims 14-15.

2. claims: 11, 12, 21

Subject matter of the above claims, as characterised by th group of SEQ ID NOs: 29, 30 and 31.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No

PCT/US2013/042470

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
CN 101629206	A	20-01-2010	NONE
CN 102433379	A	02-05-2012	NONE
WO 2011075716	A1	23-06-2011	AU 2010330777 A1 14-06-2012
		CA 2782423 A1	23-06-2011
		CN 102984935 A	20-03-2013
		EP 2521437 A1	14-11-2012
		JP 2013514783 A	02-05-2013
		SG 181114 A1	30-07-2012
		US 2013031678 A1	31-01-2013
		WO 2011075716 A1	23-06-2011